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Pod yield stability and adaptation of groundnut (*Arachis hypogaea* L.) genotypes evaluated in multi-environmental trials in Zimbabwe

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Twenty-five groundnut genotypes were evaluated to identify the types of Genotype-Environment-Interaction (GEI) for pod yield. Genotypes were evaluated under multi-environmental yield trial conducted in 2013/14 season at five environments. The objectives of the experiment were to: identify genotypes with high pod yield stability, to identify genotypes with specific/wide adaptation, identify groundnut mega environments and identify an ideal environment. ANOVA was performed using GenStat Version 14. The results of the ANOVA indicate that there was GEI. The environments (E) and the interaction between the genotype and the environment were significant. GGE biplot analysis for yield data was the performed. The partitioning of GGE through GGE bi-plot analysis indicated that principal coordinate 1 and 2 (PC1 and PC2) explained 59.22 and 20.17% of GGE sum of squares, respectively, explaining 79.39% of the total variation. This large percentage variability of GGE (79.39%) accounted by the bi-plot indicates that there was complex GEI. The environment and genotype explained 58.8 and 6.1% respectively of the total treatment variance, while the genotype by environment interaction accounted for 35.1%, indicating that the environment had huge influence on genotype performance. The results revealed the existence of mega-environments, most ideal environment and genotypes with specific and others with wide adaptation. The results indicate that certain genotypes may be released for commercial production in specific environments based on their performance.

Key words: Groundnut, genotypes, pod-yield, multi-environmental trial, genotype x environment interaction, discriminating, representative.

INTRODUCTION

Groundnuts does not only provides high quality edible oil (48 to 50%), easily digestible protein (26 to 28%), nearly half of the 13 essential vitamins (e.g. Vitamin E, K and B) and seven of the essential minerals necessary for normal

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human growth but it also produces high quality fodder for livestock (Monyo et al., 2012), and is also the richest source of thiamine and niacin which is low cereals, it is thus important for nursing mothers, babies and pregnant women. It thus plays a significant role in the livelihoods of marginal farmers through income and nutritional security (ICRISAT, 2006 and Monyo et al., 2012). Unsaturated fatty acids such as linoleic and oleic acids are also abundant in groundnuts.

The haulms are processed into groundnut cake, which is a high protein source for livestock. Peanuts are rich in energy; one pound of peanuts provide approximately the energy value of 2 Ib of beef, 1.5 Ib of Cheddar cheese, 9 pints of milk or 36 medium size eggs (Carley and Stanely, 1993). Peanuts are sold fresh as a vegetable, canned, frozen, roasted in shells, toasted and salted, used in more than 50 confections and bakery products and are ground into butter for use in more than 100 recipes. In actual fact, every part of the peanut plant is used for one purpose or another like for food, feed or agribusiness; the halls for fuel, mulch, feed and industrial uses. The leaves and stems for feed, soil conditioning, soil nutrients, and possible protein extraction for special diets; the roots are essential for soil enrichment through atmospheric nitrogen fixation and fibre; and the oil from seeds for food, lubrication and motor fuel. As much as breeding all other crops is important, this is by far one of the most crucial crops to put focus on, as it has a lot of uses than many other crops.

Groundnuts are an important crop in Zimbabwe, grown by a large proportion of smallholder farmers (36%); groundnuts are second after maize in terms of area coverage. Groundnuts can provide an important source of food and nutrition, feed and soil amendment, as well as income (Homann-Kee Tui et al., 2015).

Breeders throughout the world want to present data for candidate cultivars to the cultivar release panels for their products to be commercially recognized. In Zimbabwe data from at least five sites and at least two seasons is required. This goal is achieved by conducting a series of multi-environmental trials (MET) annually for all major crops to identify superior genotypes for the target locations (Kang, 1998). It has generally been accepted that the measured grain/pod yield for each cultivar in each test environment is in fact a measure of the environment main effect (E), the genotype main effect (G), and the genotype × environment (GE) interaction. The GE interaction results from the differences in responses of genotypes at different study locations (environments) (Gauch and Zobel, 1997; Yan et al., 2000; Yan, 2002).

This study was designed to (i) identify groundnut genotypes with high pod yield stability under different environments (ii) identify groundnut genotypes with specific or wide adaptations to certain environments (iii) examine the possible existence of mega environments among the environments which were used in this study (iv) identify most discriminating and best representative environment, that is, ideal environment.

Genotypes that always give high average yields with minimum G x E interaction have been gaining importance over increased yields whenever trials are conducted at many different environments or locations (Gauch and Zobel, 1997; Ceccarelli, 1989; Kang, 1998; Xing-Ming et al., 2007). The analysis of G x E interaction is closely related with the quantitative estimation of phenotypic stability of genotypes over different environments (Kang, 1998; Mohammadi and Haghparast, 2010). In the case that significant G x E interactions are observed, the effects of genotypes and environments are statistically non-additive, this implies that the differences between genotypes are due to the environment and not genotypes themselves. G x E interactions may, but not all the time, lead to different rank orders of genotypes in different environments, that is, they result in non-crossover and or crossover interactions (Sharma et al., 2009). Yield stability analysis is usually performed using many different models including GGE biplot analysis whenever there is a presence of G x E interaction in multi environment trials (Yan and Tinker, 2006). Many authors have described yield stability in many different ways over the years and there have also been different concepts of stability tests (Lin et al., 1986). According to Becker and Leon (1988), many researchers use the terms adaptation, phenotypic stability and yield stability in different ways. Chahal and Gosal (2002) noted that stability indicates consistency in performance that would mean minimum variation among environments for a particular genotype.

