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Phenotypic diversity, heritability and environmental sensitivity in morpho-agronomic traits of Eswatini maize (*Zea mays* L.) landraces

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Maize landraces have the highest genetic variation and adaptation to less favourable farming environments. In Eswatini, maize landraces occupy about 20% of the maize crop planted annually. The current study was undertaken to assess the morpho-agronomic diversity, heritability and genotype by environment interaction among 70 genetically diverse maize landraces collected from different farmers in the country. The maize landraces (genotypes) were grown in replicated trials at Malkerns in Eswatini for three consecutive years (environments) from 2016 to 2019. Data were recorded on 15 morpho-agronomic traits, where significant differences were observed for genotypes on individual traits in all three environments. The combined ANOVA also indicated significant differences for genotypes, environments and genotype by environment interaction in most of the traits. Close resemblance between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed in number of ears per plant, ear diameter and ear length indicating minimum influence of the environments in the expression of these traits. Broad-sense heritability ranged from 18 to 99% with anthesis silking interval with the least and ear length with the highest. Analysis of genotype by environment interaction (GEI) indicated that genotype, environment and genotype by environment interaction explained variable amounts of total variance across traits, respectively. Number of kernels per row, plant height and one thousand seeds weight were more affected by environmental changes, while anthesis silking interval and kernel size traits were less affected thus indicating greater resistance to environmental changes. Based on the deviation from regression stability parameter, accessions H328, M640 and L161 showed stability of grain yield and adaptability in the Malkerns area. Further testing of these landraces in different locations across the country's five agro-ecological zones is recommended.

Key words: Maize landraces, diversity, morpho-agronomic traits, heritability, G×E interaction, cluster analysis, principal component analysis (PCA).

INTRODUCTION

Maize (*Zea mays* L.) is regarded as the third most important cereal crop after wheat and rice in the world (Tesfaye et al., 2015). It is mostly used and traded as a leading feed and food crop including a wide range of industrial applications ranging from food processing to manufacturing of industrial products (Ranum et al., 2014). It is cultivated on more than 156 million hectares per year in nearly 100 countries within 40°S to 58°N latitude and all longitudes (FAOSTAT, 2018). It is also the most extensively cultivated crop in tropical Africa including Eswatini where it is a stable crop. It was introduced in Eswatini in the early 1930s, replacing sorghum as the stable crop. Since the introduction of these maize varieties into Eswatini, farmers have consciously and artificially selected some strains, which led to the wide phenotypic diversity present in today's maize landraces.

Global maize variability has been the attention of numerous studies in morphological, agronomic and varietal relationships (Twumasi et al., 2017). Such assessments are critical to plant genetic resources management and to crop improvement (Hellin et al., 2014; McLean-Rodriguez et al., 2019). There is wide morphological diversity available in maize landraces, and characterization of these resources is a prerequisite for the genetic improvement of its cultivars. The diversity is due to its reproductive structure, introgression from exotic germplasm, seed exchange between farmers, mutation and farmer assisted selection on diverse environments in different time scales (Rincon-Sanchez and Ruiz-Torres, 2018). The key morphological descriptors in maize are related to vegetative structure, tassel, ear and kernel characteristics (Rincon-Sanchez and Ruiz-Torres, 2018). The traits contributing to morpho-agronomic diversity are grain weight and grain yield (Drinic et al., 2012); kernel weight and days to maturity (Twumasi et al., 2017); ear height, days to silking, ear length and 100-seed weight (Barros et al., 2019); ear length and diameter (Rincon-Sanchez and Ruiz-Torres, 2018).

Understanding the extent of genetic variability existing in the germplasm is vital and leads to effective exploitation of the germplasm in crop breeding programmes (Drinic et al., 2012). Genetic variability parameters give an indication of the extent of genetic variation of quantitative traits (Bhandari et al., 2017) available for exploitation. Selection in practice is subject to the phenotypes of individuals, which are measured by the phenotypic variance (V_P). Knowledge of heritability determines the selection procedures a breeder can use, which could be suitable for the improvement of traits (Falconer and Mackay, 1996) including the consistency of a particular phenotypic observation that directs a breeding value (Dabholkar, 1999). Comparative variability of traits is assessed by estimating the genotypic coefficient of variation (GCV) and the phenotypic coefficient of variation (PCV). The GCV indicates the heritable portion, while the PCV indicates both the genetic and environmental effects on trait performance (Deshmukh et al., 1986).

