

## Full Length Research Paper

# GGE biplot analysis of genotypes by environment interaction on *Sorghum bicolor* L. (Moench) in Zimbabwe

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The genotype by environment interaction (GEI) reduces the success of genotype selection and recommendations by breeders, thus slowing down the progress of plant breeding. The understanding of genotype by environment interaction (GEI) multi-locational yield trials (MLYT) enables researchers to identify locations which are efficient in distinguishing tested genotypes, which are ideal across the test-locations as well as environments which are good representatives of the target regions of interest. The main objective of the study was to assess the genotype by environment interaction on grain yield stability of promising sorghum genotypes across five diverse environments of Zimbabwe. Sorghum yield data of twenty-seven cultivars was obtained from the replicated trials. After performing a pooled analysis of variance for grain yield across five diverse environments during the 2013/14 rainy season, the GxE interaction was significant ( $P < 0.001$ ), and this justified need for testing for GEI components using the GGE biplot analysis to enhance the understanding the effects of components. The results revealed that three mega-environments were identifiable which are Matopos, Save-Valley and Kadoma falling in one mega-environment, then Makoholi was identified as a second mega-environment and then Gwebi was identified as the third mega-environment. Gwebi had the most discriminating ability and good representativeness whereby Save Valley had a poor discriminating ability as well as least representativeness.

**Key words:** Sorghum, genotype x environment interaction, GGE, adaptation and yield stability, mega-environment, discriminating ability, representativeness.

## INTRODUCTION

*Sorghum bicolor* L. (Moench) is an important cereal crop which is ranked 5<sup>th</sup> in the world based on its use and production after maize, wheat, rice and pearl millet. The crop is predominantly grown in dry and hot regions due to its tolerance to drought. Sorghum is versatile and can be

grown as grain, forage and sweet crop and it thrives well under temperatures and humidity which are as high as 40 to 43°C and 15 to 30%, respectively as long as soil moisture is available. The crop carries natural characteristics which make it adaptable to drought

conditions. Sorghum characteristics such as dense and deep roots, ability to reduce transpiration through leaf rolling and stomatal closure among others make the crop able to survive dry periods. Hence sorghum has become a strategic crop in Zimbabwe's driest regions in the face of climate variability. Despite all the crop's advantages over other cereals under dry condition, the crop production is still very low and very low yields are being obtained. Research through the national breeding programmes has been done for years but with little progress due to limited knowledge on the relationship and effects of genotype and environment and their interaction on the crop yield performance.

It is important to show the relationship between genotypes and environments for selected traits graphically by use of a genotype by genotype by environment (GGE) biplot that allows visual assessment of genotype by environment interaction (GEI) pattern of multi-locational or multi-environment data (Yan et al., 2000; Yan and Hunt, 2001). GGE is the most recent approach for analysis of GEI and increasingly being used in GEI studies in plant breeding research (Butran et al., 2004). The model was proposed by Yan et al. (2000), and has shown extensive usefulness and a more comprehensive tool in quantitative genetics and plant breeding (Yan et al., 2001; Yan and Rajcan, 2002). The model covers very critical areas in the study of stability of multi-locational trials, like the which-won-where pattern, mean performance and stability of genotypes, discriminating ability, mega-environment investigation, and representativeness of environments.

The GGE method emphasizes on two concepts, whereby in the first concept, it clearly points out that even though the measured yield is a result of combination effect by Genotype (G), Environment (E) and genotype x environment interaction (GEI), only G and GEI are relevant and must be considered simultaneously when evaluating genotypes, thus the name GGE. The second concept is based on the biplot technique which was developed by Gabriel (1972) which is used to estimate and show the GGE of MEYT, hence the name GGE biplot. The GGE biplot is made by the first two principal components (PC), PC1 and PC2 also known as the primary and secondary effects, respectively. This is derived from subjecting the environment centred yield data (due to GGE) to singular value decomposition.

This now makes it very easy for one to see which genotype won in which environments, thus facilitating mega-environment (ME) identification (Yan et al., 2000; Yan, 2001). This is facilitated in the form of a polygon to visualize the interaction patterns between genotypes and environments (Yan and Kang, 2003), whereby furthest genotypes are connected from the biplot origin such that

all genotypes are contained in the polygon (Kaya et al., 2006). Some genotypes will be located on the vertices of the polygon and they are either the best or the poorest in one or more environments (Yan et al., 2000; Yan and Rajcan, 2002; Yan and Tinker, 2006). The rays are drawn perpendicular to the sides of the polygon dividing it into sectors, such that the vertex genotypes in each sector is also the best genotype for sites whose markers fall into respective sector so that sites within the same sector share the same winning genotype (Yan, 2002; Yan et al., 2000). GGE biplot is a visual display of the G + GE of multi-environmental data where groups of locations with similar cultivar responses are presented and it identifies the highest yielding varieties for each group. PC1 tend to correlate highly with the genotype means, the ideal cultivar is the one which possess large scores for PC1, thus indicating high average yield and small PC2 scores indicating less GEI and greater stability.

The study was however done to analyse the multi-locational yield data from across five diverse locations. The objectives of this study were to (i) to identify the genotype and environmental components that are associated with the GxE interaction across the diverse environments so as to aid better management of sorghum crop in Zimbabwe, (ii) to measure the correlation among the five test locations, (iii) to determine whether the test-locations belong to a single mega-environment or not and (iv) to rank locations based on discriminating ability and representativeness by using the genotype, genotype by environment interaction (GGE biplot analysis).

## MATERIALS AND METHODS

### Study sites

The multi-locational yield trials (MLYT) were carried out at five different locations in Zimbabwe, Matopos Research Station, Makoholi, Gwebi, Save Valley and Kadoma to assess and confirm the effects of genotype, environment and genotype by environment interaction. The locations have different agro-climatic conditions with Gwebi representing the high-potential area with good rains and soils, Kadoma representing the intermediate potential area with average rainfall, Makoholi, Save Valley and Matopos representing the low potential area with erratic and low rainfall (Table 1). According to the 2013/14 season weather data collected at study sites, the low potential areas had an average of 300 mm annual rainfall and temperatures were 34°C, whilst the high potential areas received an average of 550 mm and temperatures of 29°C. Generally, such rainfall averages depict poor season as compared to good seasons where low potential areas and high potential areas receive an average of 450 and 800 mm, respectively. The sites are also characterised by different soil types, which range from the Red-clay soil at Gwebi, Black sandy-loam soils at Kadoma and Black clay at Matopos and Sandy soils at Makoholi.

