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Contribution of temperate germplasm to the performance of maize hybrids under stress and non-stress environments in South Africa

Sphiwokuhle Shandu [1], Edmore Gasura [2], Kingstone Mashingaidze[3] and John Derera [1,4]

[1]*School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal, Pietermaritzburg, South Africa*
[2]*Department of Plant Production Sciences and Technologies, University of Zimbabwe, Harare, Zimbabwe*
[3]*Agricultural Research Council (ARC), Pretoria, South Africa*
[4]*International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria*
**Corresponding author: dereraj@gmail.com*

Increases in genetic gains are crucial to maize breeding programmes. The objectives of this study were to identify higher-yielding and stable maize hybrids across stress and non-stress environments, to identify representative test environments for testing and selection of superior maize genotypes, and to determine the contribution of temperate maize germplasm in the performance of new tropical hybrids. Respectively 42 and 72 newly developed single-cross hybrids together with check hybrids were evaluated separately for grain yield performance across stress and non-stress environments, at four locations (Potchefstroom, Cedara, Vaalharts/Taung and Makhathini) in South Africa, in the 2014/15 and 2015/16 growing seasons (seasons 1 and 2, respectively). Additive main effects and multiplicative interaction (AMMI) and genotype + genotype × environment interaction (GGE) biplots were employed. In season 1, the hybrids MO17HtHtN × CML444 and I-39 × CML444 were the most stable and high-yielding genotypes after the ideal commercial check. In season 2, the hybrids FO215W × CML444, I-42 × CML444 and U71Y × CML444 were stable and high-yielding, with FO215W × CML444 being the most ideal. These stable hybrids would be the best suited for wide adaptation across non-stress and stress environments. Hybrids containing tropical CIMMYT testers were more stable than those derived from temperate Corn Belt material. The locations Potchefstroom and Vaalharts were the most suitable environments for evaluating the performance of these genotypes across the diverse environments.

Keywords: genetic gain, grain yield stability, maize adaptability, multi-environment trials, temperate testers, temperate × tropical maize

Introduction

Maize (*Zea mays* L.) is the most widely grown food crop in South Africa. A large portion of the white maize produced serves as a staple food throughout South Africa, whereas the yellow maize produced is used mainly for animal feed (Zhai et al. 2021). Maize is grown in various and diverse environments, but most of the growing regions in South Africa are characterised by frequent droughts (Agri SA 2016), low soil fertility and limited use of improved and adapted varieties, particularly by smallholder farmers. Developing maize varieties that are tolerant to drought and low soil fertility, particularly low nitrogen (N), will mitigate the challenges posed by climate change. The International Maize and Wheat Improvement Centre (CIMMYT) and partners have made substantial progress in the breeding and identification of drought- and low N-tolerant maize varieties. However, the varieties so far developed are specific for certain regions.

Maize is a widely cultivated and adapted cereal crop; when superior varieties are developed, they are distributed to farmers in different regions with a wide range of environmental conditions. Some varieties may fail to adapt in certain regions because of geographical differences, such that superior varieties in one environment may not be consistently superior in other environments (Russell et al. 2003; Setimela et al. 2007; Makumbi et al. 2015). The varying conditions may cause varieties to rank differently from one environment to another due to the presence of genotype-by-environment interaction (G × E). The G × E complicates breeding and selection of superior and adapted varieties under stress and non-stress environments (Makumbi et al. 2015). Cultivars that show minimal G × E are phenotypically more stable, and their yield performance is relatively predictable (Yan and Tinker 2005).

Varieties with high mean performance and stability (i.e. showing consistent ranking across varying environmental conditions) are more ideal (Yan and Tinker 2005) and may be recommended for a wide range of environments. Therefore, in addition to high mean performance, breeders also account for yield stability across the range of environments to exploit the G × E effects. The G × E effect can be minimised by grouping similar locations into two or more groups (mega-environments), where maize varieties will perform consistently with minimum crossover interaction (Russell et al. 2003). Mega-environments allow

breeders to easily identify areas with similar biotic and abiotic stresses for hybrid development and germplasm exchange (Yan and Tinker 2005).

Multi-environment trials (MET) data are important in the evaluation of environments and genotypes and their interaction, to effectively identify superior genotypes and mega-environments (Yan et al. 2007). The additive main effects and multiplicative interaction (AMMI) statistical model (Gauch and Zobel 1988; Crossa 1990) and genotype + genotype × environment interaction (GGE) biplot analysis (Yan et al. 2009) are commonly used statistical tools for evaluating the response of genotypes to different environments. The difference is that GGE biplot analysis is based on environment-centred principal component analysis (PCA), whereas AMMI analysis refers to double-centred PCA (Yan et al. 2007). The GGE approach is useful for: (i) visualising the G × E relationships, which facilitates mega-environment delineation, and the 'which won where' view is useful for this visualisation (Gauch and Zobel 1997); (ii) evaluating the interrelationship among environments, to identify ideal test environments based on their discriminative ability of genotypes and the representativeness power of the test locations (Yan et al. 2007); and (iii) evaluating the interrelationship among genotypes and making comparisons for mean yield performance and stability (Yan et al. 2007). Evaluating genotypes for G × E and yield stability is important for developing and selecting maize varieties that are higher-yielding and broadly adapted. Newly developed cultivars must therefore be evaluated to determine the magnitude of G × E and to identify stable genotypes. The objectives of this study were to identify higher-yielding and stable maize hybrids across stress and non-stress environments, to identify representative test environments for testing and selection of superior maize genotypes, and to determine the contribution of temperate maize germplasm in the performance of new tropical hybrids.