The phenotypic performance of crop plants is due to its genotype (G), the surrounding environment (E) as well as the interaction of the two factors (G × E). The environments may be different locations within the same cropping season or year, different years for the same location, or a combination of the two (Annicchiarico, 2002). Several studies have confirmed that genotypes evaluated in diverse environments or different years often have significant variation in trait performance due to the response of genotypes to environmental and seasonal features such as fluctuating weather patterns and soil heterogeneity (Saltz et al., 2018). These variations in trait performance are the ones that are usually referred to as genotype × environment interaction (GEI) and they are a common occurrence whenever multi-location or multi-year experiments are conducted (Falcon et al., 2020). GEI is present whenever genotypes differ in their trait values more in some environments than others or change ranks in different environments signifying genetic variation in plasticity (Dabholkar, 1999). While GEI has been comprehensively researched in maize (Anley et al., 2013; Ndhlela et al., 2014; Abate, 2020), its presence and extent vary significantly across germplasm used and traits under study (Falcon et al., 2020). Due to their differences in heritability and sensitivity to environmental factors, these different types of traits may show different levels of GEI (Saltz et al., 2018). Traits with greater V_G are more sensitive and are expected to show greater GEI than traits with low V_G (Saltz et al., 2018). In most cases grain yield and its components have low heritability and high sensitivity to environmental changes (Falcon et al., 2020). Acceptable cultivars are expected to express a stable level for traits important for growers and consumers (Annicchiarico, 2002). Usually, the goal is to identify genotypes with large means and small sensitivities, to warrant a reliable crop under diverse conditions. Traits showing insignificant or a lack of GEI could indicate absence of genetic diversity, which predisposes genetic vulnerability of a crop to disease epidemics, insect infestations, or other stresses.

The presence of GEI reduces the relationship between phenotype and genotype, and makes it difficult to identify the genetic potential of a genotype. In addition, if significant GEI is discovered for a particular trait, one seeks to find the performance of genotypes for adaptability and stability (Dabholkar, 1999). According to Eberhart and Russell (1966), a stable genotype is defined as one which produces high mean yield, depicts regression coefficients (b_i) around unity and non-significant deviations from regression (S^2_{di}). The

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Table 1. List of the 70 studied maize landraces and the agro-ecological zones of the villages where they were collected.

Agro-ecological zone	Total No. of accessions	Name of accession
Highveld	24	H28, H100, H56, H30, H9, H143, H69, H75,H41, H25, H134, H136, H149, H135, H59, H23, H16, H67, H19, H144, H29, H93, H126, H328, H14
Wet Middleveld	21	M88, M65, M83, M80, M78, M87, M86, M99, M58, M95, M47, M109, M96, M 138, M36, M34, M21, M39, M94, M640, M50, M37, M27, M112
Dry Middleveld	15	M66, M11, M8, M104, M68, M51, M90, M44, M123, M42, M7, M57, M33, M101, M103
Lowveld	2	L22, L161
Lubombo plateau	8	L85, L131, L128, L148, L133, L125, L150, L2

regression coefficient should be simply viewed as a measure of response of a particular genotype and its sensitivity to environmental variations (Finlay and Wilkinson, 1963; Anley et al., 2013) and it does not indicate variety stability and field performance (Annicchiarico, 2002). Based on the evaluated traits, the regression coefficient values > 1.0, describe genotypes with increasing sensitivity to environmental change and greater specificity of adaptability to high yielding environments. On the other hand, the regression coefficient values < 1.0 provide a measure of greater resistance to environmental change and, therefore, increasing specificity of adaptability to low yielding environments (Saltz et al., 2018; Falcon et al., 2020). The deviation from regression is the most appropriate criterion for measuring phenotypic stability in an agronomic sense because this parameter measures the predictability of genotypic reaction to environments (Eberhart and Russell, 1966; Mahajan and Khehra, 1992; Alberts, 2004). According to this parameter, a stable genotype is the one with an insignificant deviation from regression mean squares. A genotype with $S^2_{di} = 0$ is highly predictable, whilst that with $S^2_{di} > 0$ has less predictable response (Dabholkar, 1999; Scapim et al., 2010).