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**Table 1.** Description of sites used in the multi-locational trials.

Code	Location	Altitude (m)	Longitude/latitude	Natural region
E1	Gwebi	1448	30°32'E/17°41'S	IIb
E2	Kadoma	1149	29°53'E/18°19'S	III
E3	Makoholi	1204	38047'E/19050'S	IV
E4	Matopos	1328	28028'E/20024'S	IV
E5	Save Valley	450	30°E/20°48S	V

**Table 2.** Description of sorghum genotypes used in the multi-locational trials.

Variety/line code	Code	Type and breeding status	Origin
NL9411	(G1)	Grain/Advanced	CBI-Zimbabwe
NL9803	(G2)	Grain/Advanced/CBI	CBI-Zimbabwe
NL9923	(G3)	Grain/Advanced/CBI	CBI-Zimbabwe
NL9907	(G4)	Grain/Advanced/CBI	CBI-Zimbabwe
NL9921	(G5)	Grain/Advanced/CBI	CBI-Zimbabwe
NL2014	(G6)	Grain/Advanced/CBI	CBI-Zimbabwe
ICSV93046	(G7)	Dual/Advanced/ICRISAT	ICRISAT-India
NL2015	(G8)	Grain/Advanced/CBI	CBI-Zimbabwe
NL2020	(G9)	Grain/Advanced/CBI	CBI-Zimbabwe
NL2009	(G10)	Grain/Advanced/CBI	CBI-Zimbabwe
SV4	(G11)	Grain/Released/CBI	CBI-Zimbabwe
SV2	(G12)	Grain/Released/CBI	CBI-Zimbabwe
MACIA	(G13)	Grain/Released/ICRISAT	ICRISAT-India
NL2012	(G14)	Grain/Advanced/CBI	CBI-Zimbabwe
NL9412	(G15)	Grain/Advanced/CBI	CBI-Zimbabwe
SDS6013	(G16)	Dual/Advanced/ICRISAT	ICRISAT-India
ICSR93034	(G17)	Sweet sorghum/Advanced/ICRISAT	ICRISAT-India
S35	(G18)	Sweet sorghum/Advanced/ICRISAT	ICRISAT-India
SPV1022	(G19)	Dual/Advanced/ICRISAT	ICRISAT-India
CSV15	(G20)	Dual/Advanced/ICRISAT	ICRISAT-India
NTJ2	(G21)	Sweet sorghum/Advanced/ICRISAT	ICRISAT-India
SPV422	(G22)	Sweet sorghum/Advanced/ICRISAT	ICRISAT-India
E36-1	(G23)	Dual/Advanced/ICRISAT	ICRISAT-India
PVK801	(G24)	Dual/Advanced/ICRISAT	ICRISAT-India
JJ1041	(G25)	Dual/Advanced/ICRISAT	ICRISAT-India
SEREDO	(G26)	Dual/Advanced/ICRISAT	ICRISAT-India
MATEBELE	(G27)	Sweet sorghum/Landrace	Farmers-Zimbabwe

### Experiment design and measurements

Twenty-seven genotypes of sorghum (*Sorghum bicolor*) were evaluated during the 2013/14 season in five diverse locations across Zimbabwe. The twenty-seven genotypes included three Zimbabwean released varieties, one farmer variety and twenty-three advanced lines (Table 2).

The trials were planted in a two-factor randomised complete block design (RCBD) replicated three times. Each plot comprised of 4 rows which are 5 m long with inter-row and intra-row spacing of 75 and 20 cm, respectively. Basal fertilizer of compound D with ratio nitrogen : phosphorus : potassium (N:P:K) of 7:14:7 was applied at planting at a rate of 200 kg/ha. The trials were raised under rainfed across all the sites. Topdressing with ammonium nitrate (34.5% N) was applied at a rate of 150 kg/ha after six weeks from germination.

Weeding was done using hoes at all trial locations. The data considered for analysis was from the candidates of the net plot, thus the two centre rows. The harvested panicles were sundried for two days before being tested for moisture content where 12% was the preferred average content. Grain yield data was then obtained by weighing the dried grain using a digital scale. The data was then statistically analysed by analysis of variance (ANOVA) using GenStat version 14 statistical package. The presence of significant genotype by environment interaction GEI ( $P < 0.001$ ) justified further testing for GEI components using the GGE biplot analysis to enhance the understanding the effects and components. The further partitioning of variance components was computed using the GGE model (Yan, 2001). The first two principal components (PC1 and PC2) derived from environment centred yield data were used to construct the GGE biplot (Yan et al., 2000). That enabled selection

**Table 3.** Summary of the general analysis of variance for grain yield (kg/ha) showing the level of significance for the genotype, environment and GEI of 27 sorghum varieties grown at 5 environments of Zimbabwe during 2013/14 season.

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Exp % ss
REP stratum	2	1.645x10 <sup>7</sup>	8.224 x10 <sup>6</sup>	2.74		
Genotype (G)	26	1.841 x10 <sup>8</sup>	7.081 x10 <sup>6</sup>	2.36	<0.001	15.2
Environment (E)	4	5.049 x10 <sup>8</sup>	1.262 x10 <sup>8</sup>	41.99	<0.001	41.8
Genotype x Environment	104	5.190 x10 <sup>8</sup>	4.990 x10 <sup>6</sup>	1.66	<0.001	43
Residual	268	8.056 x10 <sup>8</sup>	3.006 x10 <sup>6</sup>			
Total	404	2.030 x10 <sup>9</sup>				

\*\*\* DF= Degrees of freedom; SS= sums of square; MS= means square.

of best environments to be regarded and used as test-locations and genotypes which are high yielding and widely adapted. The GGE biplot was generated from the environment-centred yield data following the method described by Yan et al. (2001, 2007). This method enabled to determine the genotype with yields above average for a specific environment on "which-won-where" and the most discriminating environments as well as with good responsiveness as well as the correlation between environments. The best genotypes were also selected such that if the angle between the genotype and environment is less than 90°, it shows that the genotype performed above average on that particular environment, and angle above 90° depicts below average performance whilst that with equal to 90° is near average performance. In this study, comparison between two genotypes was done by connecting the two with a straight line, and followed by a perpendicular line that passes through the biplot origin (the equality line of the two genotypes).

