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Grain Yield Potential and Stability of Soybean Genotypes of Different Ages across Diverse Environments in Southern Africa

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Abstract: Soybean [*Glycine max* (L.) Merrill] is an important crop in southern Africa where it is cultivated in a wide range of agro-ecologies. Both spatial and seasonal variability is high in the region. As a result, breeders aim to release varieties with a fine balance of high productivity potential and stability. Genotype × environment interaction (GEI) limits the selection of superior genotypes in heterogeneous environments consequently slowing down breeding progress. This study determined the magnitude of GEI effects and genotype superiority index of soybean genotypes of different ages across three countries in southern Africa. Forty-two soybean genotypes that were released between 1966 and 2013 were evaluated for two seasons at thirteen diverse locations across the three countries. Additive main effects and multiplicative interaction (AMMI) and genotype superiority index tools were used to analyse both productivity and stability performance of these genotypes. The AMMI analysis showed that grain yield variation due to genotypes, environments main effects and GEI were highly significant ($p < 0.001$). Environments explained the greatest proportion (77%) of the total treatment sum of squares followed by GEI (17.4%) and genotypes (5.6%), justifying the need for multi-environmental trials over many seasons in this region. The two methods were useful in discriminating and identifying common productive and stable genotypes of different ages. The top four high-yielding (>5.0 tha^{-1}) genotypes displayed both stability and genotype superiority index. These findings have important implications for soybean genotype recommendations, breeding progress, and strategy.

Keywords: adaptation; AMMI; genotype superiority index; genotype × environment interaction; soybean; yield stability

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1. Introduction

Soybean [*Glycine max* (L.) Merrill] is an important leguminous crop which is used for human food and industrial purposes world-wide [1–3]. It is also useful as a supplement in livestock feed and in improving soil fertility through biological nitrogen fixation [4–6]. Soybean is important as a cash crop, nutrition and food security crop in many countries including southern Africa. The crop is grown by both the high and low-input farmers in variable environments. Therefore, productive and stable genotypes are desirable in soybean production.

In southern Africa, the exchange and movement of genotypes of field crops such as soybean across national borders was approved recently. In addition, some local plant breeding companies operate from multiple representative branches in more than one country which enables them to market their genotypes widely in the region. Therefore, genotypes with wide ecological amplitudes are advantageous in such situations. However, soybean is cultivated in a wide range of agro-ecologies (environments) with varying edaphic conditions, latitude and management regimes in the region. The crop is exposed to the influence of genotype by environment interaction (GEI) which can potentially affect the productivity and profitability of the crop. In addition, GEI can limit genetic progress [7]. Nonetheless, a significant GEI can be exploited for selecting stable genotypes for specific environments particularly if potential genotypes are evaluated over a range of locations and years to determine superior and stable genotypes [8,9]. It is generally expected that new genotypes would be superior for both yield and stability when grown in the region of their adaptation. This is due to the fact that breeders are expected to derive new genotypes from elite by elite crosses every year which results in incremental yield performance and stability over the years. However, this might be com-promised by the quest to balance mean performance with diversity, especially in public breeding programmes. Therefore, the objectives of this study were to determine (i) the magnitude of GEI effect on soybean grain yield; (ii) the stability and adaptation; and (iii) the genotype superiority index (GSI) (which is equivalent to the cultivar superiority index as indicated below) of elite soybean genotypes of different ages across three soybean growing countries in southern Africa.

2. Materials and Methods

2.1. Genotypes and Test Environments

Forty-two soybean genotypes, which were released in Zimbabwe during the 1966–2013 period, were utilized in the study. For convenience of the study, the genotypes were coded and their respective designated names indicated (Table 1). The genotypes largely consisted of medium maturity types which require about 106–131 days to mature. The field trials were conducted in three southern Africa countries, namely Malawi, Zambia, and Zimbabwe over two cropping seasons (2010/2011 and 2011/2012). Five and eight test locations were used during the 2010/2011 and 2011/2012 cropping seasons, respectively, resulting in a total of 13 environments (season × location combination). The locations represented the major soybean production ecologies in the region (Table 2).

