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Genotype x environment interaction analysis of soybean (*Glycine max* (L.) Merrill) grain yield across production environments in Southern Africa

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ABSTRACT

Development of high yielding and stable cultivars of various crops across the Southern African Development Community (SADC) member states is in line with the recently enacted SADC's seed harmonisation act. This study, therefore, focused on evaluating soybean [*Glycine max* (L.) Merrill] lines developed by the International Institute of Tropical Agriculture (IITA) for yield and stability across SADC test environments using the additive main effects and multiplicative interaction (AMMI) analysis. Twenty-five elite lines (five checks and 20 experimental) were evaluated at six locations across four SADC countries during the 2017/18 season in a 5*5 alpha lattice design, replicated three times at each location. The locations were: IITA-SARA, Lusaka West and Chipata in Zambia; Chitedze in Malawi; Nampula in Mozambique; and Rattray Arnold Research Station in Zimbabwe. The environment, genotype, and genotype x environment interaction (GEI) effects were highly significant ($p < 0.001$), with contributions to total observed variation of 21.04 %, 31.59 % and 47.36 %, respectively. The first two interaction principal component axes (IPCA1 and IPCA2) explained 44 % and 22 %, respectively of the variation due to GEI. Twelve genotypes (48 %) yielded above the grand mean of 3146.31 kg/ha. Check variety SC SAFARI was the highest yielder across environments followed by experimental lines TGx2014-5GM and TGx2002-23DM. Lines TGx2002-17DM, TGx2001-10DM, TGx2001-18DM, TGx2014-24FM, TGx2001-6FM and TGx2002-3DM were winners in Chitedze, Nampula, IITA-SARAH, Lusaka West, Chipata and Rattray Arnold Research Station, respectively. Since TGx2014-5GM was the most stable among all the genotypes across environments, highest yielder (4143 kg/ha) among the experimental lines and second to the highest yielding check (SC Safari), it is therefore recommended for release for production in the SADC after further evaluation. Lusaka West was the highest yielding environment and exhibited strongest interactive forces whilst Nambula had weakest interactive forces.

1. Introduction

Soybean [*Glycine max* (L.) Merrill], is the global source of high quality, inexpensive protein (40 %) and vegetable oil (21 %). The crop is extensively used as human food, animal feed and raw material for manufacturing of various industrial products (Sinclair et al., 2014). It is a good crop for rotation with cereals as it improves soil fertility and helps to break the build-up of pests and diseases that are unique to cereals (Athoni and Basavaraja, 2012). Soybean production has increased in the recent years in southern Africa, owing to the increased demand for vegetable oil, protein and soybean cake. The crop follows maize and wheat in terms of production area in the southern African region, which contributes over 50 % of Africa's total soybean production (FAO, 2017). However, despite the importance of soybean, its productivity in the southern Africa region is still low (1.1 ton/ha) compared to other producers in the world (Mohamedkheir et al., 2018).

The use of improved cultivars that are stable and well adapted to the prevailing agro-ecological conditions coupled with good management practices can help to boost productivity. This makes the assessment of cultivars for adaptability and stability a critical component in plant breeding. Therefore, performance evaluation of elite cultivars through multi-environment trials (METs) within the environments or representatives of environments in which cultivar(s) are intended to be produced is important. Analysis of MET enables breeders to detect and understand the effect of genotype x environment interaction (GEI) to the ultimate performance and performance ranking of a genotype.

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Sharifi et al. (2017) defined GEI as the variation in the performance of a genotype in different environments. Genotype x environment interaction is only important if it is significant and causes genotypes to rank differently (referred to as crossover GEI) (Fernandez, 1991). The crossover GEI is important for selection of specifically adapted genotypes, while the non-crossover type is important when selecting widely adapted genotypes (Kaya et al., 2006).

Recent developments in international seed laws and policies support seed production and sharing across nations. The recently enacted Southern African Development Community's (SADC) seed harmonisation act allows plant breeders to develop, produce and market across SADC countries (Lewis and Masinjila, 2018; Mahop, 2016). At the centre of the SADC's seed harmonisation act is the mandatory cultivar evaluation across at least two-member countries (Lewis and Masinjila, 2018; Cameron and Sparg, 2018). Environments in the four SADC countries (Zambia, Malawi, Mozambique and Zimbabwe), where the soybean lines in the current study were evaluated are highly varied in terms of latitude, altitude and rainfall. Variability in climatic conditions can cause differential responses among genotypes (Gurmu et al., 2009). Therefore, implementation of regional METs across these countries would help to understand and dissect GEI so that stable and specifically or widely adapted cultivars can be identified and recommended for production in the target environments.