## RESULTS

### Combined analysis of variance

A general combined analysis of variance (ANOVA) was performed and the results revealed that variances due to genotypes, environments and GxE interaction were highly significant ( $P < 0.001$ ) (Table 3). Environment mean yield ranged from 1752.26 kg/ha at E3 (Makoholi) to 4940.26 kg/ha at E1 (Gwebi) (Table 4). Genotype mean yield ranged from 1977.4 (G11) to 4706 kg/ha (G1) (Table 4). The GxE interaction component explained 43% of the total sum of squares and this indicates the need for further analysis for stability and adaptability to recommend genotypes which are high yielding and stable as well as genotypes which are promising and adaptable to an environment.

### Discriminating ability, environmental correlation and genotype performance per environment (GGE biplot analysis)

The similarity (covariance) between two environments is determined by both the length of their vectors and the cosine of the angle between them (Figure 1). Location E1 had good discriminating ability as shown by a long

environmental vector, followed by E3 and then E2 (KADOMA) and E4 (MATOPOS). However, E5 (Save-Valley) had poor discriminating ability, as was indicated by its short environmental vector. The study shows that E1 (GWEBI), E2 (KADOMA) and E4 (MATOPOS) were the most discriminating locations which means such sites gave more information on the performance of the varieties, while E5 (Save Valley) was the least discriminating environment. This means if the study is carried out for several seasons and same sites continue to be non-discriminating (less informative); it means the locations can be dropped and not to be used as test locations.

Information on relationships among the test environments was also given (Figure 1) as is indicated by the cosine of the angles; acute angle indicates a positive correlation, right angle and obtuse angles indicate no correlation and negative correlation, respectively. Angles between any of the three environments; E4 (Matopos), E2 (Kadoma) and E5 (Save Valley) were acute and hence showed positive correlations and the same environments E4 (Matopos), E2 (Kadoma) and E5 (Save Valley) had negative correlation with environments E1 (Gwebi) and E3 (Makoholi).

A wide negative correlation between three environments (E4 (Matopos), E2 (Kadoma) and E5 (Save Valley) and two environments E1 (Gwebi) and E3 (Makoholi) indicated a crossover GE interaction; thus, the changes in ranking order from one environment to another. Such close associations among most test environments suggests that same information in terms of performance can be obtained from fewer test locations and some may be dropped without losing any information about the cultivars under test, thus reducing experimental costs (Yan and Tinker, 2005).

The results from the study shows that genotypes G22, G12, G18, G26, G6, G19 and G27 performed above average in environments E4, E2 and E5 but below average in E3. However, G1, G2, G14, G24 and G8 performed below average in E4, E2 and E5 whilst G11 and G16 were near average in the same environments. Genotypes G14, G3 G6 and G5 performed above average in E3 whilst G13, G14, G21, and G25 performed

**Table 4.** Genotype mean and environment mean for 27 sorghum advanced genotypes yield performance evaluated across 5 environments.

Genotype	Environment	E1	E2	E3	E4	E5	Mean
G1		8327	3833	4963	3177	3230	4706
G10		6396	4072	845	3651	2316	3456
G11		2826	3127	-80	2493	1521	1977.4
G12		1911	5523	-103	4851	3393	3115
G13		7506	3741	512	3436	1905	3420
G14		6853	1737	5128	917	1760	3279
G15		2689	3729	2649	2835	2785	2937.4
G16		521	4214	1489	3262	2936	2484.4
G17		3867	2578	975	1921	1353	2138.8
G18		5586	3433	230	2996	1693	2787.6
G19		3435	3621	765	2963	2111	2579
G2		3644	2894	1124	2209	1650	2304.2
G20		5623	3526	1176	3004	2038	3073.4
G21		7239	3522	2887	2969	2446	3812.6
G22		5112	3935	638	3428	2221	3066.8
G23		7600	4958	2342	4505	3363	4553.6
G24		4208	2283	1540	1596	1274	2180.2
G25		6995	3800	3028	3218	2713	3950.8
G26		5822	3220	565	2767	1615	2797.8
G27		2218	3846	657	3103	2318	2428.4
G3		5603	1745	4074	924	1528	2774.8
G4		5883	3506	2210	2907	2310	3363.2
G5		2406	2564	2788	1619	1952	2265.8
G6		4641	3804	2032	3126	2555	3231.6
G7		6565	3194	1051	2755	1697	3052.4
G8		4369	2349	2553	1581	1612	2492.8
G9		5542	3858	1273	3325	2324	3264.4
Mean		4940.26	3430.07	1752.26	2797.7	2171.07	3018.27

above average in both E3 and E4. Genotypes G1, G23, G13, G10, G7 and G4 performed above average in E1 whilst G17 is near average in environment E3 and G3 near average in environment E1.

### Environment representativeness

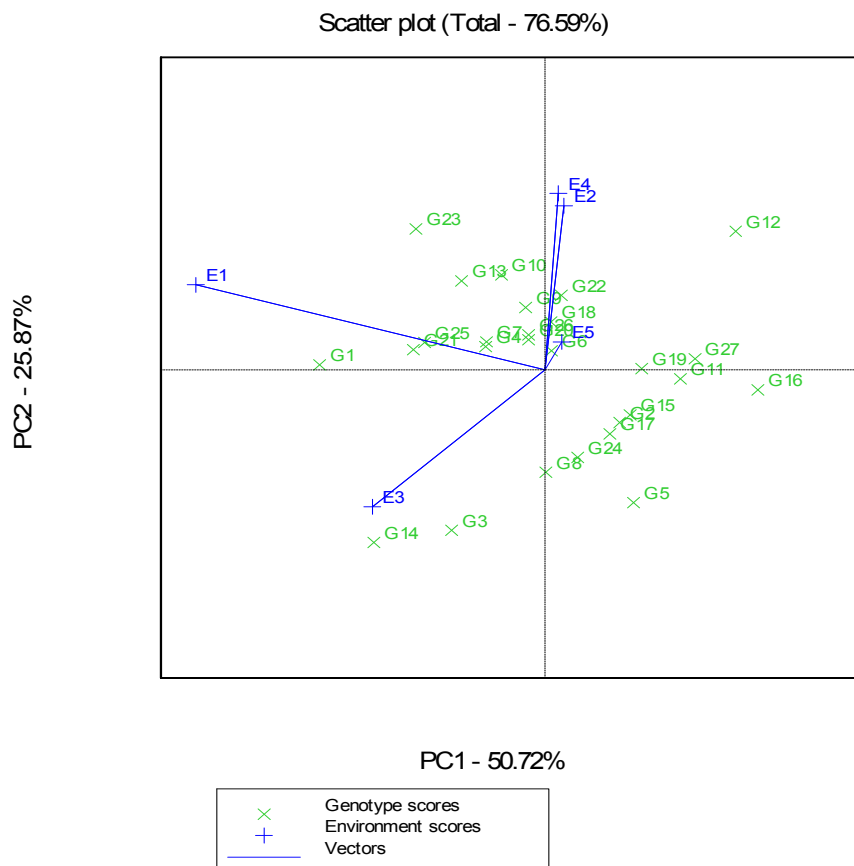
Figure 1 presents the representativeness of the test locations and a test location with a small angle to the average environmental axis (AEA) is more representative than other test locations. This means that E5 (SAVE VALLEY) is the most representative test location but with poor discriminating ability as indicated in Figure 1, whereas E1 indicated both good discriminating ability and representativeness, making it an ideal and best location for testing the sorghum genotypes. Environments E2 (KADOMA), E4 (MATOPOS) and E3 (MAKOHOLI) are the least representative. Test locations which are discriminating but non-representative like E2 (KADOMA) and E4 (MATOPOS) and E3 (SAVE VALLEY) are