Materials and methods

Germplasm and study sites

Forty-two and 72 F_1 maize hybrids were derived from a line by tester mating design in the 2014/15 and 2015/16 winter nurseries, respectively. The inbred lines and testers used are presented in Tables 1 and 2. The tables show that similar materials were used for generating crosses in the 2014/15 and 2015/16 winter nurseries, but several crosses were missing in the 2014/15 season, resulting in only 42 hybrids. In season 1 the 42 hybrids were evaluated together with three commercial checks, while in season 2 the 72 hybrids were evaluated together with four checks. Three of the checks were consistent across the seasons (Tables 1 and 2). Evaluation of the 45 and 76 hybrids (including the checks) was conducted in seven and six different environments during the 2014/15 and 2015/16 growing seasons, respectively (Table 3). These environments were characterised by variable weather conditions and soil properties (Table 4). In all environments, a pre-emergence herbicide (Bateleur® Gold, 1.3 l ha^{-1}) and a post-emergence herbicide (Basagran®, 2.5 l ha^{-1}) were used to control weeds, which was followed by subsequent manual weeding. Insect pests were controlled using Karate® insecticide, at 70 ml h^{-1}.

Experimental design and data collection

In season 1, the 45 hybrids (including three checks) were evaluated in a 5 × 9 α-lattice design with two replications; in season 2 the 76 hybrids (including the four checks) were evaluated in a 4 × 19 α-lattice design with two replications. At each location, each entry was hand-planted in a two-row plot

Table 1: Pedigrees and descriptions of the parental lines and check materials used for the development of maize (Zea mays L.) hybrids during the 2014/15 growing season

Code	Name	Pedigree	Designation
L1	B1138T	TEKOYELLOW	Line
L2	I-39	I-39	Line
L3	U2540W	M162W1.DO940Y-J34	Line
L4	M162W	K64R2.B1138T	Line
L5	K64	Pride of Saline	Line
L6	K64R-22	K64R-22	Line
L7	MO17HtHtN	MO17HtHtN	Line
L8	P594MSV	MLSxVHMO17	Line
L9	SO181Y	KO326Y2.NPPES1	Line
L10	SO713W	POWS1(S4)	Line
L11	VO500Y	POWS12.Y	Line
L12	SO1224Y	M28Y1.KO288Y	Line
L13	U71Y	M28Y2.NP	Line
L14	P612MSV	B73xVHKG/C1	Line
T1	B73	BSSS C5 (Iowa Stiff Stalk Synthetic)	Tester
T2	CML312	S89500-F2-2-2-1-1-B	Tester
T3	CML444	P43-C9-1-1-1-1-1-B	Tester
Check1	CAP9004	Capstone	Check
Check2	PAN6479	Pannar	Check
Check3	WE3127	WEMA	Check

Table 2: Pedigrees and descriptions of the parental lines and check materials used for the development of maize (*Zea mays* L.) hybrids during the 2015/16 growing season

Code	Name	Pedigree	Designation
L1	E30Y	B390YxM136Y	Line
L2	FO215W	NPPES14.O2S14	Line
L3	I-16	I-16	Line
L4	I-42	I-42	Line
L5	J80W	D800W2.HtN	Line
L6	K64	Pride of Saline	Line
L7	M162W	K64R2.B1138T	Line
L8	MO17HtHtN	MO17HtHtN	Line
L9	P614MSV	B73xVHKG/C1	Line
L10	RO421W	DO940Y-11.O2(W)	Line
L11	RO452W	DO940Y-13.NHK	Line
L12	RO544W	BO160W.3J400W	Line
L13	S198Y	M28Y1.DO620Y	Line
L14	SO181Y	KO326Y2.NPPES1	Line
L15	U127Y	M162W.1KO326Y	Line
L16	U2540W	M162W1.DO940Y-J34	Line
L17	U71Y	M28Y2.NP	Line
L18	VO495Y	POWS12.Y	Line
T1	MO17	(CL.187-2 x C103)	Tester
T2	B73	BSSS C5 (Iowa Stiff Stalk Synthetic)	Tester
T3	CML312	S89500-F2-2-2-1-1-B	Tester
T4	CML444	P43-C9-1-1-1-1-1-B	Tester
Check1	CAP9004	Capstone	Check
Check2	PAN6479	Pannar	Check
Check3	SNK2147	Sensako	Check
Check4	WE3127	WEMA	Check

of 4 m, with a spacing of 0.75 m between rows and 0.25 m between plants. Two seeds of each variety were planted per planting hole; at four weeks after emergence, all trials were thinned to a density of 53 333 plants ha^{-1} Data on grain yield and secondary traits were recorded in all trials. Grain yield was estimated on a plot basis and adjusted to 12.5% grain moisture content.

Data analysis

The MET data for grain yield were subjected to combined analysis of variance using a model appropriate for an α-lattice design. The following statistical model was used for the analysis:

$$Y_{ijkl} = \mu + h_i + E_j + h_iE_j + E_j(r_k) + E_j(r_k)(b_l) + e_{ijkl} \quad (1)$$

where Y_{ijk} is the performance of the i^{th} hybrid evaluated in the k^{th} replication nested within the j^{th} environment; μ is the grand mean; h_i is the effect of the i^{th} hybrid; E_j is the effect of the j^{th} environment; h_iE_j is the interaction between the i^{th} hybrid and the j^{th} environment; $E_j(r_k)$ is the effect of the k^{th} replication nested within the j^{th} environment; $E_j(r_k)(b_l)$ is the effect of the l^{th} incomplete block nested in the k^{th} replication also nested within the j^{th} environment; and e_{ijk} is the random error. Upon significant genotype × environment interaction (G × E) for grain yield, the AMMI and GGE biplots were employed to visually inspect the interaction, using GenStat software version 18. The AMMI and GGE biplot analyses followed the methods of Gauch (2013) and Yan and Tinker (2005), respectively. The AMMI stability value (ASV) was used to compare the stability of the