Table 1. Soybean genotypes evaluated at 13 test environments in southern Africa.

Genotype Code	Designated Name	Year of Release	Maturity (Days after Planting)	Growth Habit
G1	Sovreign	2012	127	Determinate
G2	Rhosa	1966	106	Indeterminate
G3	Bragg	1972	131	Determinate
G4	Oribi	1973	118	Determinate
G5	Buffalo	1974	125	Determinate
G6	Impala	1977	120	Indeterminate
G7	Kudu	1977	121	Determinate
G8	Sable	1980	123	Indeterminate
G9	SC Sequel	2010	121	Indeterminate
G10	Roan	1985	117	Determinate
G11	Gazelle	1988	117	Indeterminate
G12	SC Satellite	2007	118	Indeterminate
G13	Nondo	1992	126	Indeterminate
G14	SC Sirocco	2007	119	Indeterminate
G15	SCS1	1989	121	Indeterminate
G16	SC Sonnet	1994	124	Determinate
G17	SC Sonata	1997	121	Determinate
G18	SC Score	2003	123	Indeterminate
G19	Viking	1999	119	Indeterminate
G20	Bimha	1999	121	Determinate
G21	SC Scorpio	2000	118	Determinate

Table 1. *Cont.*

Genotype Code	Designated Name	Year of Release	Maturity (Days after Planting)	Growth Habit
G22	Nyati	1999	126	Determinate
G23	SC Storm	2000	121	Indeterminate
G24	SC Safari	2001	122	Determinate
G25	SC Siesta	2005	124	Determinate
G26	SC Santa	2005	125	Indeterminate
G27	SC Soprano	1998	125	Determinate
G28	SC Serenade	2006	124	Determinate
G29	SC Soma	1995	129	Determinate
G30	SC Scribe	2007	125	Indeterminate
G31	Nyala	1992	118	Determinate
G32	SC Saga	2008	122	Indeterminate
G33	SC Squire	2008	122	Determinate
G34	Duiker	1982	127	Indeterminate
G35	SC Sputnik	2012	123	Determinate
G36	SC Sepa	2012	127	Determinate
G37	SC Solitaire	1997	120	Indeterminate
G38	PAN 1867	2013	121	Indeterminate
G39	PAN 1856	2005	119	Indeterminate
G41	PAN 891	2008	116	Determinate
G42	SC Spike	2008	127	Indeterminate

Table 2. Physical and weather characteristics of the study locations.

Environment	Country	Year	Code	Latitude	Longitude	Altitude (masl)	Rainfall [1] (mm)
Rattray	Zimbabwe	2010/11	E1	−17.78	31.32	1341	686
Gwebi	Zimbabwe	2010/11	E2	−17.81	30.57	1449	712
Lusaka	Zambia	2010/11	E3	−15.42	28.11	1300	860
Mpongwe	Zambia	2010/11	E4	−13.51	28.15	1219	1000
Bvumbwe	Malawi	2010/11	E5	−15.90	35.10	1228	950
Rattray	Zimbabwe	2011/12	E6	−17.78	31.32	1341	749
Gwebi	Zimbabwe	2011/12	E7	−17.81	30.57	1449	712
Lusaka	Zambia	2011/12	E8	−15.42	28.11	1300	700
Mpongwe	Zambia	2011/12	E9	−13.51	28.15	1199	800
Bvumbwe	Malawi	2011/12	E10	−15.90	35.10	1250	768
Lilayi	Zambia	2011/12	E11	−15.53	28.30	1090	688
Trust	Zimabwe	2011/12	E12	−17.74	31.05	1527	780
Chitedze	Malawi	2011/12	E13	−13.98	33.64	1146	643

[1] Rainfall refers to total precipitation over the two seasons (each rainy season begins in November/December to April of each year) including irrigation; masl = metres above sea level; Rattray = Rattray Arnold Research Station; Gwebi = Gwebi Variety Testing Centre; Lusaka = Lusaka West Farm; Mpongwe = Mpongwe Development Centre; Bvumbwe = Bvumbwe Research Station; Lilayi = Lilayi Farm; Trust = Agricultural Research Trust; Chitedze = Chitedze Research Station.