important under circumstances when selecting genotypes that are specifically adapted if the target locations can be divided into mega-environments. However, where the target locations cannot be divided into mega-environments such test environments like E2 (KADOMA) can be useful for culling unstable genotypes.

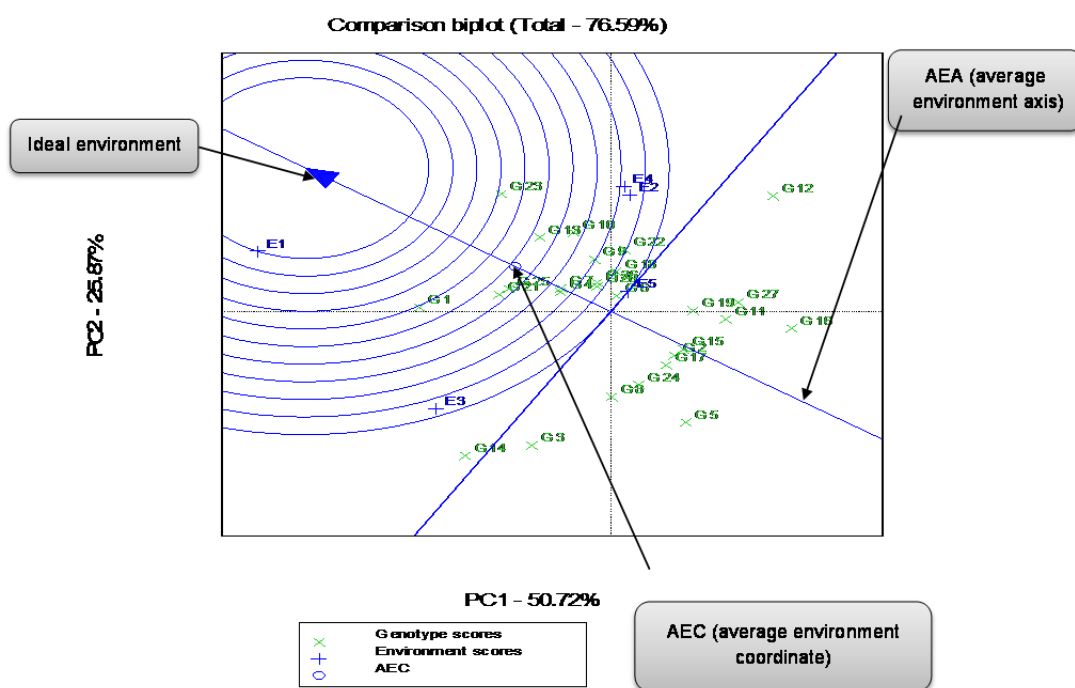
An ideal environment is the one which is on the intrinsic circle (Figure 2). So E1 (GWEBI) is found on the closer proximity or on the edge of the intrinsic circle (Figure 2). However, E3 (MAKOHOLI) and E5 (SAVE VALLEY) cannot be ideal test locations for selecting cultivars which can be adaptable for the whole region. Since this study was carried out for one season, it is of paramount importance to repeat the experiment in more seasons so as to confirm that a certain test location is ideal.

### Ranking of genotypes based on environment E1 (good discriminating ability, representativeness and ideal)

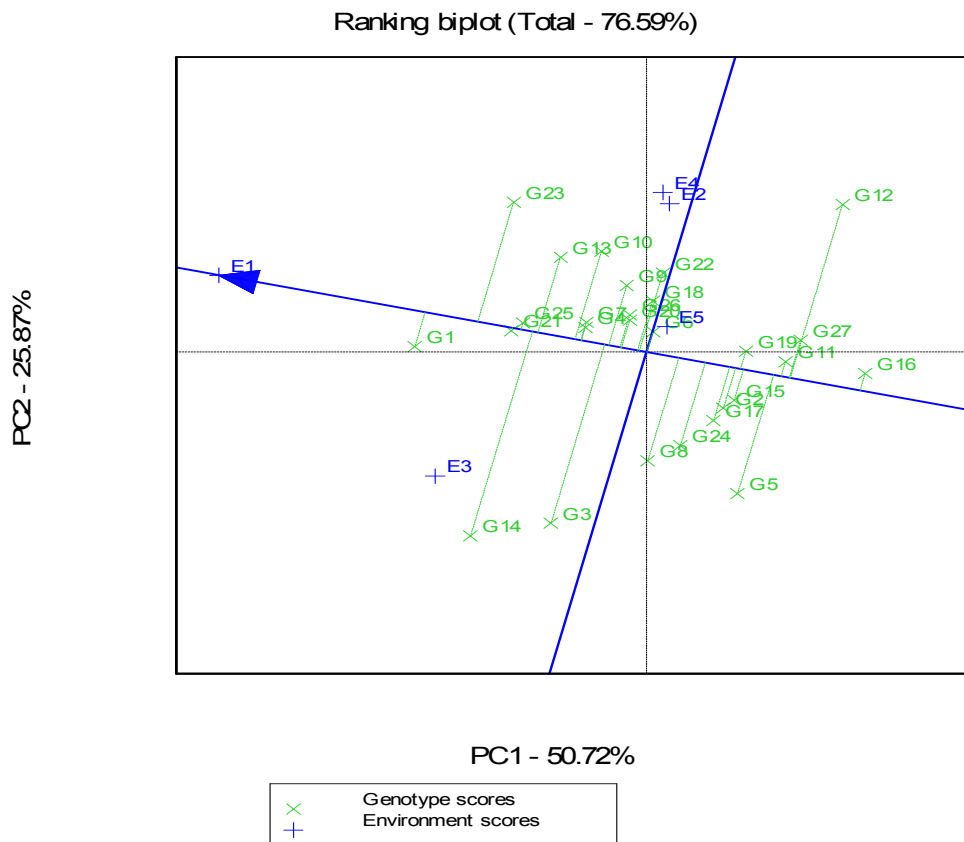
Genotypes can be ranked based on their performance in



**Figure 1.** The environment vector view of the GGE drawn to show similarities among test-environments in discriminating environments.