Table 3: South African locations and codes of the test environments used for evaluation of the maize hybrids in the 2014/15 and 2015/16 growing seasons

Location	Code	2014/15	2015/16
		Management	Management
Potchefstroom	E1	low N	low N
Taung[1]/Cedara [2]	E2	low N	low N
Vaalharts	E3	low N	low N + random drought
Potchefstroom	E4	Random drought	Random drought
Makhathini	E5	Managed drought	–
Potchefstroom	E6	Non-stress	Non-stress
Cedara	E7	Non-stress	Non-stress

1. 2014/15; 2. 2015/16

Table 4: Weather data and geographic information for the South African locations used for the evaluation of maize hybrids during the 2014/15 and 2015/16 growing seasons

Management	Site	Geolocation	Elevation (m.a.s.l)	Season	Annual rainfall (mm)			Temperature (°C) Minimum			Maximum		
					Long-term	2014/2015	2015/2016	Long-term	2014/2015	2015/2016	Long-term	2014/2015	2015/2016
NS and DT	Potchefstroom	26°74′ S, 27°08′ E	1 349	Summer	541	519	364	15	14	16	29	29	31
NS and low N	Cedara	29°54′ S, 30°26′ E	1 068	Summer	662	619	521	14	13	14	25	25	27
Combined low N + DT	Vaalharts/ Taung	27°95′ S, 24°84′ E	1 180	Summer	356	214	239	15	15	16	32	34	35
DT	Makhathini	27°39′ S, 32°18′ E	77	Winter	153	127	–	14	9	–	28	29	–

m.a.s.l. metres above sea level, DT = drought stress, NS = non-stress

genotypes (Purchase 1997):

$$ASV = \sqrt{\left[\frac{IPCA1SS}{IPCA2SS}(IPCA1\ score)\right]^2 + (IPCA2\ score)^2} \quad (2)$$

where SS is the sum of squares; IPCA1 is the first principal component axis and IPCA2 is the second principal component axis for the genotypic scores; and IPCA1SS / IPC2SS is the weight given to the IPCA1 value by dividing the IPCA1 sums of square by the IPCA2 sums of squares.

Results

Analysis of variance

The combined analysis of variance for the 2014/15 and 2015/16 seasons are presented in Table 5. These results showed highly significant effects of genotype ($p < 0.001$), environment ($p < 0.001$) and G × E ($p < 0.001$) in both seasons. Among all sources of variation, the environments accounted for the largest sum of squares, followed by the G × E, in both season 1 and season 2.

AMMI analysis of G × E

The AMMI analysis of variance showed highly significant ($p < 0.001$) main effects of genotype, environment and their interaction (G × E) in both seasons (Tables 6 and 7). Of the total variation, the environments contributed 62.4% in season 1, and 40.2% in season 2. In season 1, 6.4% of the total variation was caused by genotype effects, and 17.1% by G × E effects. In season 2, 7.0% of the total variation was caused by genotype effects, and 28.1% by G × E effects. Of the total G × E variation in season 1, 42.3% was due to IPC1, 20.1% to IPC2, and 37.6% to residual effects for that season. In season 2, the IPC1, IPC2 and G × E residuals accounted for 44.6%, 25.6% and 29.8% of the total G × E variation, respectively.

Evaluation of the test environments

The discriminative power of the test environments is shown in Figures 1 and 2. In 2014/15 (season 1) the most discriminative environment (with the longest vector) was E7 (Cedara, non-stress), followed by E1 (Potchefstroom, low N), while E5 (Makhathini, managed drought) and E2 (Taung, low N) were the least discriminating (Figure 1). In 2015/16 (season 2) the most discriminative environments were E6 (Potchefstroom, non-stress) and E3 (Vaalharts, low N + random drought) (Figure 2). Test environments E1 (Potchefstroom, low N), E2 (Cedara, low N), E4 (Potchefstroom, random drought) and E7 (Cedara, non-stress) were equally not discriminating among the hybrids (Figure 2). The most representative and the ideal test environment in season 1 was E6 (Potchefstroom, non-stress) (Figure 3), and in season 2 it was E3 (Vaalharts, low N + random drought) (Figure 4), since the biplot exhibited the smallest angle with the average environment axis.

Relationship among environments and mega-environment delineation

In 2014/15 (season 1), the interrelationship between environments was observed between E7, E4 and E6 (Figure 1), which had acute angles. The environments E1, E3, E2 and E5 were also positively correlated since they had small angles among them. In 2015/16 (season 2), a positive correlation was found between E1 and E4, while environment 3 was strongly correlated with E2. Environment E5 and E1 were negatively correlated (Figure 2). Environment E3 and E6 were not correlated since they had an obtuse angle between them (Figure 2).

The 'which won where' view of GGE biplots for seasons 1 and 2 are shown in Figures 5 and 6, respectively. The polygon divided the season 1 biplot into seven sectors with different winning genotypes; only two sectors were containing the environments. The first sector was comprised of four stress environments, which were E1 (Potchefstroom, low N), E2 (Taung, low N), E3 (Vaalharts, low N) and E5 (Makhathini, managed drought); and the winning genotype in this sector was entry 44, a commercial check (WE3127). The second sectors had three environments, which included E4 (Potchefstroom, random drought), E6 (Potchefstroom, non-stress) and E7 (Cedara, non-stress), with entry 34 (L7/T1 = MO17HtHtN/B73) as the winning genotype. Other winner (vertex) genotypes were not associated with any environment, and these were:

Table 5: Combined analysis of variance of maize grain yield among 45 genotypes tested across seven environments during the 2014/15 season, and 76 genotypes tested across six environments during the 2015/16 season in South Africa