Most biometricians and geneticists in plant breeding consider S^2_{di} as a stability parameter (Eberhart and Russell, 1966; Annicchiarico, 2002). This investigation was undertaken to estimate:

(1) The extent of phenotypic diversity and heritability in morpho-agronomic traits among 70 maize landraces collected from diverse locations in Eswatini.
(2) To evaluate the effect of genotype, environment, GEI and environmental sensitivity on morpho-agronomic traits of maize landraces.
(3) Identify maize landraces with stable and reliable grain yield for the Malkerns area in Eswatini.

MATERIALS AND METHODS

Plant

A selected set of 70 landrace accessions hereafter referred to as genotypes collected from 52 areas in all five agro-ecologies of Eswatini were used for the study. These genotypes were conserved *ex situ* at the National Plant Genetic Resources Centre (NPGRC) (Table 1).

Research site, experimental design and crop management

Seeds of diverse 70 maize genotypes were planted at Malkerns Research Station in Eswatini during the cropping seasons of 2016/2017, 2017/2018 and 2018/2019 hereafter referred to environments I, II and III, respectively. The detailed descriptions of the different environments in terms of weather parameters are shown in Table 2. All trials were planted on two row plots of 5 m long with inter and intra row spacing of 0.25 and 0.90 m, respectively. The experimental design used was the randomized complete block with 3 replications. All plots received basal fertilizer at the recommended rate of 300 kg/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 100 kg/ha. All plots were kept free of insect pests, diseases and weeds by using recommended crop protection methods.

Data collection and analysis

On each plot, 15 competitive plants were randomly selected and tagged; each plant was then evaluated for 15 morpho-agronomic traits. The following morphological traits were evaluated; number of days to pollen shed and days to silking, anthesis-silking interval (ASI), plant and ear heights, number of ears per plant, ear length and diameter, number of kernel rows per ear, number of kernels per row (a random 5 rows were selected per ear), kernel length, thickness and width, one thousand seeds weight and grain yield. Grain yield was measured in tonnes per hectare and adjusted to grain moisture content at 12.5%. All traits on individual trials in each environment were subjected to multivariate analysis of variance (MANOVA) by using GenStat 17th Edition software. Combined analysis of variance for all three environments was performed to determine the effect of genotypes, environments, and GEI on the traits across environments. In all cases, genotypes were assumed to be fixed, and environments effects as random. V_G and V_P and H^2B were estimated according to the formula proposed by Dabholkar (1999). GCV and PCV were calculated following the methods of Deshmukh et al. (1986). The PCV and GCV were classified into the

Table 2. Weather parameters at Malkerns during the 2016/2017, 2017/2018, 2018/2019 cropping seasons.

Weather parameter	November	December	January	February	March	April
			2016/2017 (Environment – I)			
Max. Temperature (°C)	31	33	32	31	28	24
Min. Temperature (°C)	16	18	14	15	13	11
Rainfall (mm)	34	44	66	72	51	28
			2017/2018 (Environment – II)			
Max. Temperature (°C)	33	31	34	27	24	17
Min. Temperature (°C)	14	18	16	15	13	10
Rainfall (mm)	60	58	70	62	45	33
			2018/2019 (Environment – III)			
Max. Temperature (°C)	31	33	32	31	28	24
Min. Temperature (°C)	16	18	14	15	13	13
Rainfall (mm)	82	87	112	95	66	48

following classes: as high (>20%), medium (10-20%) and low (<10%) as proposed by Deshmukh et al. (1986). The extent of heritability was classified as low (0 - 0.39), medium (0.40 - 0.59), moderately high (0.60 - 0.79) and very high (0.80 and above) as proposed by Dabholkar (1999). GEI and environmental sensitivity of individual traits was analysed using the Modified Joint Regression analysis as proposed by Finlay and Wilkinson (1963). In addition, the stability of grain yield of each genotype was based on the deviation from regression (S^2_{di}) method as suggested by Eberhart and Russell (1966).

RESULTS

Combined analysis of variance and variation in morpho-agronomic traits

Analysis of variance (ANOVA) of combined data revealed highly significant (P<0.01) effects of genotypes across all evaluated traits (Table 3). In addition, highly significant effects of locations, genotypes as well as genotype × environment (G × E) interactions were observed in plant and ear heights, days to silking, pollen shed and anthesis-silking interval (ASI) including grain yield and its components. Number of ears per plant, ear diameter and kernel sizes (kernel length, thickness and width) showed non-significant (P>0.05) variations over environments and G × E interaction.