**Figure 2.** The average environment coordination (AEC) view to rank genotypes relative to the centre of the concentric circles.



**Figure 3.** Ranking genotypes based on the performance of a specific environment (E1).

an environment by a line drawn that passes through the biplot origin and the environment called the axis of the environment. In Figure 3, genotypes performance is shown based on E1 (GWEBI), and the graph shows that genotype G16, G5 (NL9921) and G12 (NL9803) had a lower than average yield, whilst G6 (NL2014), G22 (SPV-422), G4 (NL9907) and G7 (ICSV93046) had a performance near the average yield and G1 (NL9411), G23 (E-36-1), G13 and G21 had performance above the average yield. So, the highest yielding genotype in E1 (GWEBI) is G1 (NL9411) whilst the lowest yield is G16 (SDS6013).

#### Ranking of environments based on the highest yielding genotype (G1 – NL9411)

Environments can be ranked based on the performance of a genotype. This is shown in Figure 4 where a line is drawn through the biplot origin and the genotype called the line of axis of genotype. The axis in Figure 4 was drawn based on G1 (NL9411), and this showed that G1 (NL9411) performed below average in E2 (KADOMA), E4 (MATOPOS) and E5 (SAVE VALLEY), whilst it performed above average in E3 (MAKOHOLI) and E1 (GWEBI).

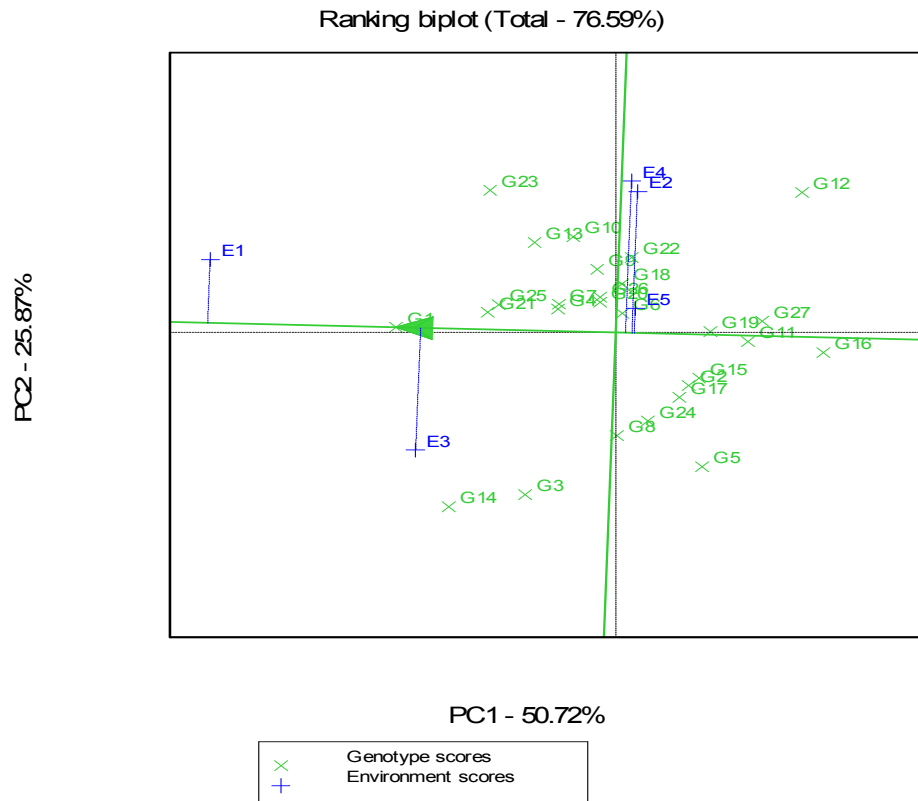
#### Comparison plot for genotypes based on the concentric circle

Figure 5 shows the comparison plot for genotypes, and an ideal genotype is one which is near or at the centre of the concentric circle. Hence in the study, the plot reflected that G23 is the most ideal genotypes as shown by its position and followed by G1 and G25. This also reflects that the genotype has high mean and it is stable. Good genotypes are those which are closer to the ideal genotypes, thus G4, G7, G13, G10, G20, G26 and G21. They are positioned closer to the ideal genotypes. However, G5 (NL9921), G11, G17, G16 and G12 are the worst genotypes as their position in the plot are located far from the concentric circle.

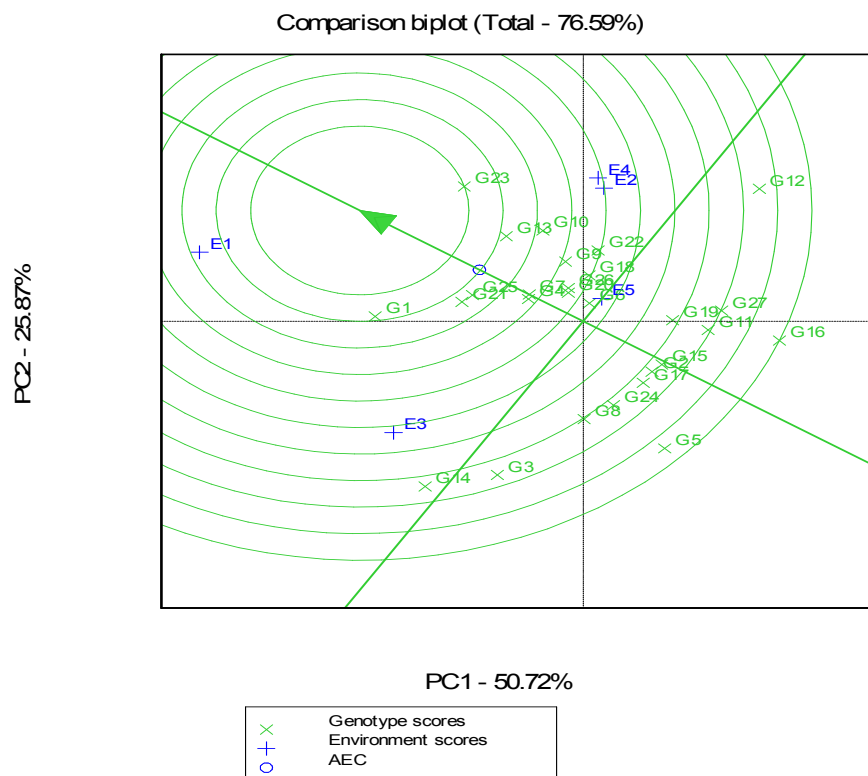
#### Comparison between performances of two genotypes