A number of analytical tools have been used to assess the stability and adaptability of genotypes across environments and these include; joint regression developed by Finlay and Wilkinson (1963), stability models by Eberhart and Russell (1966), the additive main effects and multiplicative interaction (AMMI) developed by Gauch (1992); and genotype main effects and genotype by environment interaction (GGE) biplot developed by Yan et al. (2000). The AMMI and the GGE approaches combine univariate methods for the environment and genotype additive main effects with a multivariate method for the multiplicative effect of GEI (Zobel et al., 1988) thereby providing a better interpretation of multi-environmental data set (Bhartiya et al., 2017). Both approaches use biplots to graphically visualise GEI. The AMMI model is effective in assessing the adaptability and stability of genotypes (Pacheco et al., 2005). Accuracy in the AMMI model is achieved by separation of structural variation from noise (Nassir and Ariyo, 2011). The AMMI's stability value (ASV), is helpful in identifying stable genotypes across environments (Purchase, 1997). Lower AMMI stability values are an indication of greater stability of genotypes (Anley et al., 2013).

This study constituted a preliminary adaptation and stability analysis of elite soybean lines for production in southern Africa using AMMI. The specific objectives were to (i) assess the presence and magnitude of genotype x environment interaction, (ii) identify and recommend lines that have potential for specific and wide adaptation and (iii) identify environments with strong or weak interactive forces.

2. Materials and methods

2.1. Germplasm and study sites

Twenty elite soybean lines developed by IITA, and five commercial checks (Table 1) were used in the study. The study was conducted in Zambia, Malawi, Mozambique and Zimbabwe in the 2017/18 rainy season from October 2017 to May 2018 across six environments. Descriptions of the six environments are given in Table 2 and Fig. 1.

2.2. Trial design and management

The 25 soybean lines were evaluated in a 5 × 5 alpha lattice design, replicated three times per environment. A plot consisted of four rows that were 0.5 m apart and 5 m long. The intra-row spacing was 0.05 m, resulting in a population of about 350,000 plants per hectare. Basal fertilizer (25 kg N/ha, 30 kg K_2O/ha, 60 kg P_2O_5/ha) was applied at planting and pre-emergence herbicides (Metolachlor and Imazethapyr) were applied soon after planting to prevent weeds from germinating. Weeds that germinated later in the season were both mechanically (hand weeding) and chemically (Quizalofop-p-ethyl and Fomesafen) controlled. When the crop had fully matured, the net plots (two middle rows) in each replication were harvested and the weight of seed was recorded for each plot in kg. The weight was converted to yield in kg per hectare after being corrected to 11 % moisture content as described by Mushoriwa (2013).

2.3. Data analysis

2.3.1. Analysis of variance

The grain yield data collected at each site were subjected to analysis of variance (ANOVA) followed by combined analysis of variance for all the six sites using PROC GLM in SAS 9.4 software (SAS, 2013). The replications within location were considered as random effects, whereas the genotypes were taken to be fixed effects so that the genotype (G), environment (E) and the interaction (GEI) effects could be determined to be significant or not. The combined ANOVA model used is given in Eq. (1):

$$Y_{ijkl} = \mu + G_i + E_j + R_{k(j)} + B_{l(jk)} + GE_{ij} + e_{ijlk} \quad (1)$$

Where Y_{ijkl} is the response of the ith genotype in jth environment and kth replication within environment and lth block within replication; μ is the grand mean, G_i is the genotype effect i; E_j is the environment effect j; $R_{k(j)}$ is the replication within environment effect k; $B_{l(jk)}$ is the block within replication effect l; GE_{ij} is the genotype × environment interaction effect; and e_{ijkl} is the random error.

2.3.2. Additive main effects and multiplicative interaction (AMMI) analysis and AMMI's stability value (ASV)

The AMMI analysis was carried out in Genstat version 18.2 (VSNi, 2016). An approach described by Gauch (2013) to determine if AMMI analysis could be employed for this study was used as follows: Genotype by environment interaction noise (GEI_N) was computed by multiplying the error mean square by the degrees of freedom (df) for GEI (120 × 59,221 = 7,106,520) and GEI signal (GEI_S) was then estimated by subtracting GEI_N from the sum of squares (SS) of GEI ($165023998 - 7106520 = 157,917,478$). For this study GEI was not hidden in the noise, thus AMMI analysis was used to explore the GEI. The AMMI model combines both ANOVA and PCA in assessing the stability and adaptability of genotypes. The genotype and environment main effects were taken to be additive using ANOVA, while the GEI was taken to have a multiplicative effect by PCA. Statistical significance method was used for model diagnosis and selection. The model used to determine the nature of GEI was adopted from Zobel et al. (1988) and the biplot was constructed using IPCA1 and IPCA2 scores. The model is given in Eq. (2):

$$Y_{ij} = \mu + \alpha_i + \beta_j + \Sigma_n \lambda_n \delta_{in} \gamma_{jn} + P_{ij} + e_{ij} \quad (2)$$

Where Y_{ij} is the mean yield of the ith genotype/line effect in jth environment in all replications; and the additive components are μ (the grand mean), α_i (the ith genotype effect) and β_j (the jth environment effect). The multiplicative component consists of λ_n, δ_{in}, γ_{jn} *and* P_{ij} terms, where λ_n is the singular value, δ_{in} is the eigen vector for the genotypic principal component, γ_{in} is the environmental principal component, P_{ij} are the AMMI residuals and e_{ij} is the random error.