The environments were characterized by temperatures that ranged from 13.0 °C to 30.0 °C over the two seasons. The location at the Agricultural Research Trust in Zimbabwe was the coolest while Bvumbwe Research Station in Malawi, was relatively warm. The temperatures were generally favorable for the vegetative growth and development of the crop since stressfully higher temperatures negatively affect pollen viability (and hence grain yield) [10].

2.2. Experimental Design and Management

The experiment was designed as a 6 × 7 rectangular lattice with three replications for each test environment. Planting was carried out between the last week of November up to mid-December across all of the sites and seasons. The experimental unit consisted of six rows, 5.0 m long and spaced at 0.45 m. In each row, seed was planted at 6.3 cm apart resulting in a plant population of approximately 350,000 plants ha^{-1}. Assuming that 10% of the seed did not germinate or was lost due to various factors, then number of established

plants (or the harvest plant population) was approximately 315,000 plants ha^{-1}. Standard cultural practices for soybean production that included land or seedbed preparation, hand planting, weeding, herbicide application and crop protection were applied at each test environment. Fertilizer (was applied at a rate of 400 kg ha^{-1} supplying 28 kg ha^{-1} of N, 68 kg ha^{-1} of P_2O_5 and 40 kg ha^{-1} of K_2O. The seed was inoculated with *Bradrhizobium japonicum* inoculant. Across all of the trial locations, both pre-emergence and post emergence herbicides were used. Lasso (Alachlor 384 EC) (active ingredient = chloroacetanilide) and Gramoxone (active ingredient = paraquat) were mixed and applied together as pre-emergence herbicides at planting at 5.0 L ha^{-1} and 3.0 L ha^{-1}, respectively. Basagran (active ingredient = sodium salt of Bentazon) and Bateleur Gold 650 EC (active ingredient = Sulfonanilide (Flumetsulam)) were applied as post emergence herbicides at 3.0 L ha^{-1} and 1.2 L ha^{-1}, respectively. Both herbicides were applied within six weeks post emergence as per recommendation of the manufacturer to control the weeds early. Hand weeding was carried out just before the canopying stage.

Insect pests, notably the soybean looper (*Chrysodeixis includens*) that sporadically appeared in the field trials were controlled using Thionex 35 EC (active ingredient = endosulfan) and Karate 2.5% EC (active ingredient = Lambda-cyhalothrin) which were applied at 400 mL and 266 mL in 200 L of water, respectively. The looper is common in the soybean crop. The fungicide Shavit (active ingredients = Folpet and Triadimenol), was also applied on the trials (at a rate of 266 mL per 200 L of water ha^{-1}) as a preventative measure against soybean rust (*Phakopsora pachyrhizi*) that was prevalent in the region [11–13]. The initial spraying was carried out at 50 days after planting followed by two subsequent applications at 20 day intervals, thereafter.

All of the trials were harvested manually. Due to the variation in duration to maturity, the harvesting in each experimental unit was carried out at the 95% pod maturity [14]. Consequently, the harvesting at each test location was carried out sequentially. The grain yield was obtained from a net plot (7.92 m^2) consisting of four rows measuring 4.4 m long. The grain yield was adjusted for moisture content (calculated at 11%) which is the standard practice in the region.

