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ASSESSMENT OF GENOTYPE BY ENVIRONMENT INTERACTIONS AND GRAIN YIELD PERFORMANCE OF ESWATINI MAIZE (*Zea mays* L.) LANDRACES

Victor B. Simelane*[1, 2], Angeline Van Biljon[2], Adre Minaar-Ontong[2], Thembinkosi Gumedze[3]

[1]Department of Crop Production, Faculty of Agriculture, University of Eswatini, PO Luyengo, Eswatini
vsimelane@uniswa.sz
[2]Department of Plant Sciences (Plant Breeding), Faculty of Natural and Agricultural Sciences, University of the Free State, P.O. Box 339 Bloemfontein 9300, Republic of South Africa Avbiljon@ufs.ac.za, minnara@ufs.ac.za
[3]National Plant Genetic Resources Centre, Department of Agricultural Research and Specialist Services, Ministry of Agriculture, Eswatini tg.tgumedze@gmail.com

ABSTRACT

Maize (Zea mays L.) is one of the important commercial crops of the world. Beside its uses as food and feed, maize is a priority and strategic crop to respond to the world's pursuit for alternative energy sources. In Eswatini, it ranks first in total production and yield per unit area and it is the staple crop for the majority of Swazis, especially those in rural areas. It is grown by both large-and small-scale farmers in the different agro-ecological zones of the country. The decision to recommend and distribute high yielding and adapted maize cultivars to these agro-ecological zones involves conducting multi-environment trials (METs) to identify the best cultivar across locations and years. Seventy (70) diverse maize landraces (accessions) conserved ex situ at the National Plant Genetic Resources Centre (NPGRC) were evaluated across three (3) locations during the 2016/2017 and 2017/2018 cropping seasons. The objectives of the study were to determine the extent and nature of genotype-by-environment interaction (GEI) on grain yield based on analysis of variance (ANOVA) procedures and to identify landraces that are specifically or widely adapted. The combined ANOVA indicated that the mean squares for landraces (G), years (Y), environments (E) and all interactions were all highly significant ($P \leq 0.01$) on grain yield. Landraces, environments and years explained 26.35, 32.08 and 15.66% of the total treatment variance respectively, whilst GEI accounted for 7.78%. Crossover type of GEI was observed in all evaluated landraces and based on mean grain yield across locations and years, accessions M258, M17 and M251 had the highest mean grain yields of 6.49, 6.39, 6.38 t ha^{-1} respectively. A stability analysis based on univariate or multivariate parameters is further recommended to extract more information on the GEI.

Keywords: *Maize, ANOVA, genotype by environment interaction, grain yield.*

INTRODUCTION

Maize (*Zea mays* L.) belongs to the grass Family Poaceae under the tribe Maydeae. It is the most important cereal crop in Africa and in Eswatini. In Eswatini, it is grown by both large – and small – scale farmers for both food and feed in all the agro-ecological zones of the country. Before official release, all new maize varieties from seed companies and International Agricultural Research Centres need to be evaluated at several locations and years within the different agro-ecological zones before being recommended to be grown at certain locations. The evaluation of grain yield performance of new maize varieties provides valuable information to ascertain their value for cultivation, adaptation and stability (Bassi and Sanchez-Garcia, 2017). New crop varieties evaluated in different locations or years often have significant fluctuation in yield performance due to the response of genotypes to environmental factors such as climate, soil fertility, biotic and abiotic stresses (Kang, 2004). These variations in yield performance are the ones that are usually referred to as genotype-by-environment interactions (GEI) and they are common in all multi-environment trials (METs). The principle behind GEI is that the phenotype of any living organism is determined by the effects of its genetic makeup (G), the environment (E) surrounding it, and the interaction between the genotype of the individual and the environment (G x E) (de Leon *et al*., 2016). The term genotype denotes a cultivar with materials genetically homogeneous, such as pure lines or clones, or heterogeneous, such as open-pollinated populations rather than to an individual's genetic make-up. The term environment relates to the set of climatic, soil, biotic and management circumstances in an individual trial implemented at a given location in one year or over several years (Annicchiarico, 2002).