Source of variation	Degrees of freedom	Sum of squares	Mean square	Degrees of freedom	Sum of squares	Mean square
	2014/15 season			2015/16 season		
Replications (R)	1	16.55	16.55	1	24.422	24.422
Environments (E)	6	2 154.18	359.03***	5	1 819.00	363.80***
Genotype (G)	44	220.87	5.02***	75	313.31	4.18***
Genotype × environment (G × E)	264	592.25	2.24***	375	1 279.55	3.41***
Error	314	469.06	1.49	455	1 101.84	2.42
Total	629	3 452.90		911	4 538.12	

***Significant at $p < 0.001$

Table 6: AMMI analysis of variance for maize grain yield among 45 single-cross hybrids across seven environments in 2014/15

Source	Degrees of freedom	Sum of squares	Mean square	Contribution to total variation (%)	Variation explained (% of G × E)
Genotypes (G)	44	221	5.02***	6.40	
Environments (E)	6	2154	359.03***	62.38	
Block	7	83	11.79***	2.40	
Interactions (G × E)	264	592	2.24***	17.14	
IPCA1	49	251	5.12***		42.33
IPCA2	47	119	2.53***		20.07
Residuals	168	223	1.32		37.61
Error	308	403	1.31	11.67	
Total	629	3453			

***Significant at $p < 0.001$

Table 7: AMMI analysis of variance for maize grain yield of 76 single-cross hybrids across six environments in 2015/16

Source	Degrees of freedom	Sum of squares	Mean square	Contribution to total variation (%)	Variation explained (% of G × E)
Genotypes (G)	75	318	4.24***	6.98	
Environments (E)	5	1 831	366.29***	40.18	
Block	6	74	12.31***	1.62	
Interactions (G × E)	375	1 279	3.41***	28.07	
IPCA1	79	571	7.23***		44.64
IPCA2	77	327	4.25***		25.57
Residuals	219	381	1.74		29.79
Error	450	1 054	2.34	23.13	
Total	911	4 556			

***Significant at $p < 0.001$

entry 8 (L11/T2 = VO500Y/CML312), 26 (L4/T2 = M162W/CML312) and 16 (L4/T1 = M162W/B73).

The polygon in season 2 divided the biplot into six sectors (Figure 6), with only three sectors containing environments. The first sector had one environment, E5 (Potchefstroom, non-stress), with entry 44 (L2/T4 = FO215W/CML444) as a winner genotype. The second sector was formed by three environments: E2 (Cedara, low N), E3 (Vaalharts, low N + random drought) and E7 (Cedara, non-stress); entry 52 (L4/T4; I-42/CML444) was the superior genotype in this sector. The third sector was formed by E1 (Potchefstroom, low N) and E4 (Potchefstroom, random drought), and the winning genotype in this sector was 59 (L6/T3 = K64/CML312). Other genotypes, including 13 (L12/T1 = RO544W/MO17) and 61 (L7/T1 = M162W/MO17), were not associated with any environment.

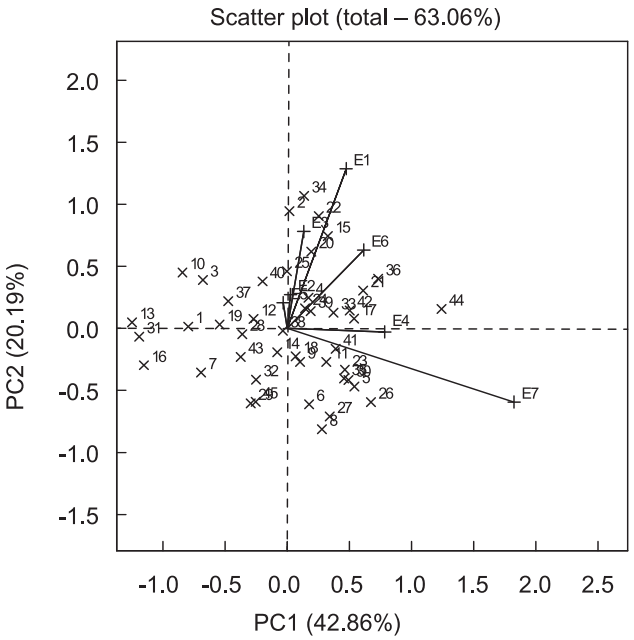

Figure 1: Representativeness of the test environments in 2014/15, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = 2

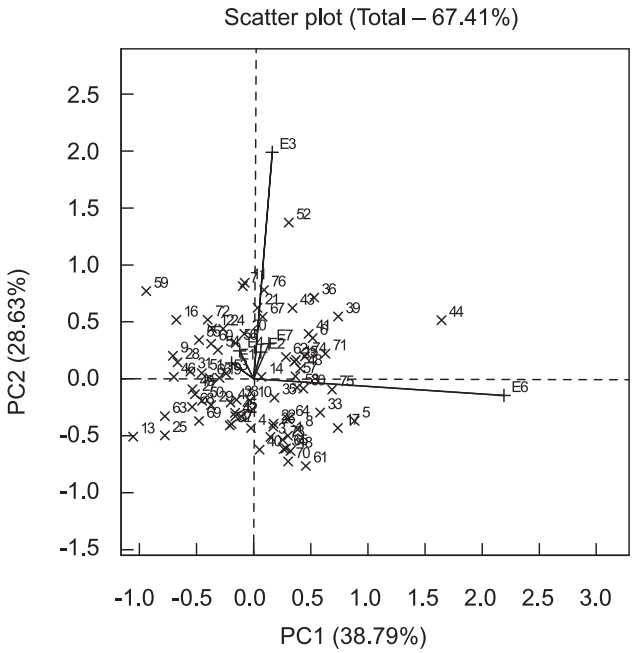

Figure 2: The vector view of the GGE biplot showing discriminative power and representativeness of the test environments in 2015/16, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = 2