Across environments, plant and ear heights ranged from 197.80 to 286.37 cm and 68.60 to 201.80 cm, respectively. Tall plants were observed on accession M24, while those from accession L223 were generally the shortest. Days to pollen shed and days to silking varied from 62.60 to 84.20 days and 63 to 88.20 days, respectively with a mean ASI of 3.74 days. Based on days to pollen shed, plants from accession L223 were generally late maturing with mean of 79.02 days, while those from accession M24 shed their pollen earlier with mean of 62.60 days. Less variation was observed in kernel traits (kernel thickness, kernel width and kernel length). Ear diameter and ear length varied from 3.60 cm (accession M3) to 5.87 cm (accession M17) and 11.16 cm (accession M22) to 23.81 cm (accession S139), respectively. Grains with the smallest kernel length were observed in accession H42 (9.20 mm) while those from accession H328 had the longest kernels (14.60 cm). Kernel width ranged from 8 mm (accession M251) to 13.20 mm (accession M19). Thick kernels were observed in accession L480 (4.80 mm) while thin kernels were observed in accession S516 (2.40 mm). Grain yield ranged from 2.71 t/ha (accession M24) to 7.13 t/ha (accession L223) with a mean of 6.38 t/ha. The coefficient of variation ranged from 3% (days to silking) to 15.60% (number of ears per plant) (Table 3).

Phenotypic, genotypic coefficient of variation and heritability

The phenotypic coefficient of variation (PCV) was high (>20%) for number for ear diameter, ear length, ASI and ear width. Intermediate PCV (10 - 20%) was observed in number of kernels per row (Table 4). Ear diameter showed the highest genotypic coefficient of variation (GCV) (70.81%) followed by ear length (42.01%) and grain yield (14.83%). The lowest GCV was recorded for days to silking (1.99%) and kernel length (2.52%). The differences between GCV and PCV were small for all traits, except ASI, kernel width and grain yield. Very high broad sense heritability estimates were noted for ear length (99%) and ears diameter (97%), while moderately high heritability was observed in number of kernel rows per ear, days to pollen shedding, plant height, grain yield,

Table 3. Combined analysis of variance (mean squares) and basic statistics for morpho-agronomic traits among 70 maize landraces evaluated across three consecutive cropping seasons (environments) at Malkerns, Eswatini.

Trait	MS				Basic statistics					
	Environments (E) (df = 2)	**Genotypes (G) (df = 69)**	**Interaction (G×E) (df = 138)**	**Pooled Error (df = 418)**	**Min.**	**Max.**	**Mean**	**St. Dev.**	**LSD (0.05)**	**CV (%)**
PH (cm)	14251.10**	1835.00**	496.10**	118.60	197.40	286.37	245.90	24.75	17.48	4.30
EH(cm)	22142.60**	1096.40**	362.30**	130.40	68.60	201.80	136.90	25.74	18.33	8.30
EPP (no.)	0.37^{NS}	0.33**	0.12^{NS}	0.14	1.98	2.80	2.42	6.32	0.63	15.60
DS (days)	1225.70**	27.70**	8.90**	1.80	63.00	88.80	72.77	1.27	3.54	3.00
DP (days)	1457.20**	46.90**	11.81**	2.30	62.60	79.02	72.66	4.95	4.67	4.00
ASI (days)	716.70**	7.20**	9.30**	4.00	-6.00	13.40	3.74	2.55	3.19	15.30
EL (cm)	11173.90**	537.10**	0.40^{NS}	2.42	11.16	23.81	18.38	2.04	2.46	8.00
ED (cm)	1.60^{NS}	95.00**	2.40^{NS}	1.20	3.60	5.87	4.53	0.42	0.42	5.80
NKR (no.)	254.10**	10.10**	2.10**	0.80	6.00	15.00	10.03	1.41	3.46	17.70
NKPR (no.)	155.29**	41.99**	23.65**	6.34	33.38	43.09	38.34	9.48	4.040	6.60
KT (mm)	0.02^{NS}	0.30**	0.04^{NS}	0.006	2.40	4.80	3.39	0.57	0.64	11.70
KW (mm)	0.04^{NS}	62.20*	33.10^{NS}	0.70	8.00	13.20	10.97	0.71	1.80	10.60
KL (mm)	0.28^{NS}	1.34**	0.51^{NS}	0.43	9.20	14.60	12.07	0.78	1.05	5.40
TSW (g)	11703.00**	6187.00**	2343.00**	1491.00	281.50	566.00	426.90	22.14	61.98	9.00
GY (t/ha)	384.10**	11.13**	3.07**	1.81	2.71	7.13	6.38	3.17	1.09	10.60