Most traits of economic importance in maize, such as grain yield, are quantitative in nature and as such their phenotypic expressions are highly influenced by the environment where the crop grows. This type of interaction brings difficulties to the selection of maize cultivars, especially because it changes the genotypic performance across environments (Mohamed, 2013) and minimizes the extent of the association between the phenotypic and genotypic values (Alwala *et al*., 2010), thus reducing selection progress (Ramagosa and Fox, 1993). This scenario thus calls for extensive testing networks, covering diverse environments. In this case, breeders test genotypes in multi-environment trials, interchanging favourable and unfavourable conditions (DeLacy *et al*., 1996; Alwala *et al*., 2010). The main purpose of the extensive variety testing is to validate variety recommendations (Mohammadi *et al.,* 2015). Furthermore, GEI permits the identification of genotypes adapted to specific environments, which may constitute good opportunities for grain growers to select production environments (Hayman *et al.,* 2013; Bassi and Sanchez-Garcia, 2017).

Eswatini is divided into four main diverse climatic zones, also known as agro-ecological zones (AEZs). The diversity of these AEZs is mainly due to the elevation which ranges from 21 to 1862m above sea level from the Highveld to the Lowveld including the year-to-year rainfall distribution patterns. This heterogeneous agro-ecology is responsible for the different performance of maize genotypes within and across environments. When environmental differences are large like in Eswatini, it may be anticipated that the interaction of genotype x environment will also be higher. This interaction may result in one cultivar having the highest yield in some environments while a second cultivar outshines in others. Hence it is important to know the amount of the interactions in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation (Gauch and Zobel, 1997; Bassi and Sanchez-Garcia, 2017). The assessment of genotypic performance of maize landraces in many environments generates valuable data to ascertain how stable and adapted genotypes are (Crossa 1990). This also helps in the estimation and prediction as to how the genotypes are expected to perform in future years and future environments (Ngirazi *et al.,* 2017). Landraces are normally genetically heterogeneous, but with high yield stability, due to inter-genotype competition and compensation under unpredictable biotic and abiotic factors (Zeven 1998). In most cases, plant breeders are usually interested in non-crossover G × E or rather the absence of G × E interaction when selecting genotypes for general adaptation and crossover GEI for specific adaptation (Matus-Cadiz *et al*., 2003). Generally, GEI is detected, evaluated and interpreted via biometrical procedures like the analysis of variance (ANOVA), univariate and multivariate stability models (Flores et al. 1998). These statistical tools, their advantages and disadvantages, as well as the interactions between them have been studied previously (Lin *et al*., 1986; Flores *et al*., 1998; Sabaghnia *et al*., 2012). The ANOVA is useful in determining the presence, size and significance of GEI especially when genotypes and environments are considered to be fixed and random respectively. It also allows for the assessment of variance components used to determine trait heritability in the broad sense. If GEI is significant, additional stability statistics can be calculated (Smith *et al.,* 2005). The main limitation of the use of the ANOVA is that it does not provide further information as to which variety or environment contributed to the interaction (Samonte *et al*., 2005). It also does not take into consideration the core structure within the GEI, thus causing difficulties to establish the true performance of genotypes across environments (Crossa, 1990). The wide genetic variability observed in maize landraces is considered the main reason for their adaptability to different environments (Mercer and Perales, 2010). Although, maize landraces are a vital foundation of adaptability alleles, there is scanty information on current studies about their adaptability and stability (Azeez *et al*., 2018), especially those grown in Southern Africa (Tandzi *et al*., 2015; Chimonyo *et al*., 2019). In this regard, a multi-location trial involving seventy local maize landraces was conducted in the cropping seasons of 2016/2017 and 2017/2018 to estimate the extent and nature of GEI for grain yield based on the ANOVA techniques. The specific objectives were to;

a) Identify maize landraces with superior yielding ability across locations and cropping seasons.
b) Examine the level and type of GEI for grain yield.
c) Determine the need of doing grain yield stability analysis on the selected maize landraces.