GGE biplot (Yan et al., 2000) is one of the best and very important tools for graphical analysis of multi-environment trials (MET) data. GGE denotes genotypic main effect (G) plus the interaction of the genotype and the environment (G x E interaction). These have been considered to be the two main sources of variation that are important to assessment of genotype performance across different locations. The biplot is constructed by plotting the first two principal components (PC1 and PC2) and these are also referred to as primary and secondary effects respectively. The PC1 and PC2 values are derived from singular value decomposition (SVD) of the environment-centered data. The GGE biplot analysis is used to identify some of the most and the least discriminating locations and representative test locations as well as the non-representative locations (Fan et al., 2006). The GGE biplot analysis methodology is a very important tool for categorizing sites that lead to optimum cultivar performance and efficient utilization of limited resources available for most of the breeding and other testing programmes (Fan et al., 2006).

The main genotype effect (G) and the genotype x environment interaction effect (GEI) is shown by the GGE bi-plot. The GGE bi-plot shows the first 2 principal components (PC1 and PC2) that are derived from subjecting environment centered yield data to singular

Table 1. Pedigree information and source of Spanish groundnut genotypes of medium seed size.

Variety/Line Code	Pedigree	Breeding status	Origin
G1	297/7/29	Intermediate line	C.B.I
G2	302A/6/2	Intermediate line	C.B.I
G3	401/92/14	Intermediate line	C.B.I
G4	262/4/3	Intermediate line	C.B.I
G5	AB/5/11	Intermediate line	C.B.I
G6	321/5/15	Intermediate line	C.B.I
G7	9607/5/14	Intermediate line	C.B.I
G8	9503/6/11	Intermediate line	C.B.I
G9	267/6/13	Intermediate line	C.B.I
G10	9607/5/10	Intermediate line	C.B.I
G11	9607/5/22	Intermediate line	C.B.I
G12	294/5/16	Intermediate line	C.B.I
G13	9503/6/5	Intermediate line	C.B.I
G14	294/5/16	Intermediate line	C.B.I
G15	374/92/16	Intermediate line	C.B.I
G16	9607/5/11	Intermediate line	C.B.I
G17	296/5/4	Intermediate line	C.B.I
G18	295/5/8	Intermediate line	C.B.I
G19	H97/3F7/1	Intermediate line	C.B.I
G20	H97/14F7/1	Intermediate line	C.B.I
G21	267/6/6	Intermediate line	C.B.I
G22	Falcon	Released	C.B.I
G23	Tern	Released	C.B.I
G24	Jesa	Released	C.B.I
G25	Ilanda	Released	C.B.I

value decomposition (Yan et al., 2001). PC1 scores of both genotypes and environments are then plotted against their respective PC2 scores. This methodology has been widely used to determine grain yield stability and identify superior, identify superior, specifically adapted, and generally adapted genotypes as well as identifying groundnut mega environments (Yan et al., 2007).

MATERIALS AND METHODS

A total of 25 genotypes (4 commercially released varieties and 21 experimental lines) were tested in 2013/14 season. All the check varieties and the intermediated experimental lines were obtained from Crop Breeding Institute (C.B.I). Ilanda and Tern are the highest yielding short season groundnut varieties in Zimbabwe and for that reason they were included as check varieties. More details on genotypes and the information on their breeding status are highlighted in Table 1.

Study site

The project was conducted at five locations; Harare Research Station (HRS), Panmure Experimental Station (PES), Gwebi Variety Testing Centre (GVTC), Save Valley Experimental Station (SVES) and Kadoma Research Station (KRS). Two of the locations belong to high veld (Harare Research Station and Gwebi VTC, the other two to middle veld (Kadoma Research Station and Panmure Experimental Station) and one belongs to the low veld (Save Valley Experimental Station). More details on the testing sites and the agro-ecological characteristics for all the locations used are shown in Table 2.

Management

The seeding rate was 100 kg/ha for all environments because the seed that was planted were Spanish varieties that have medium seed size. Compound D was applied at planting at a general recommended blanket rate of 300 kg/ha. A special request was done at all the sites that the crop was planted in a field where the previous crop was maize, and that was accomplished. Gypsum was also applied during first flowering (7 to 8 weeks after planting) at a general recommended rate of 300 kg/ha. Harvesting was done manually, were 2.4 m (0.3 m from either sides of the row) of the 3 m rows were harvested as net plot by way of hand pulling as well as hand plucking. Pod yield was then recorded after drying the groundnut pods to 12.5% moisture content by exposing the pods to the sun and moisture content was measured using the moisture meter. All other recommended groundnut production practices such as weed, pest and disease management were followed and practiced.