2.3. Data Analysis

The data sets of the grain yield were subjected to the analysis of variance (ANOVA) model using the model (Equation (1)) and the additive main-effects and multiplicative interaction (AMMI) model [15,16] (Equation (2)) in GenStat 14 software (version, 2011) [17] as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \theta_{ge} + \mathcal{E}_{ger,} \text{ (ANOVA model)} \quad (1)$$

$$Y_{ger} = \mu + \alpha_g + \beta_e + {}^{N}\sum_{n=1} \lambda\varsigma_{gn}\, \eta_{en} + \rho_{ge} + \epsilon_{ger,} \text{ (AMMI model)} \quad (2)$$

where:

Y_{ger} = the grain yield level for genotype g in environment e for replicate r
μ = the grand mean
α_g = genotype mean deviations (mean minus the grand mean)
β_e = the environment mean deviations
N = the number of singular value decomposition (SVD) axes retained in the model
λ_n = the singular value for SVD axis η
ς_{gn} = the genotype singular vector values for SVD axis n
θ_{ge} = the interaction residuals
ρ_{ge} = the AMMI residuals
$\mathcal{E}_{ger}$ = the error term and
${}^{N}\sum_{n=1} \lambda_n \varsigma_{gn}\, \eta_{en} + \rho_{ge}$ is equivalent to the interaction term in the ANOVA model.

The computation estimates the level of noise using statistics from the AMMI ANOVA approach and defined noise as the difference between yield estimate and its true mean [15].

Therefore, the percent level of noise in the GE interaction component was estimated as follows:

$$[100 \times (Interaction\ DF \times EMS)]/Interaction\ Sum\ of\ Squares\ (SS)$$

where:

Interaction DF = interaction degrees of freedom

EMS = the expected error mean square for the AMMI ANOVA

Interaction SS = interaction sum of squares.

One AMMI biplot was plotted and IPCA1 scores were plotted against genotype and environment means. The stability coefficients displaying genotype superiority index (GSI) were also computed in GenStat 14th Edition [17]. The GSI is similar to the cultivar superiority index [18]. The stability of the genotypes across the environments was estimated by the GSI which is a measure of both productivity and stability hence a favourable tool to identify the desirable genotypes for deployment and use in breeding new genotypes for the region.

3. Results

The analysis of variance showed that soybean grain yield was significantly ($p < 0.001$) affected by environments main effects, genotypes main effects and genotype by environment interaction (GEI) effects (Table 3). The treatments (genotypes + environments + interactions) accounted for 87.7% of the total grain yield sums of squares using approximately 33.3% of the total degrees of freedom. The genotypes accounted for 4.9% of the total sums of squares and 5.6% of the treatments sums of squares. On the other hand, the environments explained 67.5% of the total sums of squares and 77.0% of the treatments sums of squares. The interactions explained 15.3% of the total sums of squares and 17.4% of the treatments sums of squares. Therefore, the environments accounted for more variation than the interactions (genotype × environment interactions) while the genotypes captured the least variation. The magnitude of the GEI sum of squares was about three-fold larger than that for genotypes implying that there were significant differences in genotypic response to the test environments.

Table 3. Analysis of variance for full AMMI model for grain yield (kg ha^{-1}) of 42 soybean genotypes evaluated across three countries in southern Africa.

Source	DF	SS	Mean Square	%Total SS Explained	% Treatment Explained	% Interaction SS Explained
Treatments	545	3,795,437,270	6,964,105 ***	87.7		
Genotypes	41	210,926,715	5,144,554 ***	4.9	5.6	
Environments	12	2,922,339,401	243,528,283 ***	67.5	77	
Block	26	62,836,136	2,416,774 ***			
Interactions	492	662,171,153	1,345,876 ***	15.3	17.4	1.00
IPCA1	52	305,345,002	5,872,019 ***			46.1
IPCA2	50	82,263,682	1,645,274 ***			12.4
IPCA3	48	70,168,338	1,461,840 ***			10.6
IPCA4	46	49,375,483	1,073,380 ***			7.5
IPCA5	44	41,744,444	948,737 ***			6.3
IPCA6	42	29,959,161	713,313 **			4.5
IPCA7	40	21,735,111	543,378			3.3
IPCA8	38	20,014,050	526,686			3.0
IPCA9	36	16,705,469	464,041			2.5
Residuals	252	113,274,204	449,501	2.6		
Error	1066	469,556,239	440,484			
Total	1637	4,327,829,645	2,643,757			

; * = significant at $p \leq 0.01$; $p \leq 0.001$, respectively; IPCA, interaction principal component axis terms 1 to 9; DF, degrees of freedom; SS, sum of squares.