MATERIALS AND METHODS

Plant materials

70 genetically diverse maize landraces (genotypes) were selected from a collection of 200 accessions conserved *ex situ* at the National Plant Genetic Resources Centre. The selection was based on a molecular characterization study, where 20 simple sequence repeat (SSR) markers were used to genotype the 200 landraces and the final selection was made based on the pairwise genetic distances among the landraces. The top 35 pairs of landraces with the highest genetic distances were selected for this study. Originally, the genotypes were collected from different homesteads across the country, especially in areas growing and maintaining maize landraces (Table 1).

Table 1 Entry codes, accession numbers and collection areas of selected maize landraces evaluated.

Entry code	Accession Number	Collection area	Entry code	Accession Number	Collection area
1	H43	Ndwandwa	36	M222	Lomshiyo
2	H327	Bhunya	37	M283	Malangeni
3	L161	Big Bend	38	M701	Maliyaduma
4	H13	Mbekelweni	39	M6	Engwenyameni
5	M640	Maliyaduma	40	M22	Sigangeni
6	M3	Sihhohhweni	41	L164	Big Bend
7	M20	Ekupheleni	42	H42	Kuphuka
8	M251	Mambane	43	M627	Malanti
9	M24	Ndwandwa	44	M498	Malanti
10	M4	Nkiliji	45	M197	Nhlambeni
11	L480	Mathatha	46	L301	Siteki
12	H406	Piggs Peak	47	L222	Mbhikwakhe
13	H328	Lomahasha	48	L167	Sigangeni
14	H188	Bhunya	49	M530	Embelebeleni
15	M26	Mduyane	50	M258	Sitsatsaweni
16	M19	Zombodze	51	L166	Mathatha
17	M17	Sihhohhweni	52	H340	Piggs Peak
18	M5	Nkiliji	53	H900	Mliba
19	M257	Lukhetseni	54	H45	Lomahasha
20	H177	Lukhetseni	55	H12	Mambane
21	H400	Lomahasha	56	H14	Siteki
22	H506	Bhunya	57	M256	Embelebeleni
23	H9	Ekwakheni	58	M274	Maliyaduma
24	S139	Ekwakheni	59	M284	Mampondweini
25	S624	Ekwakheni	60	M305	Mncitsini
26	S40	Mphelave	61	L623	Mathatha
27	M484	Mvembili	62	L223	Mgazini
28	M18	Sihhohhweni	63	L525	Mathatha
29	L163	Mathatha	64	H309	Luyengo
30	L170	Sigangeni	65	M200	Ndwandwa
31	H433	Bhunya	66	S38	Dumako
32	H288	Nkamanzi	67	M466	Hhelehhele
33	S516	Ekwakheni	68	H151	Siteki
34	S210	Ekufikeni	69	H247	Nkamanzi
35	M25	Mgazini	70	S211	Makhosini

Research sites, experimental design and crop management

The selected maize genotypes were planted at Malkerns Research Station (Malkerns), Luve experimental farm (Luve) and Lowveld Experiment Station (Big Bend) in the cropping seasons (years) of 2016/2017 and 2017/2018. Details of the research sites, meteorological data, soil types and coordinates are indicated in Table 1. All trials were planted on two row plots of 5 meters long with inter-row spacing of 0.9m. All plots were overplanted and thinned to two plants per station after seedling establishment to final intra row spacing of 0.25m. The experimental design used was the randomised complete block with 3 replications per site. All plots received basal fertilizer at the recommended rate of 300kg/ha of a compound fertilizer [N: P: K, 2: 3: 2 (22)] at planting and after six weeks, side-dressed with Lime Ammonium Nitrate (LAN) (28%N) at the rate of 100kg/ha. All plots were kept free of insect pests and weeds as described in Edje and Ossom (2009).