Table 2. Description for the sites used on the multi-environmental groundnut yield trials in 2014.

Code	Location	Soil properties	Latitude	Longitude	Altitude (masl)	Rainfall data (mm)
E1	Harare	Clay	17° 48 S	31° 03 E	1506	660
E2	Gwebi VTC	MG/SCL	17° 41 S	30° 32 E	1448	880
E3	Kadoma	Clay	18° 19 S	29° 53 E	1149	818
E4	Panmure	MG/SCL	17° 16 S	31° 47 E	881	796
E5	Save Valley	Sandy-loam	20° 48 S	33° E	450	500

Experimental design

The trials were laid in a Complete Randomized Block Design (CRBD) at all the sites. Each of the twenty-five treatments with 3 replicates and that translated to seventy-five plots in total. The plot sizes were 5.4 m^2 with 5 rows of 3 m long with spacing of 0.45 m between rows. The net plot sizes were 2.16 m^2, 1 row from both sides and 0.3 m from either side were discarded.

Data collection

Data collection includes, days to 50% flowering, days to 75% maturity, diseases scores, insect pest scores, pod size, seed size, shelling percentage and pod yield. For the sake of this study, only pod yield was considered for statistical analysis. Pod yield was recorded on the net plot basis. After drying and cleaning, the weights of the pods per plot were recorded and converted to t/ha using a formula (yield in grammes × 10 000/ (Net plot × 1000 for kg × 1000 for tonnes).

Analysis of variance

Analysis of variance (ANOVA) for pod yield data was conducted using GenStat 14th Edition software to determine the G, E and GEI effects. The effects of the genotypes, environments as well as their interaction were determined from ANOVA analysis.

Yield stability analysis

To determine pod yield stability and identify superior and well adapted genotypes across locations and ideal site(s) (most discriminating and representative) as well as determining mega-environments, (GGE) bi-plots (Yan, 2001) was done using GGE bi-plot software. The GGE bi-plot methodology is composed of two concepts, the bi-plot concept and the GGE concept.

GGE bi-plot analysis

Genotype + Genotype x Environment (GGE) bi-plots were conducted using GGE bi-plot software in GenStat 14.1 to determine pod yield stability and identify superior, specifically adapted, generally adapted genotypes as well as identifying groundnut mega environments. The GGE bi-plot methodology is composed of two concepts, the bi-plot concept and the GGE concept (Yan et al., 2001). GGE biplots were also used to compare genotypes performance with a reference genotype (ideal genotype). The ideal genotype is usually an imaginary genotype that will be stable and have the highest average mean value among the genotypes. Correlation coefficients among environments were also conducted. Which-one-where pattern of multi environment yield trial was visualized using symmetric scaling within the GGE biplots (Hunt and Yan, 2002).

Discrimination ability, representativeness, mega-environmets and relationships among test environments

The relationship among environments and comparing among a set of environments with discriminating ability and representativeness was conducted using the GGE bi-plot analysis. The correlation between two environments can be approximated by the cosine of the angle between the vectors of two environments. Any two environments can be positively, negatively or not correlated if the angles between their vectors are less than 90°, more than 90° or equal to 90° respectively (Sharma et al., 2009).

RESULTS AND DISCUSSION

ANOVA and mean yield performance

Analysis of variance at 5% significance level was performed and the results indicated that genotypes (G) were not significant ($p = 0.153$), but environments (E) and genotype x environment interactions (GEI) were highly significant both at same significance level ($P < 0.001$) on pod yield of twenty-five groundnut genotypes (Tables 3 and 4). The presence of significant interaction between the genotype and the environment lead the researcher to perform pod yield stability and adaptation analysis of the different genotypes using GGE biplot analysis with the results that are presented below.

Pod yield stability and adaptability analysis

The GGE biplot methodology has been used to evaluate test environments in soybean (Yan and Rajcan, 2002), cotton (Blanche et al., 2008), and common bean (Kang et al., 2006). Using the same methodology, Ober et al. (2005) managed to evaluate physiological traits as indirect selection criteria for drought tolerance. The results on GE main effects and the first principal component scores of the interactions summary information for both genotypes and environments are shown in Figure 1. The partitioning of GGE through GGE bi-plot analysis indicated that principal coordinate 1 (PC1) and principal coordinate (PC2) significantly explained

Table 3. Analysis of variance for pod yield (t/ha) of twenty-five groundnut genotypes evaluated across five locations over a season.

Source	DF	SS	MS	% total sum of squares
Rep stratum	2	0.8646	0.4323	
Genotype	24	29.2839	1.2202	4.1
Environment	4	281.8406	70.4602***	39.7
Genotype.Environment	96	168.4375	1.7546***	23.7
Residual	248	229.8636	0.9269	
Total	374	710.2903		

Coefficient of variation (%CV) = 18.1%.