*Significant at 0.05, **Significant at 0.01, NS= Not significant, PH= Plant height, EH=Ear height, EPP=Ears per plant DS=Days to silking, DP=Days to pollen shedding, ASI=Anthesis silking interval, EL=Ear length, ED=Ear diameter, NKR=Number of kernel rows per ear, NKPR=Number of kernels per row, KT=Kernel thickness, KW=Kernel width, KL=Kernel length, 1000 SW=1000 Seed weight, GY=Grain yield.

days to silking, ear height, number of ears per plant, kernel length and 100 seed weight. Medium heritability was observed in kernel width and number of kernels per row, while ASI recorded low heritability of 18% (Table 4).

GEI and environmental sensitivity of morpho-agronomic traits

Genotype by environment interaction analysis indicated that plant height, ear height and number of kernels per row were greatly affected by the different genotypes as they contributed 46.34, 33.28 and 33.05% to total sum of squares, while kernel sizes were less affected. Grain yield, days to silking and ASI were greatly affected by the environments as they contributed 37.09, 31.99 and 239.13% to total sum of squares. Kernel sizes, number of ears per plant and number of kernels per row were less affected by environmental factors. High sensitivity to environmental changes were noted in plant height and ear height including grain yield and its components as they all contributed a range of 16.36 to 26.71% to total sum of squares. Kernel sizes and days to silking were less sensitive to environmental changes as they contributed a range of less than 1 to 5.66% (Table 5).

Grain yield sensitivity and stability of genotypes

Genotypes with sensitivity values above 1.0 accounted for 52.9% of the evaluated maize landraces which indicated that these genotypes had higher grain yield sensitivity to environmental change and are adapted to favorable environments. About 42% of the genotypes had sensitivity values below 1.0 which indicated that they had greater resistance of grain yield to

Table 4. Variance components of morpho-agronomic traits among 70 maize genotypes evaluated across three consecutive cropping seasons (environments) at Malkerns, Eswatini.

Trait	σ^2g	σ^2gy	σ^2e	σ^2p	GCV (%)	PCV (%)	h^2b
PH (cm)	148.77	125.83	118.80	203.89	4.77	5.58	0.73
EH (cm)	81.57	77.30	130.40	121.82	6.59	8.06	0.67
EPP (no.)	0.02	0.006	0.14	0.04	6.38	7.98	0.64
DS (Days)	2.09	2.37	1.80	3.08	1.99	2.41	0.68
DP (days)	3.90	3.17	2.30	5.21	2.72	3.14	0.75
ASI days)	0.23	1.77	3.74	1.27	12.91	30.09	0.18
EL (cm)	59.63	0.67	2.42	59.68	42.01	42.02	0.99
ED (cm)	10.29	0.40	1.20	10.56	70.81	71.72	0.97
NKR (no.)	0.89	0.43	0.80	1.12	9.4	10.56	0.79
NKPR (no.)	2.03	5.77	6.34	4.67	3.72	5.63	0.44
KT (mm)	0.66	0.08	0.006	0.03	5.01	5.39	0.87
KW (mm)	3.23	10.80	0.70	6.91	16.39	23.96	0.47
KL (mm)	0.09	0.03	0.43	0.15	2.52	3.2	0.62
TSW (g)	427.11	284.00	1491.0	687.44	4.84	6.14	0.62
GY (t/ha)	0.90	0.42	1.81	1.24	14.83	17.43	0.72

σ^2g=Genetic variance, σ^2gy=interaction (genotype × years) variance, σ^2e=environmental variance, σ^2p=phenotypic variance, h^2b=broad sense heritability, GCV (%)=percent genetic coefficient of variation, PCV (%)=percent phenotypic coefficient of variation, GA=genetic advance, PH=plant height, EH=ear height, EPP=ears per plant, DS=days to silking, DP=days to pollen shedding, ASI=anthesis silking interval, EL=ear length, ED=ear diameter, NKR=number of kernel rows per ear, NKPR=number of kernels per row, KT=kernel thickness, KW=kernel width, KL=kernel length, TSW=1000 seed weight, GY=grain yield.

Table 5. Joint regression ANOVA for morpho- agronomic traits of 70 maize genotypes evaluated across three environments at Malkerns, Eswatini as modified by Finlay and Wilkinson.