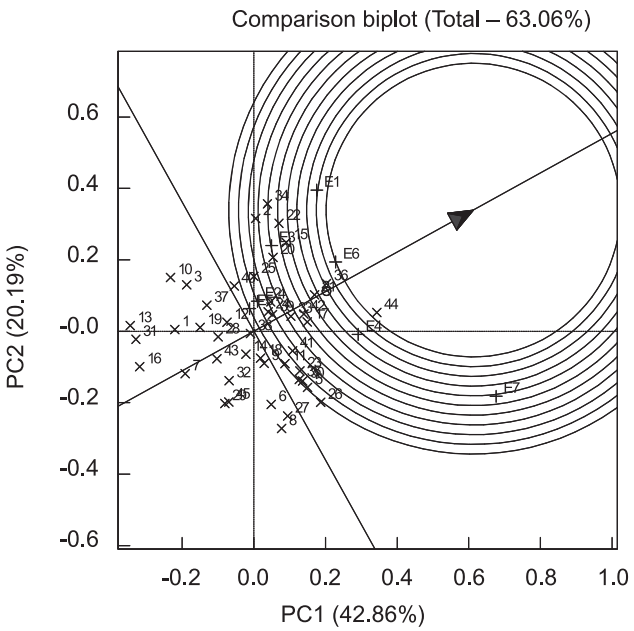

Figure 3: The biplot view for comparison of all environments with the ideal environment in the 2014/15 season, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = 2

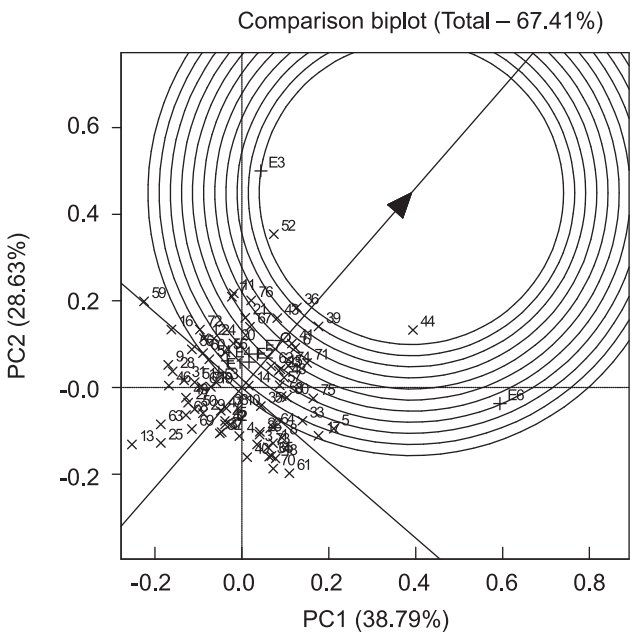

Figure 4: The biplot view for comparison of all environments with the ideal environment in the 2015/16 season, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = 2

Performance of genotypes

The biplots comparing all genotypes with the ideal genotype for grain yield mean performance and stability for 2014/15 and 2015/16 are shown in Figures 7 and 8, respectively. The experimental genotypes in season 1 (2014/15) were all outperformed by the commercial check entry 44 (WE3127), which was the most ideal genotype in this season. Following the check, other high-performing and stable genotypes were hybrids 36 (L7 × T3 = MO17HtHtN × CML444), 21 (L2 × T3 = I-39 × CML444), 22 (L3 × T1 =

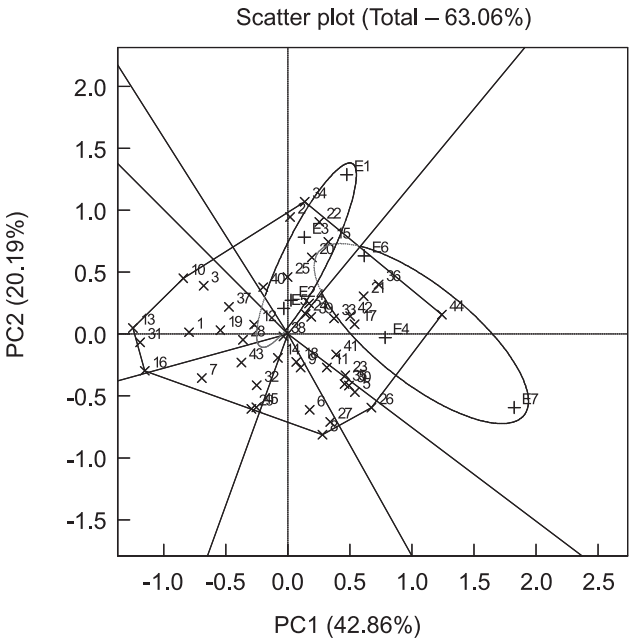

Figure 5: The 'which-won-where' view of the GGE biplot under each mega-environment in 2014/15, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = Symmetrical

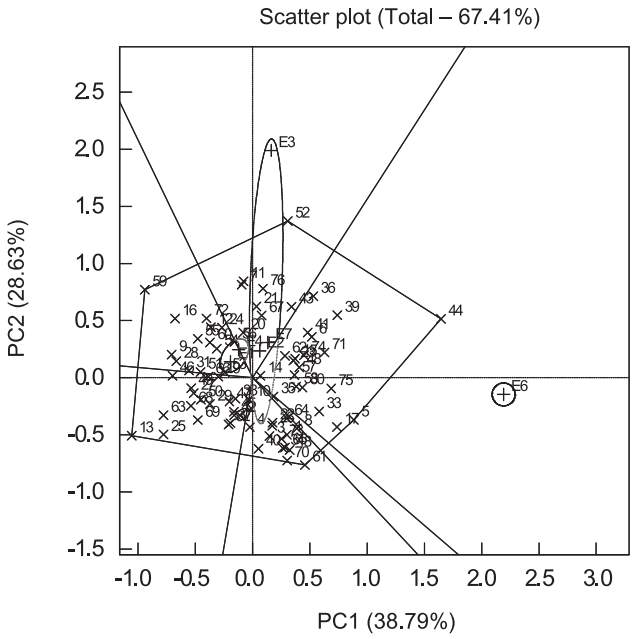

Figure 6: The 'which-won-where' view of the GGE biplot under each mega-environment in 2015/16, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = Symmetrical