Table 4. ANOVA table for AMMI model.

Source	df	SS	MS	Percentage total sum of squares	Percentage treatment	% G x E
Total	374	710.3	1.899			
Treatments	124	479.6	3.867***	67.5		
Genotypes	24	29.3	1.22	4.1	6.1	
Environments	4	281.8	70.46***	39.7	58.8	
Block	10	9.9	0.989			
Interactions	96	168.4	1.755***	23.7	35.1	
IPCA I	27	100.4	3.719***			59.6
IPCA II	25	39.6	1.584*			23.5
Residuals	44	28.4	0.646			16.9
Error	240	220.8	0.92	31.1		

Genotype + (Genotype x Environment) (GGE) biplot analysis.

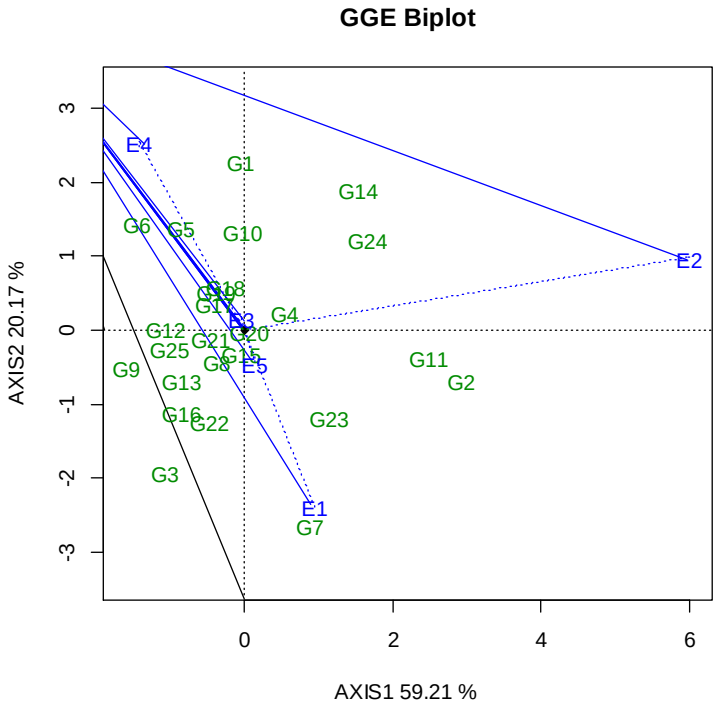

Figure 1. The discriminating ability and relationship among 5 environments based on 25 groundnut genotypes.

59.22 and 20.17% of GGE sum of squares, respectively, explaining a total of 79.39% variation. This moderate percentage variability of GGE (79.39%) accounted by the bi-plot indicates that there is strong and complex GE interaction in this multi-environment yield trial data. The presence of GEI resulted in differential pod yield performance among the groundnut genotypes across five testing environments that were used in this study (Crossa et al., 1991).

Genotypes or environments with high positive PC1 scores are high yielding or high potential locations respectively. In the biplot (Figure 1) G2 and G11 had the largest positive PC1 score indicating that they were high yielding and E2 (Gwebi VTC) had the largest PC1 score indicating that it is a high potential environment. On the other hand, genotypes or environments that had PC1 less than zero scores were identified as lower yielding or low potential locations respectively, for instance, according to the biplot (Figure 1) G9, G3 and G6 were the lowest yielders and E4 (Panmure) was a low potential environment.

The PC2 is associated with genotypic stability or instability across environments. Genotypes with low positive or low negative PC2 scores (scores near zero) are more stable than those with large PC2 scores (Yan and Tinkler, 2006). In this study, there are a lot of genotypes located on the negative side of PC1 and they included 2 check varieties (G22 and G25) as well as many experimental genotypes implying that these genotypes were low yielding. There are promising elite breeding lines that bear potential as candidate genotypes for release. Genotypes G2, G11, G14, G7, G4, G20, G15 and G10 were generally high yielding with G2 (moderately stable) being the overall best (largest PC1 score). The results agreed with (Sharma et al., 2009) who stated that higher yielding genotypes are not always the most stable across environments. On the other hand, the genotypes G9, G6, G25, G12, G3, G5, G13, G16, G22, G21, G17, G19 G8 AND G18 were generally low yielding, with G3, G6 and G5 being part of the most unstable genotypes (Figure 1). Genotypes that are not stable are not desirable as this has a negative effect on farmers' income and, in the case of staple and legume crops, contributes to food and nutrition insecurity at household and national level (Simmonds, 1991). The genotypes G12 and G21 were consistently poor performing hence the high stability. Even though G12 was most stable genotype, it was the least performing genotype (highest negative PC1 score) with low yields in different environments.