The AMMI stability values calculated using the formula proposed by Purchase (1997) were used to rank the 25 genotypes according to their stability. The lower ASVs are associated with great stability of genotypes. The model for ASV is given by Eq. (3):

$$\text{ASV} = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2}(IPCA1\ Score)\right]^2 + (IPCA2\ score)^2} \quad (3)$$

Table 1
Experimental soybean elite lines and checks evaluated in the four countries.

Genotype code	Genotype name	Source	Maturity	Growth habit	Generation
G1	TGx2001-11DM	IITA – Zambia	M	I	F_7
G2	TGx2014-21FM	IITA – Zambia	M	I	F_7
G3	TGx2002-7FM	IITA – Zambia	M	I	F_7
G4	TGx2014-5GM	IITA – Zambia	M	I	F_7
G5	TGx2002-14DM	IITA – Zambia	E	I	F_7
G6	TGx2001-24DM	IITA – Zambia	M	I	F_7
G7	TGx2001-6FM	IITA – Zambia	M	I	F_7
G8	TGx2001-13DM	IITA – Zambia	M	I	F_7
G9	TGx2002-23DM	IITA – Zambia	M	I	F_7
G10	TGx2014-19FM	IITA – Zambia	M	I	F_7
G11	TGx2001-8DM	IITA – Zambia	M	I	F_7
G12	TGx2001-1DM	IITA – Zambia	M	I	F_7
G13	TGx2001-10DM	IITA – Zambia	L	I	F_7
G14	TGx2002-5FM	IITA – Zambia	M	I	F_7
G15	TGx2014-16FM	IITA – Zambia	M	I	F_7
G16	TGx2014-24FM	IITA – Zambia	M	I	F_7
G17	TGx2001-18DM	IITA – Zambia	M	I	F_7
G18	TGx1987-62F	IITA – Zambia	M	I	F_7
G19	TGx2002-3DM	IITA – Zambia	M	I	F_7
G20	TGx2002-17DM	IITA – Zambia	M	I	F_7
CH1	Kafue	IITA – Zambia	E	D	Commercial
CH2	Lukanga	Zamseed - Zambia	M	D	Commercial
CH3	MRI Dina	MRI Syngenta	L	I	Commercial
CH4	SC SAFARI	Seed Co - Zambia	M	I	Commercial
CH5	SC SQUIRE	Seed Co - Zambia	M	I	Commercial

L = late maturity, M = medium maturity, D = determinate growth habit, I = indeterminate growth habit, IITA = International Institute of Tropical Agriculture.

Where,

ASV = AMMI's stability value; SSIPCA = Interactive Principal Component Axis sum of Squares 1 and 2; IPCA 1 and 2 Score = Interactive Principal Component Axis 1 and 2 scores.

R software version 4.0.1 (R Core Team, 2020) was used to compute bar graphs of number of genotypes vs mean grain yields across the environments.

3. Results

3.1. Combined analysis of variance

The combined analysis of variance (Table 3) showed that the genotype (G), environment (E) and genotype x environment interaction (GEI) effects were highly significant ($P < 0.001$). The environment main effect contributed 19.9 % to the total sum of squares and the contributions of genotype and genotype by environment interaction effects were 24.5 % and 35.6 %, respectively. The grand mean and coefficient of variation (CV) were 3146.3 kg/ha and 7.46 %, respectively.

3.2. AMMI ANOVA for grain yield

The AMMI ANOVA (Table 4) revealed that the genotype, environment and genotype x environment interaction (GEI) effects were highly significant ($P < 0.001$). The GEI effect accounted for 47.36 % of the total variation whilst genotype and environment main effects contributed 31.59 % and 21.04 %, respectively. The GEI was further partitioned into five IPCAs, which were all highly significant ($P < 0.001$). IPCA1 contributed 44.39 % to the GEI sum of squares. The first three IPCAs explained about 81 % of GEI variation and accounted for 65 % of the GEI degrees of freedom. GEI signal (GEI_S) was 95.7 % while GEI_N contributed 4.3 % to the total GEI sums of squares, which indicates the accuracy of the data.