Table 2 Meteorological data, soil types and coordinates of the experimental locations

Environments	Years	Altitude (m)	Average rainfall (mm)	Geographic coordinates		Average temperature (ºC)	
				Latitude	Longitude	Max.	Min.
Malkerns	2016 2017	775.08	660.6	26º 05' 20'' S	30º55' 23''E	25.4	12.7
Luve		587	473.4	26º 16' 21'' S	31º 28' 21'' E	32.4	13.2
Big Bend		108	226.5	26º 49' 18'' S	31º 56' 27'' E	34.7	14.0
Malkerns	2017 2018	775.08	950	26º 05' 20'' S	30º55' 23''E	27.2	14.3
Luve		587	628.0	26º 16' 21'' S	31º 28' 21'' E	31.5	13.0
Big Bend		108	423.3	26º 49' 18'' S	31º 56' 27'' E	33.8	12.6

Source: Eswatini Meteorological Services (2018)

Data collection

Data was collected on per plot basis on the following grain yield (GY) parameters based on the methods of Badu-Apraku *et al.*, (2012);

a) Field weight (FW): Weight of all harvested ears per plot.
b) Grain weight (GW): Weight of shelled kernels from all ears per plot.
c) Shelling percentage (SHELL): The ratio between GW and FW multiplied by 100.
d) Grain moisture content (GM): The ratio of weight of water to the weight of solids in a given grain sample as measured by a grain moisture meter.

The following formula was used to calculate grain yield (at 12.5 moisture content) per plot which was converted to tonnes per hectare (t/ha);

$$GY\ (\frac{t}{ha}) = FW * SHELL\ (\%)\,\frac{100 - GM}{100 - 12.5} * \frac{10\ 000}{3.6}$$

Statistical analysis

Individual location analysis of variance for grain yield was performed for all trials using GenStat statistical software with genotypes considered as fixed effects, year and location effects as random. The Least Significant different (LSD) at 0.05 level of significance was used for mean separation tests. Before analysing the combined data across all sites and years, the Ratio and Bartlett's tests were performed on the grain yield data to assess homogeneity of error variances. The effects of genotypes, environments and years as well as all their interactions were determined using the ANOVA technique.

The following statistical methods were implemented to assess the significance level of grain yield of the genotypes, environments and their interactions;

a) Individual site analysis for each year. This was done for all six separate trials planted across the three separate environments for the 2016/2017 and 2017/2018 years. The linear model used for individual site analysis was;

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$$

where μ is the overall mean grain yield, G_i, E_j and GE_{ij} denotes the effects of the genotype, environment and G x E interaction respectively, and e_{ij} is the mean random error related with rth plot where the ith genotype was planted in the jth test location.

b) The combined analyses of the trials (across two years and three environments) was done in order to evaluate differences between genotypes across environments and years, and also to decide whether there was any significant difference among environments and different years.

Broad sense heritability (repeatability) (h^2b) was calculated as;

$$h^2b = \sigma^2_G/[\sigma^2_G+(\sigma^2_{GE}/e) + (\sigma^2_E/re)$$

Where σ^2_G, σ^2_{GE} and σ^2_E denote the genetic, GEI and environmental variances respectively. The number of replications and environments are denoted by e and r.

RESULTS

2016/2017 cropping season

All three trials revealed highly significant ($P \leq 0.01$) variations among maize genotypes for grain yield. During the cropping season, the landraces contributed more to total variation with 99.61, 96.43 and 96.19 % at Malkerns, Big Bend and Luve respectively. At Malkerns grain yield ranged from 2.22 t/ha (accession H3440) to 8.35 t/ha (accession L223), 1.35 t/ha (accession M257) to 6.79 t/ha (accession M274) at Luve and 0.61 t/ha (accession L623) to 5.44 t/ha (accession M258) at Big Bend (Table 3).

Across the three environments, highly significant ($P \leq 0.01$) differences were observed in landraces, locations and the interaction (Table 5). Accession M258 was ranked first with an average grain yield of 6.46 t/ha followed by accession M251 and M17 with 6.39 t/ha and 6.09 t/ha respectively. Accession M257 performed poorly in all sites, with the lowest mean grain yield of 1.66 t/ha.

Table 3 Mean squares from analysis of variance and percentage sum of squares contribution to total sum of squares for grain yield of 70 maize landraces tested across three environments in Eswatini during the 2016/2017 cropping season.