In Figure 6, two genotypes, G1 (NL9411) and G12 (SV-2 released variety) were connected and the graph shows that G12 had high yield in E2 (KADOMA), E5 (SAVE VALLEY) and E4 (MATOPOS) whilst G1 (NL9411) produced high yields in E1 (GWEBI) and E3 (MAKOHOLI). This clearly shows that the genotypes



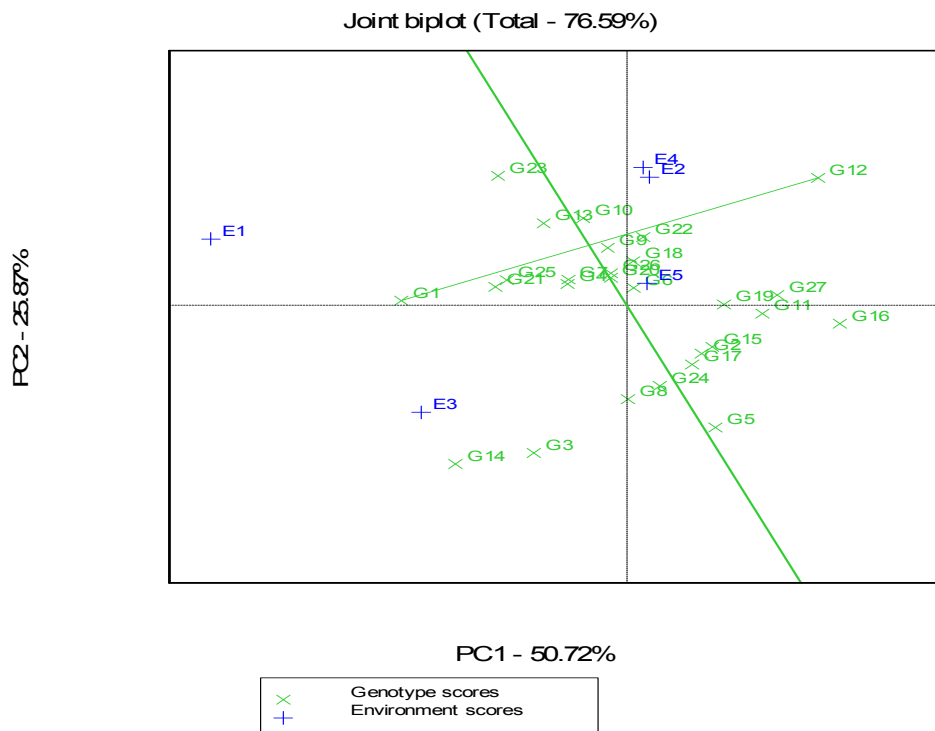


**Figure 4.** Ranking environments based on the performance of a genotype.



**Figure 5.** The average environment coordination (AEC) view to rank genotypes relative to the centre of the concentric circles.





**Figure 6.** View of two genotypes in their performances in individual environments.

changed their rankings in those different environments thus explaining an example of crossover interaction. The same biplot was also used to measure the difference between the genotypes that varies by environment being proportional to the distance of the environment to the equality line. The biplot shows that the difference between G1 and G12 was relatively large in E4 (MATOPOS) (MATOPOS) and E1 (GWEBI) as well as in E2 (KADOMA) and E3 (MAKOHOLI) but very small in E5 (SAVE VALLEY).

### Comparison of genotypes in two environments

The vertical and horizontal axis can be used to determine which variety performed above average or below average on two environments with one plotted on the horizontal axis and the other one plotted on the vertical axis. In Figure 7, E1 (Gwebi) was plotted on the x-axis and it shows that all the genotypes on the right of the vertical axis performed above average whilst those on the left side of the vertical axis performed below average. In this case, genotypes like G1, G13, G23, G14, G3, G7, G21 and G18 performed above average in that particular environment while G16, G5, G11, G15, G12, G27 and G19 performed below average. E4 (Matopos) was plotted on the y-axis and it shows that all genotypes which are above the horizontal axis performed above average and those below the horizontal axis performed below average

in E4. The genotypes which performed above average include G1, G11, G15, G27, G12, G22, G10, G23 and G25 while genotypes like G16, G5, G19, G2, G24, G3, G14, G21 and G7 performed below average in E4. Genotypes lying on the equality or diagonal line performed equally in both environments for example G20. The perpendicular divided the environments into two groups meaning that each of these genotypes (G1 and G12) would yield better than the other at environments with markers on its side of the perpendicular (Yan et al., 2000).

### Ranking plot based on mean performance and stability

Mean performance and stability of the genotypes can be predicted within a single mega environment when the genotype metric is preserved (SVP=1) (Figure 8). Predictions are mainly based on the average environment coordination (AEC) view of the biplot. In Figure 8, the single arrowed line is the AEA which shows the direction to higher mean yields across the tested environments. In this study, the graph shows that G23 and G1 had the highest mean yield, whereas G6 (NL2014) gave a mean yield almost similar to the grand mean and G16 and G5 gave the lowest mean yield. Stability and high performance make a candidate the best genotype. In this biplot (Figure 9), G17, G2 and G15 were most stable