3.3. IPCA scores, AMMI stability values and mean yields

Lusaka West (E2) followed by IITA-SARAH (E1) had more genotypes above the grand mean of 3146.31 kg/ha (Fig. 2). Nampula (E6) was the least and recorded a mean grain yield of 2739.79 kg/ha. Mean grain yield across environments ranged from 2444.66–4250.87 kg/ha (Table 5). Across environments the check CH4 (SC SAFARI) was the highest yielder with 4251 kg/ha followed by experimental line G4 (TGx2014-5GM) with 4143 kg/ha. Experimental lines G20 (TGx2002-17DM) and G2 (TGx2014-21FM) recorded the lowest yields of 2492 kg/ha and 2445 kg/ha, respectively. Twelve genotypes (CH1, G6, CH3, G16, G7, G14, CH2, G1, CH5, G9, G4 and CH4) yielded above the grand mean (3146 kg/ha) and the remaining 13 were below the average yield. The ranking of genotypes was different across environments. The lines G7, G17 and G20 had larger IPCA1 scores of -22.05, -22.43 and 30.13. The lowest IPCA1 scores were observed for genotypes G3 (0.05), G4 (0.12) and G11 (-0.40). The AMMI stability values for genotypes ranged

Table 2
Description of the six sites used for evaluation in the four countries.

Code	Environment name	Country	longitude	Latitude	Elevation (masl)	Total rainfall (mm)	Average Temperature (° c)	Soil type
E1	IITA-SARAH	Zambia	E28°30′	S15°30′	1193	703	27.0	Red clay loams
E2	Lusaka West	Zambia	E28°33′	S15°67′	1301	826	26.5	Red clay loams
E3	Chipata	Zambia	E32°39′	S13°40′	1098	1249	24.1	Loamy sand
E4	RARS	Zimbabwe	E31°14′	S17°40′	1341	880	27.4	Red clays
E5	Chitedze	Malawi	E33°38′	S13°59′	1100	929	24.0	Sand clay
E6	Nampula	Mozambique	E39°19′	S15°16′	366	489	30.5	Loamy sand

RARS = Rattray Arnold Research Station, IITA = International Institute of Tropical Agriculture, SARAH = Southern African Region Administration Hub, masl = metres above sea level, mm = millimetres.

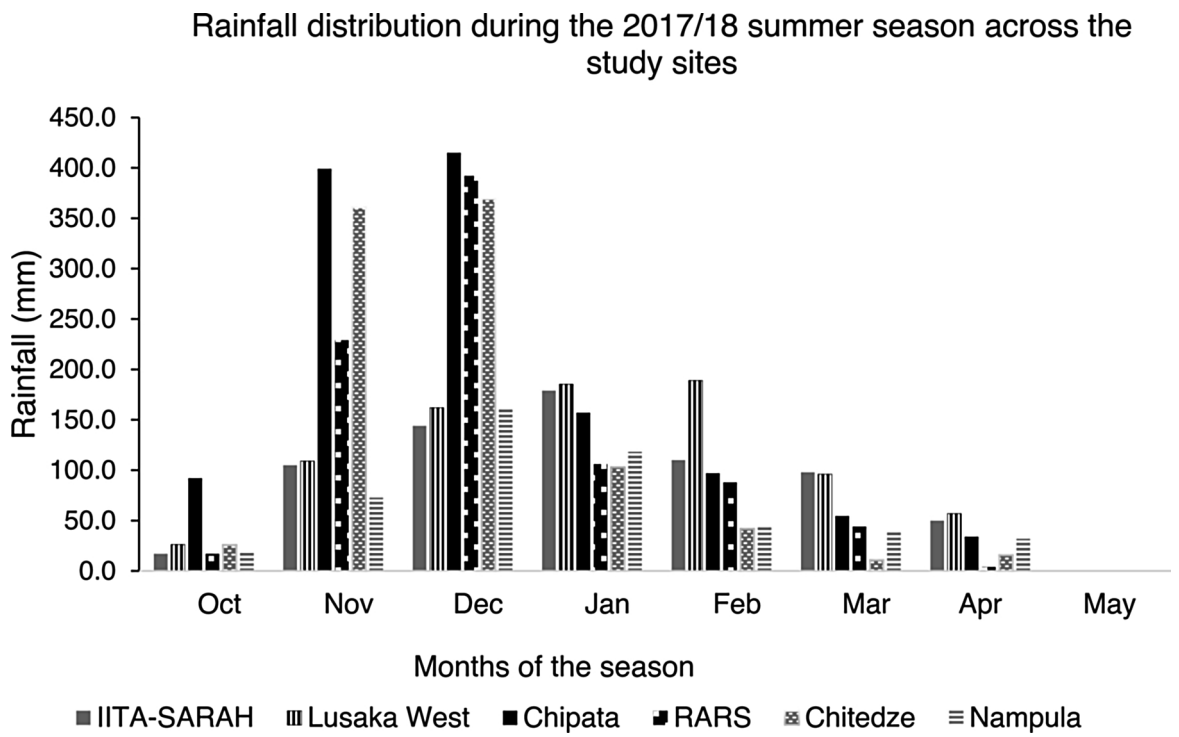

Fig. 1. Rainfall distribution across the six sites for the 2017/18 summer seasons.