The application of AMMI model for partitioning of GEI showed that the first six multiplicative terms of AMMI were significant (Table 3). However, IPCA1 explained 46.1% of the total interaction sum of squares using about 10.6% of the total interaction degrees of

freedom. When IPCA2 was fitted, the two IPCAs explained 58.5% of the total interaction variation using approximately 20.8% of the total interaction degrees of freedom. When the third IPCA was added, the model explained 69.1% of the total interaction using about 30.6% of the total interaction degrees of freedom. The first four IPCAs explained 76.6% of the total interaction variation using approximately 39.9% of the total interaction degrees of freedom. The IPCA5 and IPCA6 were significant and accounted for less than 10% of the sum of squares of the interactions. On the other hand, multiplicative axis from IPCA7 to IPCA9 including the residual captured mostly noise.

The model selection was based on firstly the proportional contribution of each IPCA to genotype × environment interaction and the ratio of noise sum of squares to residual sum of squares. The proportion of noise sum of squares for AMMI3 to its residual sum of squares was almost 1.0 making AMMI3 the most suitable model. In addition, the sum of squares of the first three terms were greater than that of genotypes and highly significant ($p < 0.001$). Although AMMI3 was the best model, the biplot analysis was generated from IPCA1 since it explained 46.1% of the total interaction sum of squares.

The ranking of the first four AMMI selections per environment for grain yield indicated that the highest (7628 kg ha^{-1}) and lowest (3112 kg ha^{-1}) grain yield per environment was attained at Mapongwe in Zambia (E4) and RARS in Zimbabwe (E1), respectively (Table 4). The results also showed that both old and new genotypes were among the top performers with respect to both yield and stability. The genotype G28, which was released in 2006, was among the top four ranked genotypes in at least seven environments followed by genotype G27, which was released in 1998. In addition, genotype G28, attained >5000 kg ha^{-1} in at least five environments (Table 5). Nonetheless, only three genotypes (G4, G9 and G33) among the bottom 21 failed to produce ≥5000 kg ha^{-1} in at least one test environment indicating that there was a strong environmental influence on grain yield. In terms of the GSI, genotype G25 was the most superior followed by genotype G1 while genotype G16 performed the least (Table 5).

Table 4. Ranking of the first four AMMI selections per environment for grain yield.

Environment	Environment Code	Season	Mean (kg ha^{-1})	Rank			
				1	2	3	4
Rattray	E1	2010/11	3112	G29	G22	G15	G42
Gwebi	E2	2010/11	3291	G27	G26	G28	G42
Lusaka	E3	2010/11	5717	G27	G26	G28	G37
Mpongwe	E4	2010/11	7628	G1	G36	G39	G27
Bvumbwe	E5	2010/11	6714	G26	G28	G35	G27
Rattray	E6	2011/12	4662	G14	G15	G6	G16
Gwebi	E7	2011/12	3617	G16	G23	G28	G21
Lusaka	E8	2011/12	3898	G40	G7	G8	G25
Mpongwe	E9	2011/12	3300	G22	G16	G28	G7
Bvumbwe	E10	2011/12	3941	G28	G25	G21	G8
Lilayi	E11	2011/12	4924	G14	G7	G21	G28
Trust	E12	2011/12	4476	G16	G31	G5	G26
Chitedze	E13	2011/12	3753	G15	G17	G14	G1

Rattray = Rattray Arnold Research Station; Gwebi = Gwebi Variety Testing Centre; Lusaka = Lusaka West Farm; Mpongwe = Mpongwe Development Centre; Bvumbwe = Bvumbwe Research Station; Lilayi = Lilayi Farm; Trust = Agricultural Research Trust; Chitedze = Chitedze Research Station.