The genotypes formed at least four groups on the bi-plot (Figure 1): 'G25, G8, G9, G13, G17, G18 and G19' generally low yielding, and moderately stable (near zero PC2 scores); 'G6, G5, G16, G22, G3 and G1'generally low yielding and highly unstable (variable) across environments (high positive and negative PC2 scores). Genotypes 'G15, G2 and G11' were generally high yielding, and moderately stable across environments (high positive PC1 scores); 'G20 and G4' were generally high yielding, and stable genotypes (absolute PC2 scores near zero) across environments (positive PC1 scores). This indicates that these genotypes may be suitable for growth in a wide range of environments. The genotypes 'G7, G10, G14, G24 and G23' formed the other group which consisted of generally high yielding and unstable genotypes across environments. The superior, high yielding and stable experimental genotypes 'G20 and G4' can be used to crossing with other genotypes (especially those that are high yielding and unstable, because only traits of being stable need to be introduced) to improve pod yield and stability across environments. This is important and appropriate especially considering that the superior genotypes differed in their genotypic background; and therefore probably there are high chances that these genotypes could provide opportunities for genetic gain through recombination of superior alleles.

Genotypes G12, G21 and G20 had the most consistent performance, being high stable with G20 being high yielding and G12 and G21 being low yielding because their absolute PC2 scores were almost at the zero line (Figure 1). Therefore, these three genotypes had little interaction across environments indicating that G20 had broad adaptations and G12 and G21 are well adapted to the low potential environments (Akcura et al., 2011). According to Akcura et al. (2011), genotypes with PC2 values near zero would have had little interactions across environments and vice versa for environments.

Projected lines perpendicular to the AEA measures the stability of the genotypes in either direction. Genotypes with smallest perpendicular lines with AEA are called stable cultivars (Yan and Tinker, 2006). Genotypes G20 and G4 were the most stable and productive genotypes in the different environments (shortest perpendicular line) (Figure 2). G12, G21 and G25 were also very stable genotypes but low yielding. Genotypes, G10 and G23 were moderately stable in the environments (moderately shorter perpendicular lines with AEA). G1 and G7 were the most unstable high yielding genotypes across the environments (longer per perpendicular lines to the AEA). The rest of the genotypes were low yielding, among them some were unstable, moderately and some highly stable (Figure 2). The following genotypes yielded above average: G2, G11, G14, G24, G23, G4, G7, G1, G10 and G20 (according to their ranking order) with G2 and G11 being the highest yielders (Figure 2).

An ideal genotype (centre of the smallest concentric circle), is usually an imaginary genotype that is both high yielding and high stable across all the environments (Yan and Tinker, 2006). The best genotypes are identified basing on the concentric circles like those in Figure 3. According to the GGE biplot above G11 (highlighted in blue circle) was found to be the best genotype as it fell on the circumference of the smallest inner concentric circle. This implies that this genotype was the most stable and

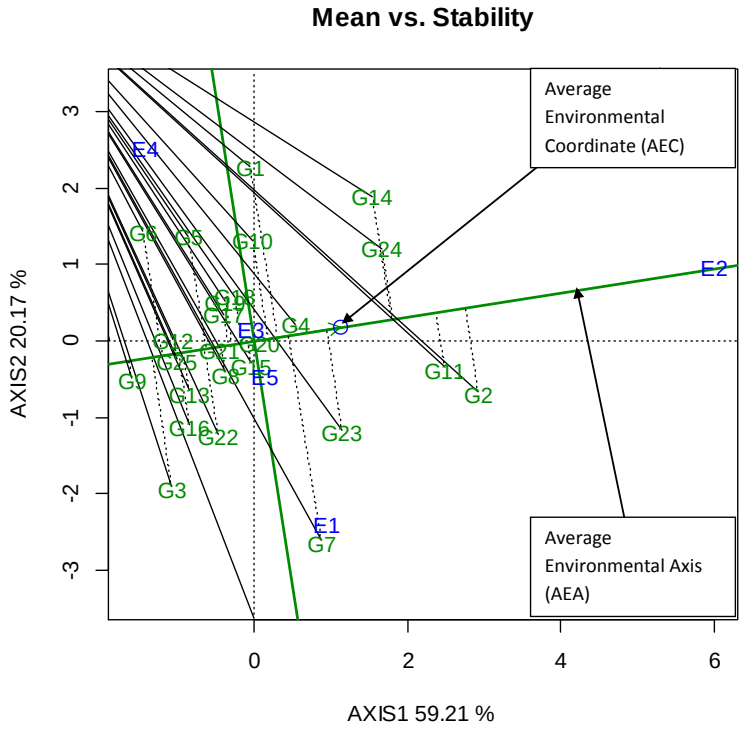

Figure 2. Ranking plot based on mean performance and stability.