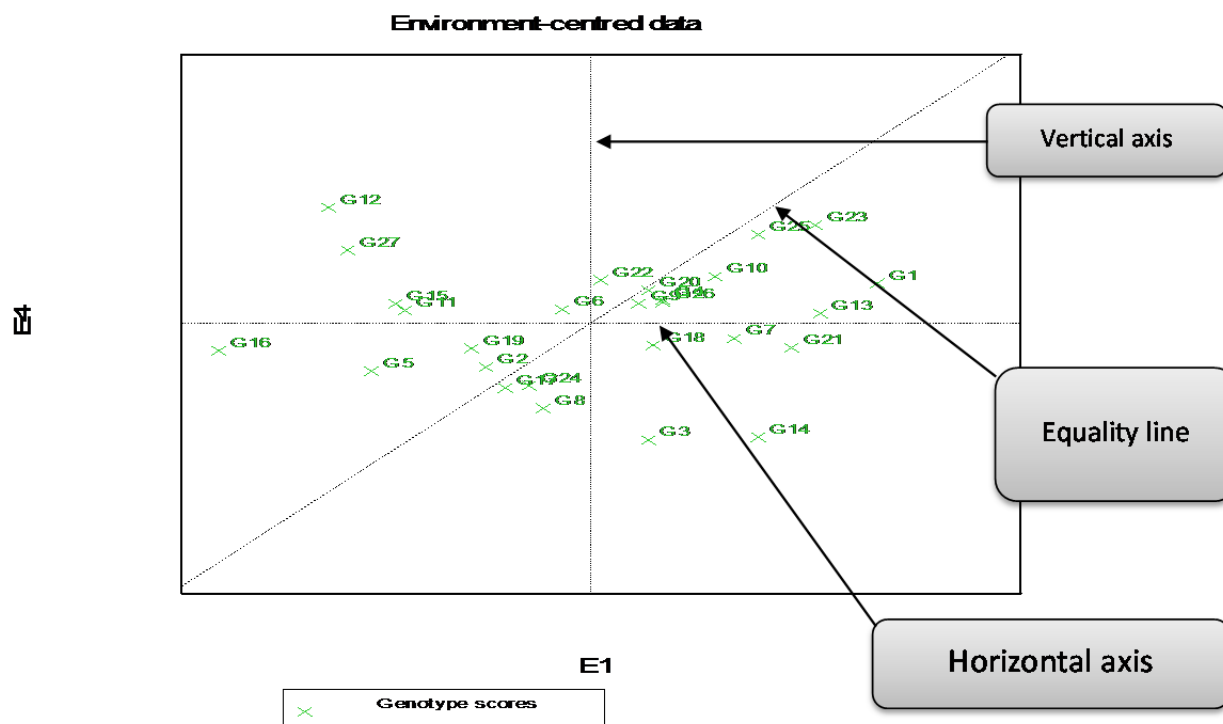


Figure 7. Centered scatter plot for genotype in two environments (E1 and E4).

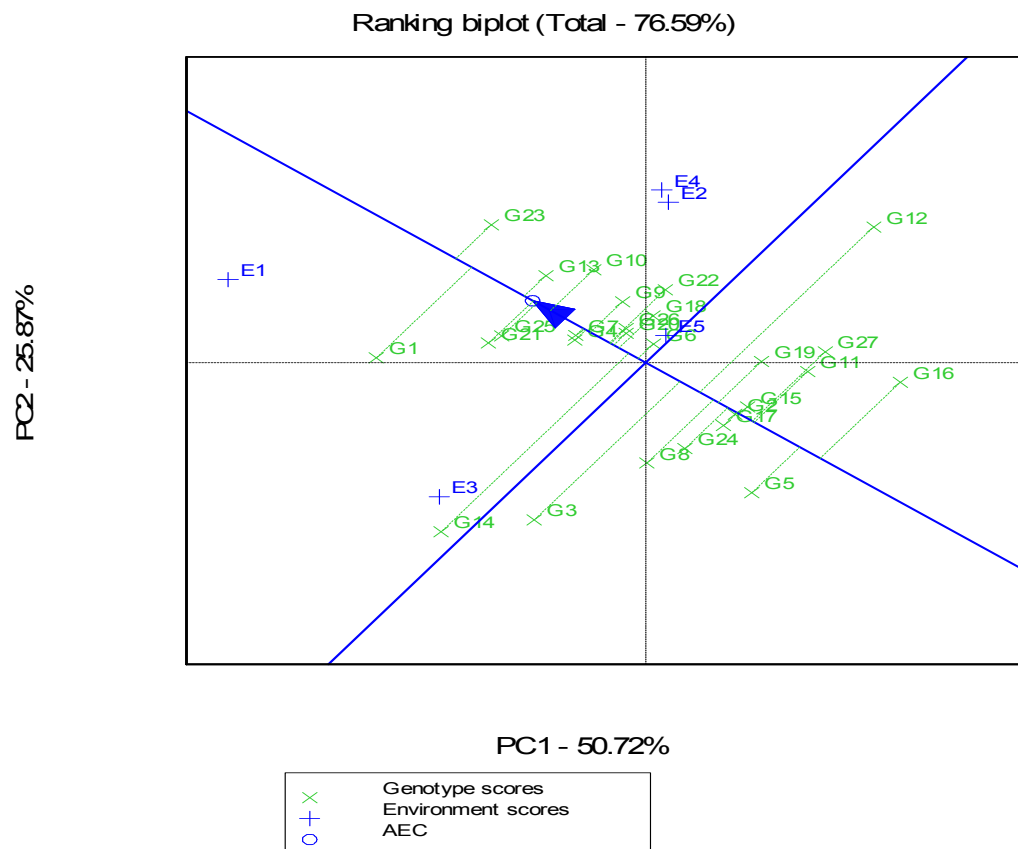
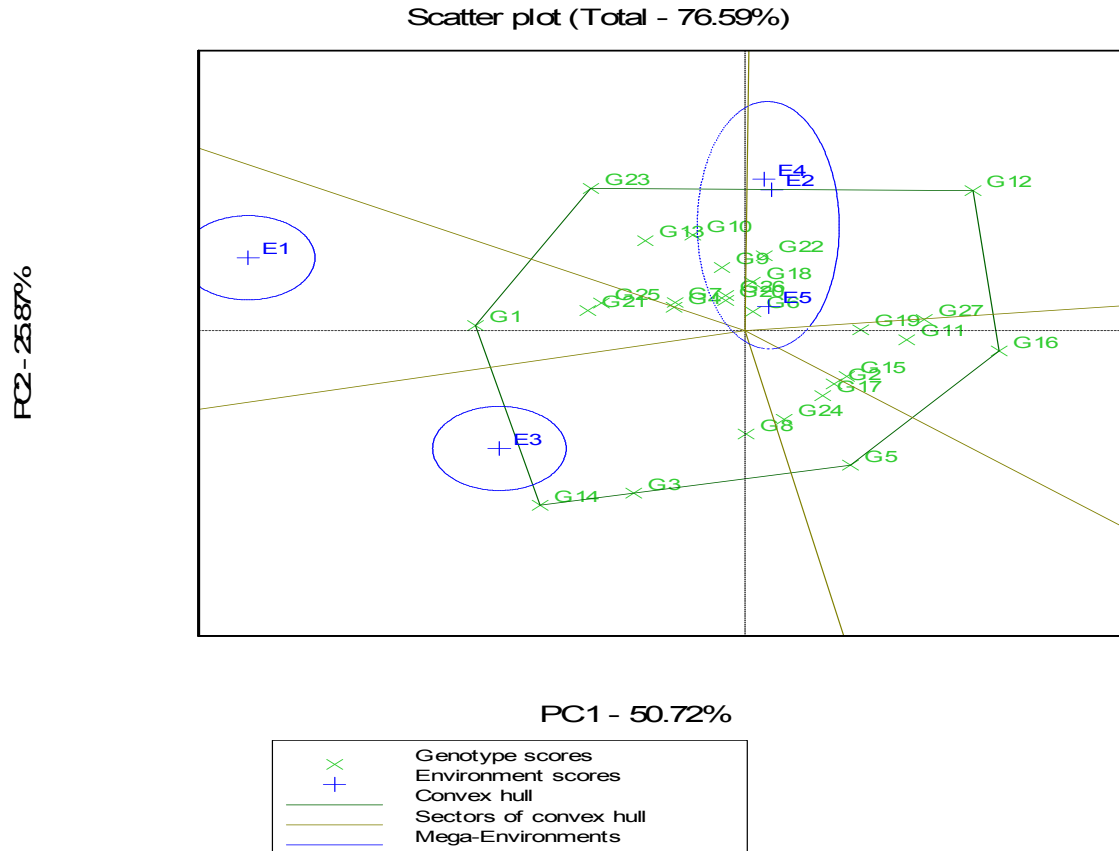