Table 3
Combined analyis of variance for grain yield of 25 genotypes across the sites.

Source	DF	SS	MS
Env	5	73316846.5	14663369.3***
Rep(Env)	12	2747445.5	228953.8***
Blk(Env*Rep)	72	5165481.2	71742.8ns
Gen	24	90320032.3	3763334.7***
Env*Gen	120	131267734.1	1093897.8***
Error	216	11890128.3	55046.9
Total	449	368215531.1	
Mean yield	3146.31 kg/ha		
CV%	7.46		

Env = Environment main factor, Rep(Env) = Replication within an environment, Blk(Env*Rep) = incomplete block within an environment, Gen = Genotype main factor, Env*Gen = Environment x Genotype environment, DF = Degrees of freedom, MS = Mean square, SS = Sum of squares, ***Significant at P < 0.001, ns = not significant, CV = Coefficient of variation.

from 1.3 for G14 to 61.4 for G20.

3.4. First four AMMI selections in the six environments

The best four selections from each test environment are presented in Table 6. The check CH4 appeared in the top four in environments E2 (Lusaka West), E1 (IITA-SARAH), E3 (Chipata) and E4 (RARS) whilst experimental line, G4 appeared in the top four in environments E2, E3, E4 and E6 (Nampula, Table 6). Lines G20, G1, CH5 and G9 appeared in the top four in one environment each, namely E5, E6, E3 and E1, respectively.

3.5. AMMI biplots

The first two principal components, IPCA1 and IPCA2, explained 66.25 % of the total GEI variation (Fig. 3). The length of the vector of an environment from the biplot origin is proportional to the amount of GEI. The environments with longer vectors elicit strong interactive forces, while those with shorter vectors elicit weak interactive forces.

Table 4
AMMI analysis of variance for grain yield across the six sites.

Source of variation	DF	SS	MS	Total variation %	GEI explained %	GEI Cumulative %
Treatments	149	348,412,476	2,338,339***			
Block (Env)	12	2,747,446	228,954***			
Genotypes, G	24	110,071,631	4,586,318***	31.59		
Environments, E	5	73,316,846	14,663,369***	21.04		
Interactions, GEI	120	165,023,998	1,375,200***	47.36		
IPCA 1	28	73,248,019	2,616,001***		44.39	44.39
IPCA 2	26	36,080,975	1,387,730***		21.86	66.25
IPCA 3	24	24,835,867	1,034,828***		15.05	81.30
IPCA 4	22	16,929,608	769,528***		10.26	91.56
IPCA 5	20	13,929,530	696,476***		8.44	100.00
Error	288	17,055,610	59,221			
Total	449	368,215,531	820,079			

GEI = Genotype by Environment interaction, IPCA = Interaction principal component axis, *** Significant at P < 0.001, MS = Mean squares, SS = Sum of squares, DF = Degrees of freedom.

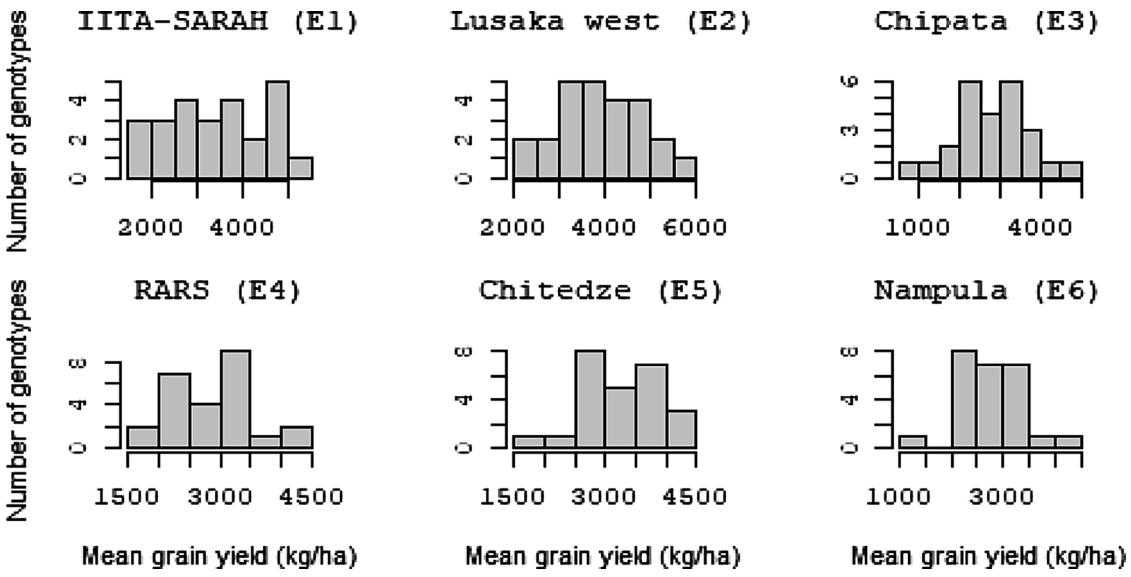

Fig. 2. Number of genotypes and their mean grain yields per environment.