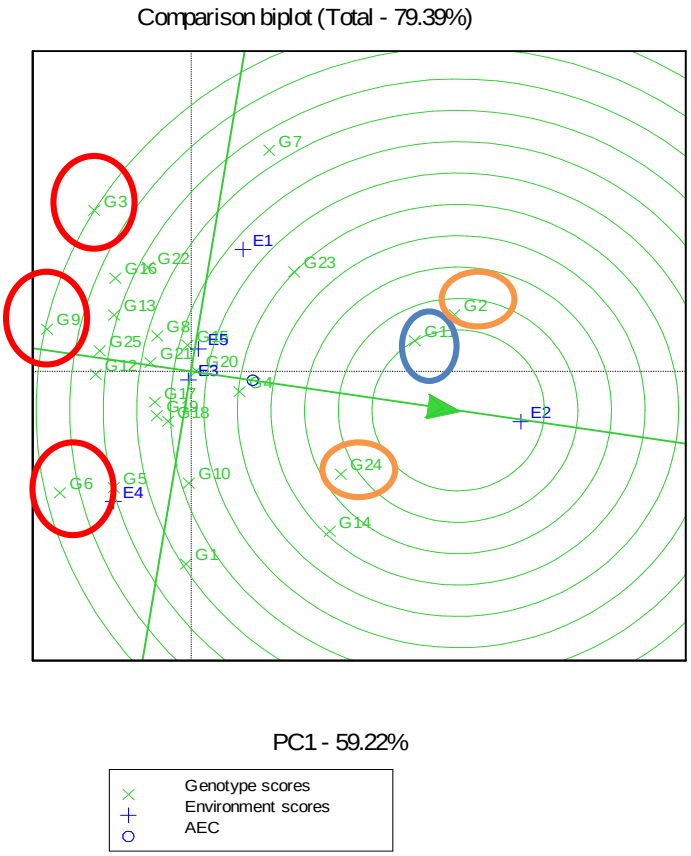

Figure 3. Comparison Plot for genotypes (relative to the ideal genotype).

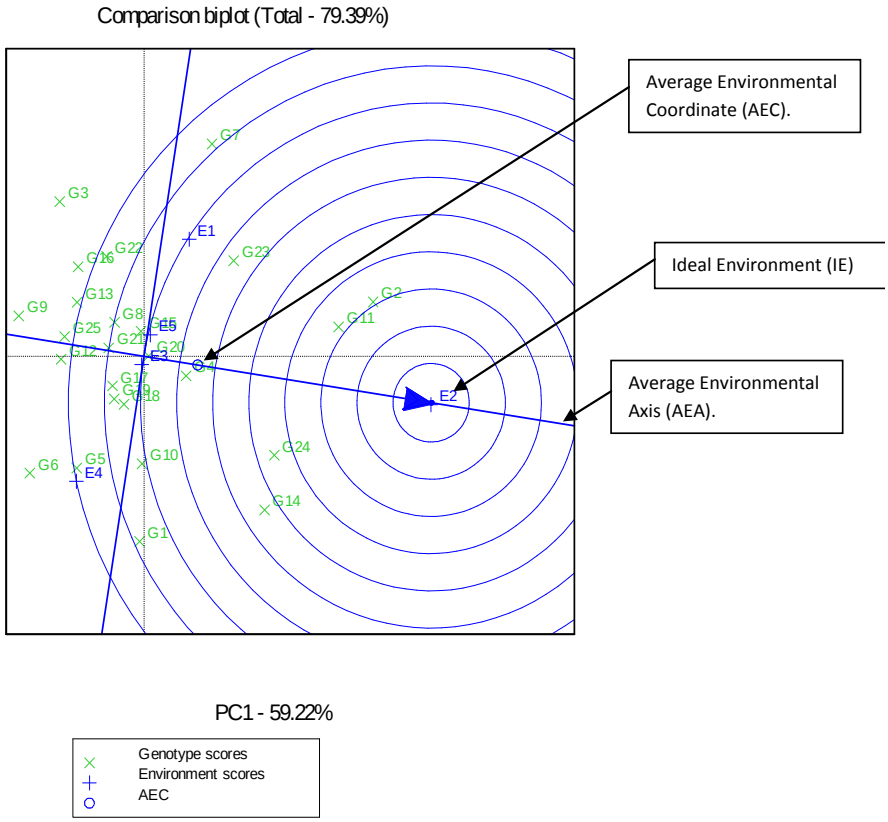

Figure 4. Discriminating ability vs. representativeness of test environments; average environment.

high yielding at the same time (Yan and Tinker, 2006). The best genotype according to this study may not be the most stable cultivar. Genotypes G2 and G24 (highlighted in oranges circles) were the next best genotypes as they lied on the circumference of the second concentric circle and just outside the second concentric circle respectively. The implication is that these two genotypes failed to strike a balance between high yielding and stability as G11 did (Yan and Tinker, 2006). According to the biplot (Figure 3), G9, G3 and G6 (highlighted in red circles) were the most unfavourable and most undesirable genotypes as they lie in the last outer concentric circle.