Figure 8. Ranking plot based on mean performance and stability.



**Figure 9.** The which-won-where view of the GGE biplot to show which genotypes performed best in which environments (mega-environment Identification).

but low yielding, whereas genotypes G4, G7, G26 and G20 are the most stable and high yielding; hence, can be selected as the most favourable genotypes. However, G12 and G14 are the most unstable even though G14 is above mean yield more than the low yielders but G17, G2 and G15 are stable.

**Mega-environments (which-won-where)**

An important feature of the GGE biplot (which-won-where) was also predicted. In mega-environment identification process, furthest genotypes are connected together to form a polygon, and perpendicular lines are drawn to form sectors which will make it easy to visualise the mega-environments. Mega-environment concept requires multi-year data, but in this study, mega environment study was carried out and the results (Figure 9) indicated three mega-environments thus three environments, E2 (KADOMA), E4 (MATOPOS) and E5 (SAVE VALLEY) formed one mega-environment, while E1 (GWEBI) and E3 (MAKOHOLI) formed two separate mega-environments, respectively. The winning genotypes for each sector are those positioned at the vertex. G12 is

the winning genotype for the mega-environment which consists of E2 (KADOMA), E4 (MATOPOS), E5 (SAVE VALLEY), while G14 is the winning genotype for E3 (MAKOHOLI) mega-environment and G1 (NL9411) winning genotype for the E1 (GWEBI) mega-environment. The equality line between G14 and G5 shows that the G14 was better than G5 in all environments. On the line that connects the two is G3 which also means the three can be ranked G14, G3 and G5 in all the environments.

**DISCUSSION**

As the pooled ANOVA showed the presence of GEI for the sorghum grain yield, it means a breeder faces challenge of selection genotypes for advancement and or release, hence further testing for genotypes with wider and specific adaptation and locations with good discriminating ability and representativeness was done. This is similar to the study which was done by Gasura et al. (2015), where they tested 20 sorghum varieties and there was a large effect of GEI about seven times larger than the effect of genotypes. The GGE biplot analysis showed that IPCA1 accounted for 50.72% and IPCA2

accounted for 25.82%, both accounting for a sum of 76.59% (Figure 1) and this showed similarity with study of Gasura et al. (2015) where PC1 and 2 explained 36.8 and 29.5%, respectively. The biplot analysis identified the discriminating ability and representativeness as well as the correlation of environments (Sujay et al., 2014) and genotype average performance and the results showed the importance of testing and comparing genotypes so as to select the ones with specific and wide adaptation accordingly and environments which are representativeness to reduce experimenting costs by discarding unrepresentative locations and those with poor discriminating abilities. The greater IPCA1 shows greater discriminating ability of an environment. This gives the importance of determining the discriminating ability to enhance separation through differences in performances of different genotypes. The results revealed that E5 though low yielding but gave more information on the tested genotypes than the other environments as was also detected by Yan and Kang (2003) when they used the GGE vector view plot. So this study provides important information on selecting and releasing best and ideal genotypes which are good for production in specific and widely adapted environments as well as determine the most effective and necessary environments which gives more information on varieties in future breeding trials.

Identification of mega-environments (Figure 9) was studied also and very important information on which-won-where was unveiled in the results obtained. The mega-environment identification involved a situation whereby one or more environments with similar or homogenous characteristics were bunched into one big location, like in this study where E2, E4 and E5 were bunched into one environment meaning in the future, costs of raising multi-locational trials will be reduced by putting that effect into consideration. Which-won-where (Yan et al., 2007) identified best winners for the mega-environment or sector. This enables the researcher to have specific and valid justification to recommend genotypes which are good for that particular environment (Gasura et al., 2015). This also means the genotypes can be tested in those few mega-environments and still good yield data results can be obtained. The GGE biplot also gave information which is important if a researcher has to make decisions and conclusions about specific correlations among environments and genotypes. The study results gave a better understanding of how biased a researcher can be if there is GEI and fails to do further GEI biplot analysis. The GGE have a lot of information which validates appropriate environment for testing and appropriate genotypes for selection and recommendation (Sujay et al., 2014), there was effective evaluation of environments and genotypes and evaluation of genotypes based on the mean performance and stability across environments which is important required information for a researcher.

In conclusion, the results showed that the grain yield performance of the 27 genotypes was significantly influenced by environment, genotype and their interaction. A further analysis on the adaptability and stability across the 5 environments was done. G1, G23, G21 and G25 showed both high yielding and stability across the test environments. These have been identified as possible candidates for advancement, for release and for use as parents in future breeding programmes. Test environments E1-Gwebi, E2-Kadoma and E4-Matopos were the most discriminating locations which means they gave more information on the performance of the varieties. However, only E1-Gwebi showed good discriminating ability, and representativeness, making it the most ideal environment in this multilocational yield trials.

## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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