Trait	Genotypes		Environments		Sensitivities		Residual	
	MS	%SS	MS	%SS	MS	%SS	MS	%SS
PH (cm)	1835.04**	46.34	14251.14**	10.43	981.85**	24.79	103.01	18.43
EH(cm)	1096.38**	33.28	22142.6**	19.48	630.68**	19.14	130.68	28.11
EPP (no.)	0.33**	22.76	0.37	0.74	0.17	11.94	0.13	64.55
DS (days)	27.71**	24.96	1225.68**	31.99	6.29	5.66	5.86	37.39
DP (days)	0.14**	18.79	0.88**	3.42	0.14	18.98	0.06	58.81
ASI days)	7.17	10.05	716.67**	29.13	7.54	10.58	5.05	50.22
EL (cm)	7.84**	27.18	55.51**	5.58	2.58	8.93	2.37	58.3
ED (cm)	0.14**	19.2	0.88**	3.5	0.14**	19.2	0.06	58.31
NKR (no.)	9.88**	33.05	6.01	0.6	3.51	11.76	2.3	54.6
NKPR (no.)	41.99**	30.65	155.29**	3.29	36.59**	26.71	7.61	39.35
KT (mm)	0.28**	1.37	660.19**	94.75	0.14	0.67	0.09	3.21
KW (mm)	1.73**	0.93	6237.22**	97	0.82**	0.44	0.43	1.62
KL (mm)	1.34**	23.28	0.28	0.14	0.59	10.22	0.54	66.36
TSW (g)	6187.35**	30.41	11702.59**	1.67	3962.4**	19.48	1390.58	48.44
GY (t/ha)	10.07**	26.64	483.65**	37.09	6.18**	16.36	1.06	19.91

*Significant at 0.05; **Significant at 0.01; MS = Mean sum of squares; %SS =% contribution to total sum of squares; PH=Plant height; EH=Ear height; EPP=Ears per plant; DS=Days to silking; DP=Days to pollen shedding; ASI=Anthesis silking interval; EL=Ear length; ED=Ear diameter; NKR=Number of kernel rows per ear; NKPR=Number of kernels per row; KT=Kernel thickness; KW=Kernel width; KL=Kernel length; TSW=1000 Seed weight; GY=Grain yield.

environmental change. Genotypes H12, L166 and H433 had sensitivity values very close to 1.0 which indicated that they had average grain yield stability. Genotype H433 was associated with high grain yield of 6.88 t/ha thus indicating its good general adaptability. The most stable genotypes with the lowest deviation from

Table 6. Mean yield, environmental sensitivity (b_i), stability (S^2_{di}) and stability ranks for 70 maize genotypes evaluated across three consecutive cropping seasons (environments) at Malkerns, Eswatini.