Best test environment for groundnut genotypes

GGE biplot is a data visualization tool, which graphically shows a GxE interaction in a two way table (Yan et al., 2000). The analysis of GGE biplot is useful for: 1. mega-environment identification (e.g. “which-won-where” pattern), that help to recommend specific genotypes to their suitable mega-environment 2. Evaluation of genotypes performance (genotypic stability) and 3. The environmental evaluation (the power to discriminate among genotypes in target environments) (Yan and Kang, 2003; Yan and Tinker, 2006). Lines that connect the environment to the origin of the biplot are known as the environmental vectors (EV). The length of the environmental vectors is proportional to their standard deviation which is a measure of discriminating ability of a particular environment (Yan and Tinker, 2006). In this particular study, environment E2 (Gwebi VTC) had the longest environmental vector, implying that, it was most discriminating environment (Figures 1 and 4). Environments E4 (Panmure) and E1 (Harare) also had long environmental vectors, meaning that they also have the capacity to discriminate genotypes according to their genotypic performance. Environments E5 (Save Valley) and E3 (Kadoma) had the shortest environmental vectors (Yan and Tinker, 2006), implying their inability to discriminate varieties basing on their genotypic performance (Figures 1 and 4). Any two environments can be positively, negatively or not correlated if the angles between their vectors are less than 90°, more than 90° or equal to 90° respectively (Sharma et al., 2009) respectively. Each environment was connected to the bi-plot origin using a vector to determine the discriminating ability of test environments. Environments with longer vectors are known to be more discriminative of the genotypes than those with short vectors discriminative (Sharma et al., 2009). An environment with a small angle to the average environment axis (AEA) is

more representative of other test environments. Ideal test environments should have near zero PC2 scores (more representative of the average environment) (Yan et al., 2001). Therefore, the biplot shows that E1 (Harare) and E5 (Save Valley), E3 (Kadoma) and E4 (Panmure) are positively correlated, E1 (Harare) and E2 (Gwebi VTC) are slightly positively correlated, E3 (Panmure) and E2 (Gwebi VTC) are not correlated and the same applies for E2 (Gwebi VTC) and E4 (Panmure) (the angle is about 90°). Environments E1 (Harare) and E4 (Panmure), E4 (Panmure) and E5 (Save Valley) as well as E1 (Harare) and E3 (Kadoma) are negatively correlated, E1 (Harare) and E5 (Save Valley) are negatively correlated to E3 (Kadoma) and E4 (Panmure) shown by the biplot (the angle between the environmental vectors is more than 90°). Environments E2 (Gwebi VTC) and E5 (Save Valley) as well as E2 (Gwebi VTC) and E3 (Kadoma) are not correlated. Similarity of the environments in their discriminating ability is obtained when there is a combination of similar environmental vector length and an acute cosine angles between the vectors (Yan and Tinker, 2006). Therefore, there was dissimilarity in discriminating ability among all the environments; this is shown in the biplot (Figure 1) by the combination of different lengths in the environmental vectors and the large angles between the environments with similar lengths of the environmental vectors (Yan and Tinker, 2006).

The GGE methodology has been used to target cultivars to specific environments in rice (Samonte et al., 2005), that is, specific adaptation. The length of the environmental vectors is proportional to their standard deviation which is a measure of discriminating ability of a particular environment (Yan and Tinker, 2006). An environment whose environmental vector has a smaller angle with the Average Environmental Axis (AEA) is known to be representative. Being representative is the ability of the environment to allow the genotypes to perform more or less the same as they would do in any other environment in the study. In this study, environment E2 (Gwebi VTC) is an ideal environment because it is both representative (smaller angle to the AEA) and highly discriminating (longer EV). This environment is an ideal environment because it lies at the centre of the first inner concentric circle (Figure 4). The same figures shows that, environments E1 (Harare) and E4 (Panmure) were only discriminating (longer EV) but not representative (larger angles to the AEA). These environments can be used to select for specifically adapted genotypes. E3 (Kadoma) and E5 (Save Valley) were neither discriminating (short environmental vectors) nor representative (large angle with the AEA) (Figures 1 and 4) (Yan and Tinker, 2006).

Mega-environment identification (which-won-where pattern)

A polygon connects all the furthest (the highest yielder in one or more environments) genotypes (Yan and Tinker, 2006). The GGE biplot (Figure 5) shows that there are 3 mega environments, of which two of the mega environments were intersecting at the biplot origin implying that they belong to one complex mega-environment. These results coincide with the conclusion that was reached by Rukuni et al. (2006) when they said Zimbabwe is a very small country but is very diverse, hence the reason why it is divided into 5 agro-ecological zones. In this study, genotypes G2, G14, G1, G6, G9, G3 and G7 were the highest yielders in one or more sectors, hence the furthest points on the polygon (Yan and Tinker, 2006). Perpendicular lines divide the polygon into sectors; hence in this case there are seven sectors. Sectors are the ones that are used to visualize mega environments. In view of the GGE biplot (Figure 5) based on G x E data exhibits crossover interaction, that is, there are different genotypes winning in different sectors. According to the GGE biplot Figure 5, for the locations that were used in the study there are three groundnut mega environments. Environment E2 (Gwebi VTC) was allocated its own mega environment; hence this was the only environment that was both discriminating and representative. Gwebi VTC is generally a high potential location, and according to Souta (2012) and Ceccarelli and Grando, (1997), high potential environments are usually highly discriminating and best representative. Environment E3 (Kadoma) and E4 (Panmure) were clustered into same mega-environment. Environments E1 (Harare) and E5 (Save Valley) were also clustered into the same environment. Harare is generally high potential location that under normal conditions it was not supposed to have been clustered (but could have been clustered with Gwebi VTC) into the same mega environment with Save Valley which is inherently a low potential area due to its unfavourable climatic conditions and type of soil. Ideally high potential locations are generally highly discriminating and representative (Yan and Tinker, 2006). The reason for this phenomenon is the delay in planting that transpired at Harare, leading to the crop spending most of its growing time exposed to the decreasing temperatures in this environment. The crop at Harare also experienced mid-season drought during flowering, pegging periods as well as early podding, hence the reduction in the pods that where set and automatically achieved low yields that match those at Save Valley. Winning genotypes for each sector are located at the vertex. Genotypes G2, G14, G1, G6, G9, G3 and G7 are the ones that are on the vertex meaning that they the winning genotypes of those particular sectors.