Source	DF	Environments					
		Malkerns		Luve		Big Bend	
		MS	%SS	MS	%SS	MS	%SS
Replications	2	0.01	0.001	0.14	0.08	0.23	0.14
Genotypes	69	6.18**	99.61	4.98**	96.19	4.61**	96.43
Error	138	0.01	0.39	0.096	3.72	0.08	3.43
Total	209		100		100		100
CV (%)		2.3		8.00		11.00	
LSD(0.05)		0.18		0.50		0.46	
Yield range (t/ha)		2.22–8.35		1.35–6.79		0.61–5.44	

Key: ** = P<0.01 DF = degrees of freedom
MS = Mean sum of squares
%SS = percent sum of squares (contribution to total sum of squares)

2017/2018 cropping season

Highly significant differences ($P \leq 0.01$) for grain yield were observed among the genotypes across all environments during the cropping season. As observed in the previous season, differences in genotypes explained most of the variation observed as it explained 85.62, 88.49 and 96.14 % of total sum of squares at Malkerns, Luve and Big Bend respectively. At Malkerns grain yield ranged from 2.86 t/ha (accession H328) to 10.73 t/ha (accession L223), 2.39 t/ha (accession H328) to 7.69 t/ha (accession M24) at Luve and at Big Bend it ranged from 1.26 t/ha (accession H328) to 6.44 t/ha (accession M258) (Table 4).

Across the three locations, highly significant ($P \leq 0.01$) differences were observed in landraces, locations and the interaction (Table 5). Accession M24 was ranked first with an average grain yield of 6.94 t/ha followed by accession L223 and M484 with 6.90 t/ha and 6.09 t/ha respectively. Accession H328 performed poorly in all sites, with the lowest mean grain yield of 2.17 t/ha.

Table 4 Mean squares from analysis of variance and percentage of variance components for grain yield of 70 maize landraces tested across three locations in Eswatini during the 2017/2018 cropping season.

Source	DF	Environments					
		Malkerns		Luve		Big Bend	
		MS	%SS	MS	%SS	MS	%SS
Replications	2	0.79	0.32	0.18	0.14	0.07	0.02
Genotypes	69	6.08**	85.62	3.34**	88.49	5.07**	96.14
Error	138	0.49	14.06	0.21	11.37	0.10	3.82
Total	209		100		100		100
CV (%)		10.60		8.7		8.7	
LSD(0.05)		1.14		0.75		0.51	
Yield range (t/ha)		2.86–10.73		2.39–7.69		1.26–6.44	

Key: ** = P<0.01 DF = degrees of freedom MS = Mean sum of squares
%SS = percent sum of squares (contribution to total sum of squares)

Table 5 Mean squares and basic statistics of the combined analysis of variance for grain yield of 70 maize landraces (genotypes) tested across three environments in Eswatini during the 2016/2017 and 2017/2018 cropping seasons (years)

Cropping seasons (years)	Sources	DF	MS
2016/2017	Replications	2	
	Genotypes (G)	69	14.58**
	Environments (E)	2	237.06**
	GxE	138	0.59**
	Residual	418	0.06**
	Total	629	
	Mean yield (t/ha)	3.74	
	Range (t/ha)	1.66 – 6.46	
	LSD (0.05)	0.38	
	CV (%)	9.10	
	Heritability (%)	95.95	
2017/2018	Replications	2	0.48
	Genotypes (G)	69	7.40**
	Environments (E)	2	484.06**
	GxE	138	3.54**
	Residual	418	0.27**
	Total	629	
	Mean yield (t/ha)	5.21	
	Range (t/ha)	2.17 - 6.90	
	LSD (0.05)	0.38	
	CV (%)	9.10	
	Heritability (%)	89.81	

Key: ** = P<0.01 DF = degrees of freedom MS = Mean sum of squares
%SS = percent sum of squares (contribution to total sum of squares)