Environment E2 (Lusaka West) had the strongest interactive forces followed by E1 (IITA-SARAH) and E5 (Chitedze). The environment E6 (Nampula) had the weakest interactive forces. The genotypes that are clustered together behaved almost similar across environments. Thus, genotypes G1, G18, G13, G14 and G4 had almost similar yield performances.

A genotype and an environment with markers in the same direction from the origin have a positive GEI, in opposite directions a negative interaction, and at right angles a small interaction. Thus, genotypes G16, G17 and G20, had the positive GEI with environments E2, E1 and E5, respectively. Likewise, genotypes CH4 and G6 had negative GEI with E6 and E3, respectively.

The first IPCA (IPCA1) was plotted against the means for both the genotype and the environment (Fig. 4). Genotypes were distributed below and above the mean grain yield between IPCA1 values of -20 to +30. The environments and genotypes on the left side of the origin had mean yields below the grand mean, whilst those on the right side of the origin yielded above the grand mean. Environments E5 (Chitedze) and E2 (Lusaka West) had large positive IPCA1 values and had mean yields above the grand mean. Environment E2 was classified above the grain yield of all environments and the genotypes that had the same IPCA sign and values close to E2 were G4, G16, G1, G14 and CH1. Environment E6 (Nampula) had the lowest mean yield and a positive small IPCA value close to zero whilst E4 (RARS) had a negative small

Table 6
Best four genotypes in each of the six environments.

Environment	Mean GYD (kg/ha)	IPCA1 Score	1	2	3	4
E1	3372.15	−45.55	G9	CH4	G7	G15
E2	3876.49	15.01	CH4	G4	G16	G12
E3	2780.33	−24.36	CH5	CH4	G5	G4
E4	2857.89	−1.97	G4	CH2	CH4	G7
E5	3251.22	43.04	G20	G10	G16	G6
E6	2739.79	13.83	G1	G4	G14	G9

Mean GYD = Mean grain yield. E1 = IITA-SARAH, E2 = Lusaka West, E3 = Chipata, E4 = Rattray Arnold Research Station (RARS), E5 = Chitedze and E6 = Nampula.

Table 5
Mean yields of top ten and bottom three yielding soybean lines across environments, IPCA scores and ASVs for genotypes.

GEN CODE	E1	E2	E3	E4	E5	E6	Mean GYD	IPCAg1	IPCAg2	IPCAg3	IPCAg4	IPCAg5	ASV
Top Ten													
G4	4078.05	5107.53	3659.42	**4348.43**	3796.52	3867.77	4142.95	0.12	−2.97	7.87	−9.24	−10.05	2.98
G9	**5291.80**	4708.86	2882.64	3288.39	3432.74	3315.60	3820.00	−14.22	−12.44	−18.21	−1.84	0.12	31.43
G1	3874.71	4251.63	2265.94	3345.75	3815.84	**4241.82**	3632.61	5.97	1.33	−14.86	−20.91	2.20	12.19
G14	3311.87	4299.34	3455.5	2732.61	3239.96	3174.65	3368.99	0.47	0.89	9.70	−4.78	13.21	1.31
G7	4748.02	3204.51	3288.17	3411.78	2691.59	2722.36	3344.40	−22.05	6.50	−7.66	0.72	−7.04	45.23
G16	3532.02	5055.68	2338.45	2208.06	4079.71	2671.69	3314.27	11.66	−22.14	−5.00	8.01	7.39	32.42
G11	3295.52	3755.09	3609.63	2280.02	3546.01	2965.36	3241.94	−0.40	5.76	6.48	10.66	19.71	5.81
G5	3506.27	2431.22	3725.63	3123.46	2758.27	3139.57	3114.07	−11.58	24.54	2.60	−4.51	6.15	33.99
G17	4518.94	3992.86	2763.67	2571.74	1927.51	2856.53	3105.21	−22.43	−8.33	−5.60	−12.23	4.74	46.29
G3	2722.47	4289.67	3082.26	2504.79	2612.79	2064.00	2879.33	0.05	−7.37	16.6	3.59	0.94	7.37
Bottom three													
G18	2756.98	3250.38	1642.62	2119.49	2937.09	2475.86	2530.40	6.70	0.09	−7.52	−7.12	1.62	13.60
G20	1732.13	3113.41	859.24	2693.94	**4171.82**	2383.41	2492.33	30.13	5.42	−13.22	0.64	−14.73	61.41
G2	1845.61	2698.46	2193.69	2193.67	3522.05	2214.48	2444.66	14.84	11.80	1.61	6.03	4.00	32.36
Top two checks													
CH4	4877.84	**5656.33**	4313.77	3758.91	3897.56	3000.80	4250.87	−9.48	−15.37	8.98	11.83	−3.25	24.64
CH5	4506.12	4420.10	**4549.19**	3336.51	2628.26	3003.16	3740.56	−22.74	−1.36	16.43	0.24	2.75	46.18
Mean GYD	3372.15	3876.49	2780.33	2857.89	3251.22	2739.79	3146.31						