The biplot of the AMMI-1 showed that genotype G25 had the largest positive (>10) interaction with the environments while G4 had the largest negative interaction with environments (Figure 1). Genotype G28 was the overall best performer, combining relative stability and high yield. In addition, genotypes G15, G25, G28, and G42 were relatively stable and produced above average yield but genotype G12 was the most stable since its mean yield was equal to the grand mean. The test environments showed variability in both main effects and interaction. Environments E3, E4, E5, E6, E11, and E13 were classified above the mean grain yield of all of the environments whereas the remainder performed below the average yield (i.e., less than the grand mean yield level). Genotypes

and environments with the same sign on the IPCA axis interacted positively whereas those with different signs interacted negatively.

Table 5. AMMI IPCA1 scores and grain yield (kg ha^{-1}) of the top 21 soybean genotypes across 3 countries in southern Africa.

GCN	IPCA1	Mean (kgha^{-1})	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13	CSI
G28	0.5	5208	3594	3839	5497	5155	5827	4905	4126	4628	4395	5436	5618	4127	4056	565,077
G1	7.3	5098	4229	3610	4770	6440	5172	4863	4019	4624	3329	4765	5379	4816	4482	524,178
G25	−3.3	5084	3122	3507	4182	5649	5447	5175	3963	4725	3931	5107	5285	4798	4461	521,833
G15	4.4	5059	3692	3661	5028	5685	4865	5295	4071	4427	3031	4406	5334	4919	4849	579,880
G27	17.8	4937	3148	4264	5854	5915	5650	4718	3645	3543	3772	3264	5558	4805	3539	865,860
G21	−7.3	4924	3323	3439	4785	4590	4649	4930	4121	4547	4212	5022	5655	4158	4081	738,208
G14	−5.0	4868	2502	3280	4464	5147	5068	5754	4014	4181	3117	4704	5880	4160	4512	855,125
G42	2.0	4853	3630	3703	4877	5424	5385	4822	3761	4706	4023	4325	5419	2854	3659	918,895
G16	−21.2	4810	3040	3401	3165	2869	5110	5210	4369	4199	4398	4852	5349	6292	3772	1,292,158
G23	9.5	4801	3408	3688	4959	5133	5362	5132	4295	3371	2762	4025	5206	5033	3541	954,777
G35	10.9	4755	3187	3442	5181	5133	5825	4754	3543	3537	2622	4537	4589	4827	4132	982,732
G22	10.2	4748	3958	3692	4620	5401	4837	4232	3215	3730	4402	3959	4240	5082	3852	989,227
G26	16.9	4729	3384	3926	5742	4837	6039	4264	3704	3360	2641	3644	4753	5266	3414	1,108,735
G18	4.9	4722	3480	3494	4747	5685	4046	4336	3782	4410	3662	3842	5352	4179	3865	945,962
G17	4.2	4684	3206	3622	4253	5661	4258	4943	3493	4349	3017	2902	5263	4909	4516	1,050,160
G11	−5.7	4652	3085	3602	4217	4585	4477	4866	3390	4590	3956	3328	5395	4256	4223	1,037,688
G30	−1.7	4633	3547	3172	4739	3836	5542	5137	3933	3816	2475	4882	4572	4022	4050	1,235,065
G29	17.0	4632	4229	3566	4669	5424	5244	4318	3430	3329	2973	3852	3754	5182	3748	1,211,673
G24	12.1	4613	3557	3435	4459	5653	4764	4606	3771	3352	3207	3897	4639	4698	3434	1,120,157
G32	−0.7	4587	2989	3235	4131	4873	4282	4482	3991	4101	2968	3957	5285	5068	3764	1,094,081
G19	−7.0	4573	2519	3496	3949	4087	5204	4848	3723	4206	3396	3577	5542	4779	3618	1,196,375
Overall Means			3112	3291	4680	5104	5098	4662	3617	3898	3300	3941	4924	4476	3753	
$LSD_{0.05}$		561	520	478	630	850	617	607	620	726	795	521	531	635	655	
C.V. (%)		6.0	10.0	9.0	14.0	12.0	12.0	8.0	11.0	20.0	15.0	16.0	10.0	12.0	12.0	