Combined analysis of variance across environments and cropping seasons

The analysis of variance of grain yield for the combined analysis across environments and years showed highly significant ($P \leq 0.01$) differences among genotypes, environments, years and all their interactions. Partitioning of total sum of squares indicated that environments accounted for approximately 33%, followed by genotypes (27%) and years (16%) respectively. On the interactions, GEI accounted for 8 % of total sum of squares followed by genotypes by environments by years (GEY) with 5 % and genotypes by years (GY) with 4.84% (Table 6). Overall, Malkerns was the most favourable environment on both years with the highest mean grain yield of 5.69 t/ha with accession L223 being the most productive genotype with mean grain yield of 9.54 t/ha. Accession H328 produced the lowest grain yield of 2.64 t/ha and was the least performing across environments and years. At Luve, the observed mean yield was 4.60 t/ha with accession M274 performing well with the highest yield of 6.75 t/ha and accession H328 being the lowest in performance with 2.18 t/ha. Big Bend had an overall mean grain yield of 3.13 t/ha with accession M258 producing the highest yield of 5.94 t/ha and accession L623 producing the lowest yield of 1.08 t/ha. When focusing on the cropping seasons, the years 2017/2018 were more productive compared to the years 2016/2017 season in terms of mean grain yield. The mean grain yield observed during the 2016/2017 cropping season was 3.74 t/ha with accession M258 producing the highest yields of 6.46 t/ha and accession M257 being the lowest yielding at 1.66 t/ha. The 2017/2018 cropping season had a mean grain yield of 5.21 t/ha with accession L223 producing the highest mean grain yield of 6.90 t/ha and accession H328 producing the lowest grain yield of 2.17 t/ha.

Table 6 Mean squares of the combined analysis of variance and percentage of the variance components for grain yield of 70 maize genotypes tested across six environments of Eswatini during the 2016/2017–2017/2018 cropping seasons

Cropping season (Years)	Sources	DF	MS	%SS
2016/2017 - 2017/2018	Replication	2	0.66	0.03
	Genotypes (G)	69	16.62**	26.35
	Year (Y)	1	681.37**	15.66
	Environments (E)	2	698.20**	32.08
	GxY	69	5.35**	4.84
	GxE	138	2.48**	7.78
	YxE	2	22.92**	1.05
	GxYxE	138	1.65**	5.24
	Residual	838	0.17	3.22
	Total	1259		
	Mean (t/ha)		4.47	
	Range (t/ha)		1.99 – 6.49	
	LSD (0.05)		0.66	
	CV (%)		9.10	

Key: ** = P<0.01 DF = degrees of freedom MS = Mean sum of squares

DISCUSSION

The high and significant mean square values for locations across the three years indicated that the grain yields observed on genotypes was greatly affected by variations among environments. The significant GEI indicates the presence of a wide range of variations between genotypes and between seasons, and that different genotypes responded differently to varying environments (Annicchiarico, 2002). Based on percent contribution to variability, the combined analysis of variance indicated that environments contributed more to total sum of squares, indicating a much broader range of environment main effects than genotype main effects. In most variety trials at multi-locations, environment accounts for the maximum variation (Zhang *et al*., 2006; Zerihun, 2011). This scenario is a clear indicator of the overwhelming influence of the environment on yield performance of the maize genotypes in Eswatini. These findings are consistent with observations made by other researchers (Beshir, 2009; Tonk *et al*., 2010; Ndhlela *et al*., 2014; Mohammadi *et al*., 2015). The magnitude of GEI sum of squares was greater than that of genotypes, indicating that there were substantial differences in genotypic responses across environments. These results are also in line with those obtained by others (Ramburan *et al*., 2011; Ndhlela *et al*., 2014). However, in this study, the contribution by GEI as a percentage of total sums of squares was lower than what has been reported by three other research teams (Sabaghnia *et al*., 2008; Ramburan *et al*., 2011; Ndhlela *et al*., 2014). Likewise, the highly significant values for the interaction between location and year showed that unpredictable environmental conditions dominated across environments and across years. All these are responsible for the existence of GEI, where genotypes showed instabilities in their response to different environmental conditions. Furthermore, the significant interaction indicated the presence of unstable genotypes.