ASV = AMMI stability value, IPCAe = Interaction principal component axis scores for environments, IPCAg = Interaction principal component axis scores for genotypes, Mean GYD = Mean grain yield. E1 = IITA-SARAH, E2 = Lusaka West, E3 = Chipata, E4 = Rattray Arnold Research Station, E5 = Chitedze E6 = Nampula.

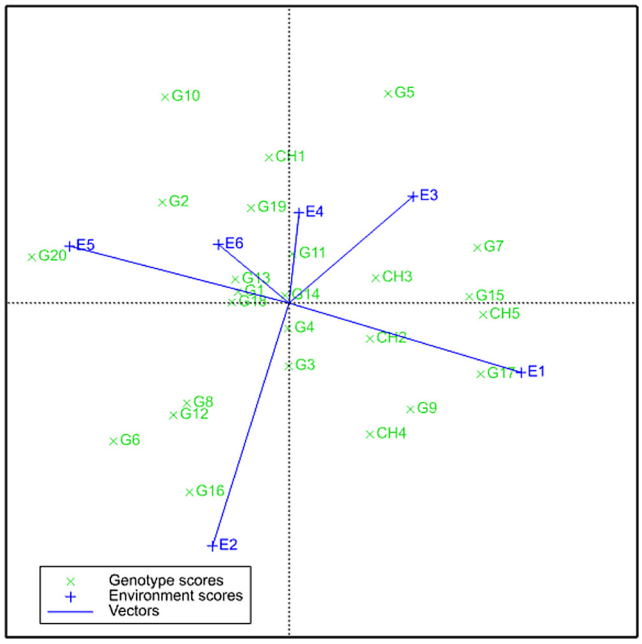

Fig. 3. AMMI2 biplot analysis of GEI.

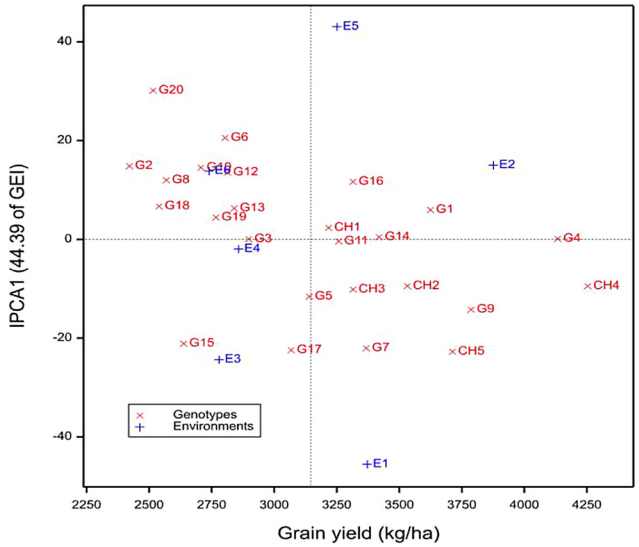

Fig. 4. AMMI1 biplot showing environment and genotype yield means plotted against IPCA1 scores.

IPCA value close to zero with mean yield less that the grand mean. Environment E1 (IITA-SARAH) had the largest negative IPCA1 value and mean yield above the grand mean. Genotypes with negative IPCA1 values and above average yields included CH4, G9, CH5, G7, CH2 and CH3. Overall, out of the 25 genotypes, 12 (48 %) genotypes yielded above the grand mean and 13 (52 %) genotypes yielded below the grand mean.

4. Discussion

The general ANOVA revealed that the genotype (G), environment (E) and genotype by environment interaction (GEI) were highly significant indicating that the lines had significantly different mean performances and ranking in the test environments. The fact that GEI was the largest contributor to the total variation (47 %) and there were different winning genotypes for each environment indicates the presence of crossover type of GEI (Fig. 3 and Table 6). The presence of crossover GEI justifies the need for stability analysis (Yan and Tinker, 2006). In other studies, Atnaf et al. (2013) and Bhartiya et al. (2017) also reported a higher contribution of GEI to total variation with values of 60 % and 41 %, respectively. On the contrary Gurmu et al. (2009); Rakshit et al. (2012); Temesgen et al. (2015); Gurmu (2017) and Vaezi et al. (2017) found the environment to be the highest contributor to the total variation. Tukamuhabwa et al. (2012) and Mushoriwa (2013) also found the presence of crossover GEI in their studies as they found different winning genotypes in the different test environments. Presence of crossover GEI could be attributed to the differences among the genotypes and the environmental conditions of the six sites in four countries. The environments are characterized by differences in altitudes, weather conditions, soil types and rainfall distributions (Fig. 1 and Table 2).