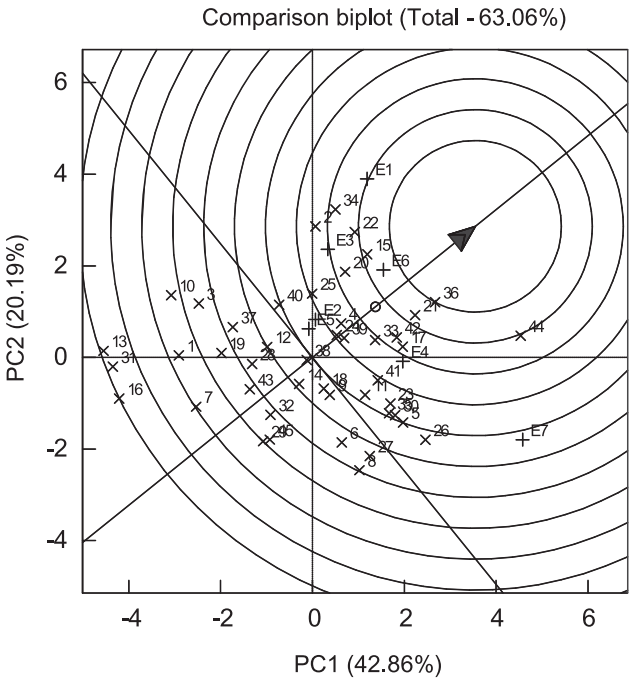

Figure 7: Biplot view comparing all genotypes with the ideal genotype across environments in 2014/15, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = 1

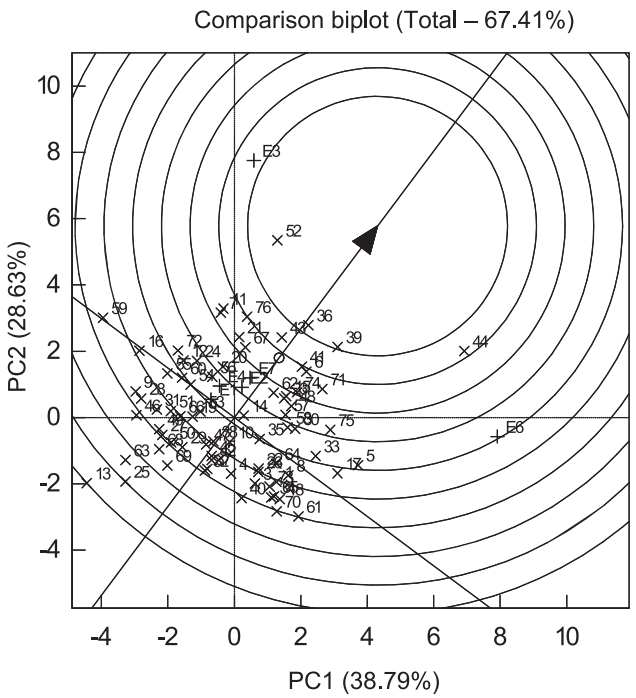

Figure 8: Biplot view comparing all genotypes with the ideal genotype across environments in 2015/16, constructed based on: Transform = 0; Scaling = 0; Centering = 2; SVP = 1

U2540W × B73) and 17 (L14 × T2 = P612MSV × CML312). In season 2 (2015/16) the most ideal genotypes were entry 44 (L2 × T4 = FO215W × CML444); other higher-yielding and stable genotypes included entry 52 (L4 × T4 = I-42 × CML444), 36 (L17 × T4 = U71Y × CML444), 39 (L18 × T3 = VO495Y × CML312) and 43 (L2 × T3 = FO215W × CML312).

Entry 44 (L2 × T4 = FO215W × CML444) in season 2 was also the most superior genotype with the lowest ASV of 0.84. High-yielding but unstable genotypes included entry 15 (L13 × T3 = U71Y × CML444) in season 1, and entry 11 (L11 × T3 = RO452W × CML312) in season 2. Out of a fraction of the hybrids that performed consistently in both season 1 and season 2 (Tables 1 and 2), none of them performed among the best in either season.

Discussion

Analysis of variance to describe G × E

The significant mean squares observed for G × E effects indicated differential response of the genotypes in different environments. The greater magnitude of the sum of squares due to environments indicated the presence of large variability among sites used in evaluating genotypes —thereby indicating possible sites for identifying superior and adapted genotypes. The large contribution of environments in influencing a genotype's performance and stability across environments has been reported in several studies (Setimela et al. 2007; Ndhlela et al. 2014; Makumbi et al. 2015; Abakemal et al. 2016; Sserumaga et al. 2016). Gauch and Zobel (1997) stated that in standard mega-environment investigations, environmental effects generally account for the greatest total sums of treatments, which is about 80%, whereas the genotype and G × E effects each contributed almost 10%. Based on the AMMI analysis in both season 1 and 2, the first two IPCAs accounted for more than 50% of the G × E, suggesting that by using only the first two PCs to explain meaningful G × E patterns, the best-fit model for AMMI could be predicted (Gauch and Zobel 1997).