S/N	Name	Mean (t/ha)	b_i	S^2_{di}	Stability ranks	S/N	Name	Mean (t/ha)	b_i	S^2_{di}	Stability ranks
1	H43	5.26	1.08	0.37	15	36	M222	5.07	0.18	0.23	7
2	H327	6.10	1.52	0.58	29	37	M283	6.68	0.30	0.64	30
3	L161	8.06	1.41	0.13	3	38	M701	7.64	2.29	1.91	60
4	H13	6.04	-0.17	0.79	35	39	M6	5.60	1.63	0.57	28
5	M640	5.32	0.87	0.12	2	40	M22	6.75	1.84	2.83	67
6	M3	5.20	0.67	0.31	9	41	L164	5.74	1.08	2.48	63
7	M20	5.63	1.10	0.99	43	42	H42	5.50	0.01	0.48	23
8	M251	7.87	0.34	0.88	40	43	M627	6.88	1.62	2.53	64
9	M24	7.91	1.76	1.01	45	44	M498	7.02	1.12	0.57	27
10	M4	7.35	0.68	0.18	4	45	M197	6.17	1.29	0.35	13
11	L480	5.10	-0.07	0.32	10	46	L301	4.74	0.78	0.65	31
12	H406	5.48	1.36	0.36	14	47	L222	4.89	0.74	0.47	22
13	H328	3.46	0.63	0.08	1	48	L167	5.97	0.86	0.99	44
14	H188	5.44	1.14	0.32	10	49	M530	7.20	1.72	0.82	38
15	M26	6.47	0.19	1.06	46	50	M258	7.23	-0.04	1.07	47
16	M19	8.57	1.69	2.23	62	51	L166	5.71	0.95	3.59	68
17	M17	6.95	-0.28	0.82	37	52	H340	5.75	2.11	0.55	26
18	M5	6.57	1.24	0.53	24	53	H900	7.30	1.21	0.92	41
19	M257	5.03	1.35	0.34	12	54	H45	4.94	1.20	0.46	21
20	H177	6.30	0.72	0.77	34	55	H12	6.04	1.03	1.47	54
21	H400	6.11	2.01	0.39	17	56	H14	7.66	1.55	0.30	8
22	H506	6.13	0.22	1.74	58	57	M256	5.72	1.43	0.76	33
23	H9	6.20	0.63	1.33	53	58	M274	7.29	-0.32	1.55	55
24	S139	5.92	0.77	0.79	36	59	M284	6.03	1.47	0.43	19
25	S624	6.43	1.21	2.54	65	60	M305	6.37	-0.87	0.53	24
26	S40	4.66	0.79	0.95	42	61	L623	7.00	2.27	4.10	70
27	M484	6.69	-0.46	1.11	48	62	L223	7.18	1.60	1.86	59
28	M18	6.08	0.44	0.88	39	63	L525	6.47	1.35	0.37	16
29	L163	6.54	0.88	1.31	52	64	H309	6.95	0.74	1.73	57
30	L170	7.74	1.28	3.64	69	65	M200	6.84	1.48	0.22	6
31	H433	6.88	0.97	1.28	51	66	S38	6.08	1.81	0.67	32
32	H288	5.69	0.62	1.22	49	67	M466	7.07	0.82	0.44	20
33	S516	6.85	1.28	2.06	61	68	H151	6.62	0.81	2.74	66
34	S210	6.21	1.72	1.23	50	69	H247	6.53	1.56	0.40	18
35	M25	10.36	1.22	0.20	5	70	S211	7.67	1.56	1.62	56

regression were H328 ranked first, M640 ranked second and L161 ranked third (Table 6).

DISCUSSION

The significant variation observed among genotypes for the different traits studied indicated the presence of genotypic differences. The wide range in days to pollen shedding (63 to 84 days) of the genotypes, for example, suggests possibility for breeding maize cultivars for the various agro-ecological zones of Eswatini with differing rainfall and length of growing season. Wide diversity in ear and plant heights observed in this study is consistent with other studies (Barros et al., 2019; Sesay et al., 2016; Sesay et al., 2018) who were working with Brazilian and Ivorian maize landraces, respectively. The narrow diversity values in kernel sizes observed in this study were also consistent with other similar studies (Jaradat and Goldstein, 2013; Bisen et al., 2017; Arwailayah et al., 2019).

The estimates of PCV in all the morpho-agronomic traits evaluated on the maize landraces were consistently greater than those of the GCV. This scenario is an indicator that environmental conditions influenced their phenotypic expression. Similar observations were reported by others (Ogunniyan and Olakojo, 2015; Sesay et al., 2016; Sesay et al., 2018; Arwailayah et al., 2019). In the current study, ear diameter and ear length exhibited the highest GCV and PCV values. The results also indicated that there were narrow differences between the PCV and GCV of both traits (including male and female flowering dates) which indicated that the traits were under the influence of genetic factors and less influenced by the environment. Very high heritability estimates were observed in ear length and ear diameter and they were accompanied by high to moderate genotypic and phenotypic coefficients of variation, which indicates that most likely the heritability was due to additive gene effects and selection may be effective in early generations, preferably in simple recurrent selection programmes. The result is in line with the findings of Ogunniyan and Olakojo (2015), Sesay et al. (2016) and rwailayah et al. (2019). The ASI indicated moderate levels of heritability which indicated that this trait was mainly influenced by environmental factors like weather patterns and this was also reported by Ngungi et al. (2013).