The high mean yield observed at Malkerns was expected since the Malkerns Valley is regarded as the prime agricultural area in Eswatini and it comprises of the best soils and climatic conditions conducive for crop production (FAO/WFP, 2015). This is also true for Luve, situated in the dry Middleveld of the country where moderate rains with sporadic dry spells are common. The least mean yields observed at Big Bend were also expected since the Lowveld is characterised by drought spells and extreme heat waves thus not conducive for rain fed crop production. According to Oseni and Masarirambi (2011), the government of Eswatini through the Ministry of Agriculture had advised that maize should not be grown in the Lowveld under rain fed conditions because of the drought spells and severe heat wave experienced in that agro-ecological zone. Furthermore, the same authors outlined that farmers in the Lowveld were advised to at least grow sorghum and millet which can withstand drought and higher temperatures. Among the environments, no landraces showed consistent yield superiority, which constitute a major limitation to the identification of superior genotypes for narrow or wide adaptation (Badu-Apraku *et al*., 2003). The same pattern was observed on both cropping season as no accession showed consistent yield superiority among the cropping seasons. The observed significant genotype by year interaction is comparable in effect to genotype by environment (Mohammadi, 2017). It is a challenge because the breeder cannot develop programmes for different years, and as a way forward, the breeder would have to conduct trials over several years and select the genotype with superior average performance over the years for recommendation (Annicchiarico, 2002; Mohammadi, 2017). Unfortunately, conducting one trial per year for more years will delay the breeding programme and the solution would be to include more locations per year and reduce the number of testing years (Acquaah, 2012).

In the current study, six trials were conducted in two cropping seasons which lead to the identification of candidate genotypes based on mean performance across environments and seasons. Accessions M258, M17, M21and M251 had the highest mean grain yields across environments and seasons. Hence, these four genotypes can be considered for commercial and small-scale production in the wet, dry and Lowveld areas of the country. This will be more advantageous to growers since they can grow more than one cultivar in each cropping season. This approach will reduce the effects of the fluctuations attributed to GEI. In all three environments across the two cropping seasons, different genotypes had the highest mean grain yields which indicated the presence of crossover GEI. This is also an indicator for the presence of GEI due to year to year weather conditions as well as variation among the testing environments. Additionally, the crossover GEI indicated the existence of different mega environments in which different winning genotypes can be selected. As indicated earlier, the GEI presence is a challenge for breeders to find genotypes that are consistently good performing in diverse locations. As such, this indicates a need for analysing stability of genotypes across environments. Such a stability analysis will facilitate the identification of widely adapted genotypes and those that are specifically adapted to high potential environments.

CONCLUSION

One of the factors affecting maize production in Eswatini is the recommendation of inappropriate maize varieties to specific growing environments. Targeting the appropriate cultivars to environments where they will perform better is very important to minimize the impact of GEI. The analysis of variance is a very powerful tool in determining the existence, magnitude and significance of GEI. The significance of the analysis of variance in GEI studies is that the variance component associated with the various sources of variation, including genotype and GEI can be predicted.

In this study seventy diverse maize genotypes were used to examine the extent and nature of GEI for grain yield and thereafter to select the best maize genotypes for the maize growing environments of Eswatini. The maize genotypes were evaluated in a multi-location yield trials conducted across two years and three environments. From the results of the combined analysis of variance, differences among the testing environments were high as specified in its percentage contribution to variation. Furthermore, the highly significant values for the interaction between environment and year indicated that unpredictable environmental conditions prevailed across environments and across cropping seasons. Among the genotypes evaluated, accessions M258, M17, M251 and M484 can be considered as candidate varieties for commercial production as open pollinated varieties as they performed well across environments and cropping seasons. Among the specific environments, Malkerns was the best and Big Bend the worst in terms of grain yield. Again, no genotype showed consistency in grain yield advantage in all environments which indicated the presence of GEI due to year to year and environments fluctuations. Some genotypes showed consistent performance across Malkerns and Luve but not with Big Bend.

The results of this study confirmed that the main problem in selecting superior maize genotypes in Eswatini is related with the unpredictable environmental conditions. Hence, under such conditions, it is important to look for stable genotypes by using appropriate stability analysis techniques that will help to get more information on the GEI.

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