Discriminative ability and representativeness of test environments

Test environments with longer vectors are more discriminative of the performance of genotypes across environments than environments with short vectors (Yan et al. 2007). The environment that had the longest vector length of all test environments in season 1 was E7 (Cedara, non-stress) followed by E1 (Potchefstroom, low N); these were the most discriminative environments among genotypes. In season 2, the most discriminative environments were E6 (Potchefstroom, low N) and E3 (Vaalharts, low N + random drought). Therefore, testing genotypes in these environments may give sufficient information on the genotype's differences compared with the least discriminative environments. In this study, it was observed that the least discriminating environments, which had shorter vectors and located closer to the biplot origin (Yan et al. 2007), were mainly stress environments, including low N and managed drought-stress environments. Gauch and Zobel (1997) state that stress environments with low productivity are prone to large errors but remain useful for selection, especially for stress tolerance (Bänziger et al. 2006). Abakemal et al. (2016) also indicated that lack of discriminating power of the environments is generally attributable to unfavourable seasonal conditions; therefore, genotypic differences based on short environmental vectors may not be reliable.

Environments that are more representative are selected based on the cosine of the environmental vector and the average environment axis (AEA). The AEA passes through the average environment (indicated by a small circle) and the biplot origin relative to the genotype mean performance. As stated by Yan and Tinker (2005), environments with long vectors and small angles with the AEC abscissa are more representative of mega-environments and are ideal for testing and selecting superior genotypes. In this study, the most representative environments were E6 (Potchefstroom, non-stress) in season 1, and E3 (Vaalharts, low N + random drought) in season 2. These two environments were also identified as ideal environments for evaluating genotypes. The ideal environment should be both highly discriminative among genotypes and representative of the mega-environment (Yan et al. 2009). The small circle located on the AEC abscissa and with an arrow pointing to it represents the average environments; the ideal environment is located at the centre of a set of concentric lines, which measures the distance between each environment and the ideal environment (Abakemal et al. 2016). Environment E6 (Potchefstroom, non-stress) in season 1, and environment E3 (Vaalharts, low N + RD) in season 2 were each in close proximity to the ideal environments, and hence were identified as the best environments for evaluating genotypes. These environments showed a greater discriminative and representative power and may be chosen over other sites for use as suitable test environments, especially when resources are limiting. Vaalharts combined both low N and drought stress; thus, this environment could easily differentiate among inbred lines because, in general, it represented the actual farmers' fields where drought and low N stress generally concurrently occur. To test for performance of genotypes under low N conditions, Vaalharts should be prioritised. Vaalharts is located in a mid-altitude area, characterised by low average annual rainfall and high temperatures during the dry season; this site therefore has potential for selecting for stress tolerance in maize. In the study by Setimela et al. (2007), Potchefstroom was likewise among the most-representative locations; its general representative power of test environments has therefore been proven, suggesting that Potchefstroom should always be considered as a test environment, particularly for non-stress trials. In this study, the identified ideal environments were the non-stress environment in season 1 and the stress environment in season 2. Bänziger et al. (2006) postulated that to achieve breeding progress, test environments should include both low and high-yielding areas, because the selection of genotypes only under high-yielding environments is usually associated with poor performance if selection is done under poor environments. The identified environments therefore represent the average performance across all locations and are generally good test environments.

Relationship between test environments and mega-environments

From the GGE biplot, useful information on the relationship between the test environments was detected. According to Yan and Tinker (2005), the cosine of the angle between the vectors of two environments approximates the correlation between them. An acute angle implies a strong positive correlation between two environments; conversely, an obtuse angle is an indication of a strong but negative correlation. An angle formed by two environments at a right angle (90°) indicates an absence of correlation. The observed relationship indicated the possibility of grouping similar environments.

The 'which won where' view of a GGE biplot was used to visualise the higher-yielding genotypes in different environments (Yan and Tinker 2005). The study revealed that the target environments could be delineated into mega-environments, with different winning genotypes. Yan and Tinker (2005) defined a mega-environment as a group of environments that share the same set of superior genotypes. The seven environments in season 1 were divided into two mega-environments. The first mega-environment was formed mainly by low N stress environments, comprising E1 (Potchefstroom, low N), E2 (Taung, low N) and E3 (Vaalharts, low N), but not E5 (Makhathini), which was a managed drought-stress environment; the higher-yielding hybrid for this mega-environment was entry 34 (L7 × T1 = MO17HtHtN × B73). The second cluster was mainly formed by non-stress environments (E6 and E7), except one random drought environment (E4, Potchefstroom), with entry 44 (commercial check, WE3127) as a winner genotype. The presence of mega-environments suggests that the sets of environments in a mega-environment can give similar information regarding the performance of genotypes; accordingly, one environment can be dropped without losing any useful information on genotype performance (Yan and Tinker 2005). The observations from season 1 thus suggest that in mega-environment 1, when resources are limiting, the number of low N environments may be minimised by dropping some test environments, particularly those that provide little or no information (least-discriminating) regarding the performance of genotypes. For example, E2 (Taung, low N) was the least-discriminating test environment within a mega-environment; consequently, it could be easily dropped without losing information on the genotype's performance. The observed delineations by stress and non-stress environments align with the results of previous studies (Setimela et al. 2007).