Significant genotypic variations were observed for all morpho-agronomic traits indicating opportunity for selection of superior genotypes based on trait of interest. Similar variations in grain yield and other agronomic traits response in maize germplasm to different environments have been reported (Anley et al., 2013; Ndhlela et al., 2014; Abate, 2020). Significant environmental variations were observed for most of the traits except ears per plant, ear diameter and kernel sizes. The different performance of genotypes across environments could also be indicative of wide variations in testing location (years) due to unpredictable variations in climatic conditions. Similar observations on significant environmental variations in maize inbred lines and open pollinated maize varieties were reported by others (Falcon et al., 2020; Abate, 2020). Significant GEI in plant and ear height, days to silking and pollen shed, ASI, grain yield and its components indicates the presence of fluctuation of genotypes performances across environments or testing sites. In addition, this indicates that for that particular trait, specifically adapted genotypes in more specific environments can be identified. Similar results were reported by other authors (Alberts, 2004; Anley et al., 2013; Abate, 2020). Number of ears per plant, traits related to ear and kernel sizes were not statistically significant for the interaction of genotypes and environments. This gives them properties that are desirable for classification purposes because they are less affected by environmental fluctuations. Similar observations were reported by Falcon et al. (2020).

Plant and ear heights, number of kernels per row and grain yield tended to show greater environmental sensitivity and this might be due to their higher heritability. This is also supported by the high standard deviations values indicating wide variations in performance across environments. Kernel thickness and width exhibited lower environmental sensitivity values, which might be due to the large genetic effects and less environmental effects controlling the expression of the trait. Similar observations were noted in previous works (Hung et al., 2012; Falcon et al., 2020). The same scenario was also seen in number of kernels per row which is normally determined earlier in the crop's development, but the final number of kernels per row is influenced by stress during the silking period, which can lead to kernel abortion (Peiffer et al., 2014). Based on grain yield, the regression coefficients of 37 maize landraces were greater than unity and thus these genotypes are sensitive to environmental changes and can be recommended for cultivation under favourable conditions. About 42% of the evaluated maize landrace had regression coefficients of less than unity and thus insensitive to environmental changes. Such genotypes can be recommended for cultivation in poor environments. The same observations were noted by Falcon et al. (2020) in maize inbred lines. Most of the genotypes had higher grain yield sensitivity to environmental changes, while some had greater resistance of grain yield to environmental changes. Genotypes H12, L166 and H433 had regression coefficients equal to unity, which indicate average sensitivity to environmental changes.

There were inconsistencies in grain yield rankings of genotypes across environments. This gives rise to cross over type of GEI indicating that there was unpredictable genotype grain yield performance across environments. The interaction of genotypes with environmental factors (climatic conditions) is an important consideration for plant breeders. The statistically non-additive GEI suggests dependence of grain yield differences among genotypes on the environment (Annicchiarico, 2002). A strategy to reduce GEI involves selecting cultivars with a better stability across a wide range of environments in order to better predict their behavior (Annicchiarico, 2002; Abate, 2020). Variations in the deviations from regression indicated the extent of grain yield stability among the evaluated genotypes. Thus, based on the deviation from regression, the most stable genotypes were H328, M640 and L161. These genotypes are expected to perform reasonably well under a range of conditions, normally experienced at Malkerns. These genotypes can also assist the maize producer in risk avoidance (Annicchiarico, 2002). Maize growers recognize yield stability as the most important socio-economic objective to reduce crop failure, especially in Eswatini which is characterized by low-input agricultures often faced with erratically and unpredictable climatic conditions.

Conclusion

Understanding the extent of genetic variability existing in breeding materials is vital and leads to effective utilization of the breeding materials in crop breeding programmes.

Genetic variability parameters give an indication of the extent of genetic variation of quantitative traits available for exploitation. From the results of the study, it can be concluded that significant variability was present in days to maturity traits and grain yield and its components. The estimates of PVC in all the morpho-agronomic traits evaluated on the maize landraces were consistently greater than those of the GCV indicating that environmental conditions influenced their phenotypic expression. Heritability estimates are of remarkable significance to the breeder, as its extent indicates the precision with which a genotype can be recognized by its phenotypic expression. Ear length and ear diameter showed very high heritability accompanied with high to moderate genotypic and phenotypic coefficient of variation which indicates that most likely the traits were under the influence of additive gene effects. Plant and ear heights, number of kernels per row and grain yield tended to show greater environmental sensitivity, while kernel sizes exhibited lower environmental sensitivity values. Most of the evaluated maize landraces showed grain yield sensitivity to environmental changes, while the rest were insensitive. There were inconsistencies in grain yield rankings of genotypes across environments, which prompted the need to identify stable genotypes. Grain yield stability of genotypes as measured by the deviation from regression parameter varied across genotypes. However, genotypes H328, M640 and L161 were found to have stable yield performance across environments.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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