IPCA, interaction principal component analysis 1; E1, Rattray Arnold Research Station, 2010/11; E2, Gwebi Variety Testing Centre, 2010/11; E3, Lusaka West Farm, 2010/11; E4, Mpongwe Development Centre, 2010/11; E5, Bvumbwe Research Station, 2010/11; E6, RARS, 2011/12; E7, Gwebi Variety Testing Centre, 2011/12; E8, Lusaka Farm West, 2011/12; E9, Mpongwe Development Centre, 2011/12; E10, Bvumbwe Research Station, 2011/12; E11, Lilayi Farm, 2011/12; E12, Agricultural Research Trust, 2011/12; E13, Chitedze Research Station, 2011/12; GCN, genotype code name.

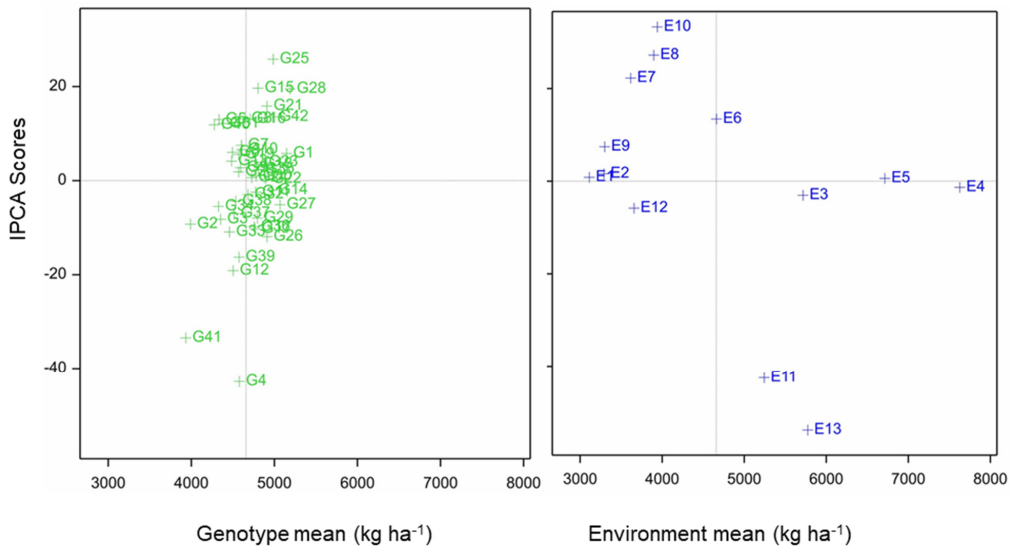

Figure 1. AMMI-1 biplot of IPCA 1 scores against grain yield for 42 soybean genotypes and 13 environments. E1, Rattray Arnold Research Station, 2010/11; E2, Gwebi Variety Testing Centre, 2010/11; E3, Lusaka West Farm, 2010/11; E4, Mpongwe Development Centre, 2010/11; E5, Bvumbwe Research Station, 2010/11; E6, Rattray Arnold Research Station, 2011/12; E7, Gwebi Variety Testing Centre, 2011/12; E8, Lusaka Farm West, 2011/12; E9, Mpongwe Development Centre, 2011/12; E10, Bvumbwe Research Station, 2011/12; E11, Lilayi Farm, 2011/12; E12, Agricultural Research Trust, 2011/12; E13, Chitedze Research Station, 2011/12; G1 to G42 represent the test genotypes.