The presence of cross over GEI complicates selection and recommendation of genotypes to environments. According to Yan and Tinker (2006), GEI can be exploited by (i) identifying genotypes that are best suited to specific environments, (ii) identifying best performing genotypes that are stable across environments (wide adaptation) and/or (iii) partitioning the environments into mega-environments followed by identify genotypes that are adapted to the mega-environments. The last option can best be explored with mean performance data of genotypes for at least two or more years/seasons in order to assess repeatability across years (Yan and Tinker, 2006). Hence, the analysis of the current study was limited to the first two options because it was implemented over a single season. However, the observed large percentage contribution of GEI to total variation compared to genotype contribution suggests the probable presents of different mega-environments (Zobel and Gauch, 1996).

Lusaka West (E2), IITA-SARAH (E1) and Chitedze (E5) had stronger interactive forces whilst Nampula (E6) and RARS (E4) had weaker interactive forces. In addition to that, Lusaka West and IITA-SARAH had the highest mean yields among the environments and more genotypes that performed above the grand mean. Therefore, by virtue of these characteristics, Lusaka West and IITA-SARAH can be considered as the best environments to use for soybean evaluation. This concurs with Mushoriwa (2013) who recommended Lusaka West as a good site for conducting multi-location soybean evaluation. The superiority of Lusaka west and IITA-SARAH over other sites could be attributed to the combination of the presence of suitable soils and receipt of enough rainfall that was evenly distributed throughout the growing period as compared to other sites.

The AMMI stability values (ASV) and IPCA scores were used to classify the genotypes according to stability (Table 5). Gurmu et al. (2009) and Annicchiarico (2002) defined a stable and widely adapted genotype as the one with ability to perform consistently and produce mean performance that is above average in all test location. According to this criterion, the most stable lines were G14, G4 and G11. These genotypes could be potential sources of stability alleles, therefore could be utilised in breeding programmes in that respect. All the three lines have the indeterminate growth habit and have medium maturity period, which makes them suitable for the prevailing climate change and weather variability.

Line G4 (4143 kg/ha) could appeal to both farmers and breeders because it was both stable and high yielding, ranked second highest after the check SC Safari (CH4) (4280 kg/ha). Wide adaption is desirable character to farmers because it enables them to salvage something in case of environmental and seasonal changes. Line G4 can be considered for wide adaptation in Southern Africa as it featured in top four ranking in four out of the six environments. Lines G16, G17 and G20, had the positive GEI with environments Lusaka West (E2), IITA-SARAH (E1) and Chitedze (E5), respectively. Therefore, these could be recommended for deployment to the respective targets environments and used as breeding resources in the respective environments. However, further studies are required over more years to confirm these findings and to assess the repeatability of the detected GEI (Yan and Kang, 2003). In another study, Al-Assily et al. (2002) reported three out of

five cultivars being widely adapted and discovered four out of thirty cultivars that exhibited wide adaption. Unlike our findings, Asfaw et al. (2009) reported no genotype with wide adaptation.

5. Conclusion

The study showed that GEI was the highest contributor to the total variation. The type of GEI present was crossover as it resulted in genotypes ranking differently in each environment. Lusaka West followed by IITA-SARAH were identified as exhibiting strong interactive forces and had many genotypes performing above the grand mean. Therefore, the two environments could be useful in selecting good genotypes and culling out unwanted genotypes. Line TGx2014-5GM, which is medium in maturity, was identified as both the highest yielding (4143 kg/ha) among the test lines and stable across the six sites making it a potential candidate for release in the four southern African countries or possibly be used in future breeding programmes as a source of high yielding and stability genes. Lines G16, G17 and G20 had the positive GEI with environments Lusaka West (E2), IITA-SARAH (E1) and Chitedze (E5), respectively. Therefore, they were recommended to be utilised as resources for breeding for specific adaptation in the respective environments. Further evaluation of these materials for more seasons is recommended to assess repeatability of GEI.

CRediT authorship contribution statement

Bubala Mwiinga: Conceptualization, Methodology, Investigation, Formal analysis, Software. **Julia Sibiya:** Funding acquisition, Resources, Supervision, Writing - original draft, Conceptualization, Methodology, Project administration. **Aleck Kondwakwenda:** Conceptualization, Formal analysis, Writing - review & editing, Visualization, Investigation, Data curation. **Cousin Musvosvi:** Conceptualization, Formal analysis, Writing - review & editing, Investigation, Supervision. **Godfree Chigeza:** Supervision, Funding acquisition, Investigation, Software, Validation.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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