Conclusion

GGE biplot analysis made the reseacher to understand that there were high levels of interaction between the environments and the genotypes. Environment explained much of the variation amoung the genotypes, and this

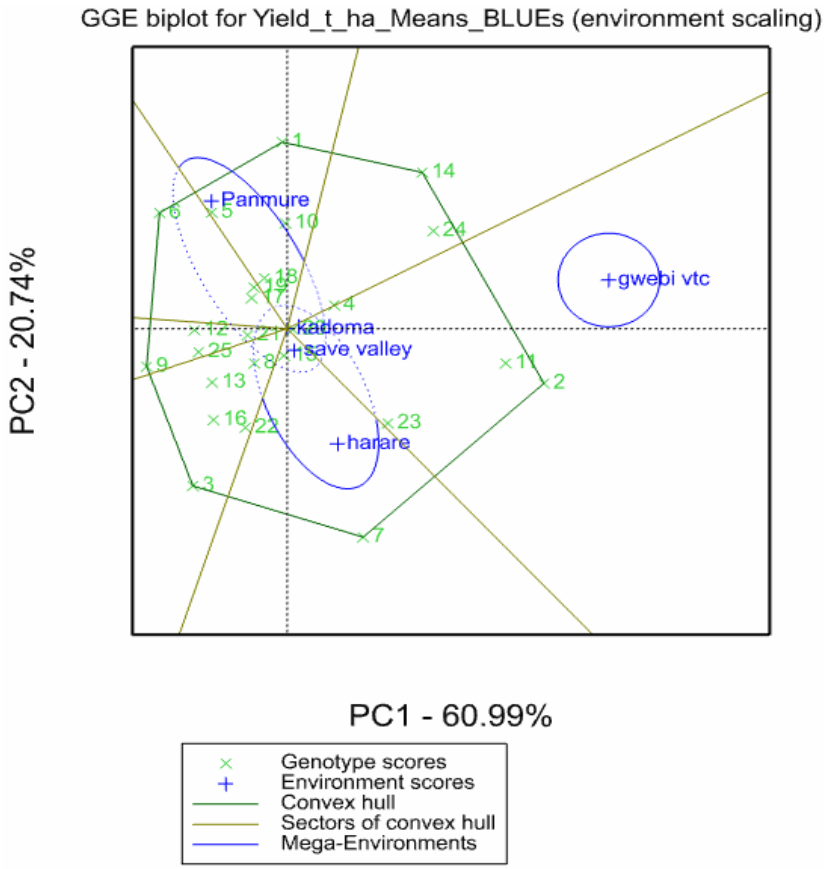

Figure 5. Which-Won-Where pattern.

was evidenced by the high percentage contribution to the total sum of squares.

Widely adapted genotypes were identified to be G20 and G4, with G4 being the most productive. These two genotypes are then recommended for further testing and released to be grown across all the environments. G12, G21 and G25 were also highly stable but cannot really be recommended for production across the environments since they were yielding below average. On the other hand G2 and G11 were identified to be the most productive genotypes but lacked stability. The two genotypes were recommended for further testing and released specifically for high potential environments because they were more adapted in those environments, since government policy allows this kind of decisions to be made.

Ideal environment was identified to be Gwebi VTC. The implication of this is that this environment is both highly discriminating therefore can be used in the early generation genotypic screening. It also shows that this environment is representative of others; so as to save resources this location can be used with a few other locations to acquire data for release. In the event that there are no enough resources to establish trials at all the sites, either Kadoma or Save Valley can be chose since they represent each other. Three mega environments were identified and these were: i. E2 (Gwebi VTC), ii. E1 (Harare) and E5 (Save Valley) and iii. E3 (Kadoma) and E4 (Panmure). There is need to validate of this information through the use of more sites and seasons is recommended.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

Abbreviations

GEI, Genotype-environment-interaction; **E**, environment; **G**, genotypes; **PC1**, principal coordinate 1; **PC 2**, principal coordinate 2; **ANOVA**, analysis of variance.

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