Results from season 2 classified the six environments into three mega-environments, with E6 (Potchefstroom, non-stress) forming one mega-environment; E2 (Cedara, low N), E3 (Vaalharts, low N + random drought) and E7 (Cedara, non-stress) formed the second mega-environment, while E1 (Potchefstroom, low N) and E4 (Potchefstroom, random drought) formed the third mega-environment. In the second mega-environment, E3 (Vaalharts), which combined both random drought and low N stress might be chosen over Cedara. This environment is the most ideal environment with high discriminative power among genotypes, and was also more representative of the test environments. Gauch and Zobel (1997) state that too many or too few mega-environments might reduce average yield; therefore, four mega-environments are generally ideal for testing genotypes. However, in this study, the fewer mega-environments identified may be considered ideal because of the total number of environments used. Some genotypes, such as entries 8 (L11 × T2 = VO500Y × CML312), 26 (L4 × T2 = M162W × CML312) and 16 (L4 × T1 = M612W × B73) in season 1, and entries 13 (L12 × T1 = RO544W × MO17) and 61 (L7 × T1 = M162W × MO17) in season 2 were superior (vertex) genotypes but were not associated with any mega-environment. This result suggested that these genotypes could exhibit either poor or good performance for grain yield depending on the environment (Kaya et al. 2006; Setimela et al. 2007). According to Yan and Tinker (2005), dividing test environments into mega-environments and recommending genotypes is more reliable and recommended if crossover interactions are repeatable across the years. For this study, the pattern was not repeatable, particularly owing to differences in the genotypes evaluated in the two seasons; this outcome indicates a need for an additional experiment to validate the pattern and then identify key environments and recommend genotypes based on MET data. Where the G × E pattern is not repeatable, different test environments are recommended for evaluating genotypes.

Performance of the maize genotypes

A comparison biplot was used to compare genotypes with ideal genotypes. The biplot accounted for 63.06% of the variation in grain yield in season 1, and 67.41% in season 2. The AEC abscissa ranks genotype relative to the direction of higher mean performance and stability (Yan et al. 2007). The AEC abscissa passes through the biplot origin, and the average environment is indicated by a small circle defined by the average PC1 and PC2 scores across the environments (Yan et al. 2009). Genotypes with high mean performance and stability within a mega-environment are considered 'ideal' genotypes (Yan et al. 2007); the term stability relates to the consistent rank of a genotype across environments. The check hybrid entry 44 (WE3127) was the best genotype in season 1; entries 36 (L7 × T3 = MO17HtHtN × CML444), 21 (L2 × T3 = I-39 × CML444) and 22 (L3 × T1 = U2540W × B73) were the most stable hybrids among experimental hybrids after the commercial check.

Unlike in season 1, most experimental hybrids evaluated in season 2 outperformed the commercial checks; this indicated the superiority of the newly developed hybrids over the commercial checks. These hybrids include entry 44 (L2 × T4 = FO215W × CML444), which was the most stable hybrid. An ideal genotype has the longest vector of all genotypes and has zero to minimal G × E interaction (Yan and Tinker 2005). Furthermore, the ASV was used to check stability of hybrids in season 2; a low ASV value closer to zero is an indication of a stable genotype (Purchase 1997). Based on the ASV, entry 44 (L2 × T4 = FO215W × CML444) was the most-stable genotype with the lowest ASV (0.84). This hybrid was identified as late

maturing (data not shown), with superior performance across non-stress, drought and low N environments. This result agrees with Setimela et al. (2007) who similarly found that the late-maturing, moisture- and low-soil-fertility-tolerant cultivars were adapted in most regions. These results suggest that the identified hybrids with high mean grain yield and stability are broadly adapted and could therefore be used to improve yields across a wide range of stress and non-stress environments. Broad adaptations are associated mainly with genotype than with G × E effects (Gauch 2013); such genotypes eliminate the need for subdividing the test environments into mega-environments (Gauch and Zobel 1997).

Some higher-yielding genotypes, such as entry 15 (L13 × T3 = U71Y × CML444) in season 1 and entry 11 (L11 × T3 = RO452W × CML312) in season 2, were not among the most stable, suggesting that they may have specific adaptation to certain stress or non-stress environments. Higher-yielding but unstable genotypes were previously reported by other investigators (Badu-Apraku et al. 2012; Makumbi et al. 2015; Sserumaga et al. 2016); such genotypes have a narrower adaptation which is greatly influenced by G × E (Gauch 2013). Our study included a wide range of non-stress, low N and drought environments; therefore, these genotypes may be less responsive particularly under stress environments, which could therefore make them unstable. Moreover, it was observed that the most-stable genotypes were mainly those involving the tropical CIMMYT testers than the temperate Corn Belt testers MO17 and B73. Some hybrids involving the temperate testers were high yielding, yet they were mainly unstable. Use of temperate material in South Africa is currently negligible because differences in environmental conditions may interfere with photoperiod reaction and the overall performance of the temperate-derived hybrids. Hybrids containing temperate material might therefore be recommended only for specific environments.

Conclusions

The results indicated that yield performance of maize single-cross hybrids was influenced largely by G × E effects. However, superior genotypes with high mean yield and stable performance could be identified. Hybrids derived from tropical CIMMYT testers were more stable than those containing temperate Corn Belt testers. The most stable and high-yielding experimental hybrid was FO215W × CML444. The identified stable hybrids require further testing before recommendation for release; whereas the identified higher-yielding but unstable genotypes could be considered for specific environments in selected regions. The study further indicated the possibility of delineating the test locations into mega-environments and then identifying the ideal target test locations. Potchefstroom and Vaalharts were the most suitable environments for evaluating the performance of genotypes under non-stress and stress conditions, respectively.

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Geolocation information

Potchefstroom: 26°74′ S, 27°08′ E; Cedara: 29°54′ S, 30°26′ E; Vaalharts/Taung: 27°95′ S, 24°84′ E; Makhathini: 27°39′ S, 32°18′ E.

ORCID

Sphiwokuhle Shandu —http://orcid.org/0000-0003-3955-1515
Edmore Gasura — http://orcid.org/0000-0002-8228-4486
John Derera — http://orcid.org/0000-0003-3715-0689

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