4. Discussion

The AMMI analysis of variance for the 42 genotypes that were evaluated across 2 seasons and 13 test environments revealed strong evidence that environment, genotype, and genotype × environment effects were significantly different from each other. Furthermore, the results revealed that the environment component had larger influence on the performance of soybean genotypes, indicating the necessity for testing soybean genotypes at multi-location sites and over years [19]. The huge influence by the environment illustrated its impact on controlling the expression of grain yield. The bottom line was that the environments contributed more to the phenotypic value which has affected the selection efficiency and breeding progress. The presence of GEI complicated the selection process of superior genotypes and reduced the selection efficiency in a soybean breeding program [15]. The magnitude of GEI effect was five times larger than that for the genotypes indicating differences in genotypic responses to test environments. However, although the environment accounted for the highest variation, one could expect the GEI to be higher than what was observed since the environments were sampled from three countries thus, greater variability was expected. Generally, the more variable the environments, the greater the GEI [16]. Nonetheless, the GEI variation (17.4%) was close to the expected, possibly implying that most of the genotypes were widely adapted. This was supported by the clustering pattern of a considerable number of genotypes around the grand mean yield with IPCA values close to zero.

The results of the study also showed a low GEI in respect of the expected proportion of the components of the treatment sum of squares (70:20:10). Therefore, genotypes that combined both high grain yield and stability (G1 and G15) were recommended for cultivation in all areas that were represented by the test locations. In contrast, the genotypes that exhibited high IPCA scores (G2, G4, G5, G7, G16, G17, G18, G31, and G40) were recommended for specific adaptation. The low IPCA values revealed poor interaction with the test environments that were used in the study, thus indicating less responsiveness to environmental changes. However, at least eight genotypes that were grouped in the top third of the mean yield table could be classified as the best genotypes combining both high stability and above average yield performance [20]. On the other hand, genotype G12 which attained the highest stability rating (IPCA score = 0) and combined low GEI and average yield suggested that it was the most suitable for cultivation across sites and seasons. However, its low yield potential makes it unattractive to farmers. The genotypes that showed large interaction with environments were classified as unstable and hence unpredictable in performance but could be recommended for specific adaptation. The differences among the test environments and their clustering patterns could be attributed to differences in latitude, altitude, climatic conditions, duration of the cropping season as well as seasonal effects. Often, the long duration of the cropping season is correlated with high yielding potential [21]. However, lengthy cropping seasons can be prone to meteorological fluctuations as well as the negative effects of soil moisture stress [22–24]. For instance, in both chickpea and soybean, pod abortion increased under terminal drought stress [25,26]. Most of the environments produced the least interaction effects suggesting that they were ideal for evaluation and selection since the performance of the genotypes can be stable. In addition, both the IPCA scores and GSI identified genotype G1 and G25 as the highest yielding and most stable. Therefore, the two stability parameters could be used for simultaneously selection for high yield and stability.

The results also showed that the newly released genotypes (which were released during 2005, 2006 and 2012), were generally superior in performance than most of the older genotypes, except G15 which was released in 1989. Therefore, it can be argued that there was sound breeding progress in the region which resulted in a significant build-up of high allele frequency for adaptation, productivity and stability. The performance pattern increased significantly since the genotypes from the earlier decades were generally poorly adapted and unstable as revealed by large IPCA scores and high genotype superiority indices. However, there are surprises of older genotypes outperforming the most recent

(2012 and 2013) genotypes. The genotype G28 was found to be relatively best yielding. In addition, the genotype possesses desirable characteristics which include good quality seed, high number of nodes per plant and good standability. It is generally large seeded (average 100 seed weight approximately 25.0 g). Although G25 was released in 2005, it attained high grain yield. However, it is susceptible to soybean rust and frogeye leaf spot (*Cercospora sojina*) suggesting that it would be costly to produce where these diseases are endemic. Based on our pedigree information, both G1 and G25 were derived from high yielding genetic backgrounds utilizing elite × elite crosses while some of the other subsequent genotypes were derived from elite × exotic or disease resistant crossing combinations.

The outstanding performance of the genotypes G1 and G25 is partly since both were derived from parents with a high yielding background. The parents of both genotypes were selected on the basis of high additive breeding values. The selection of good parents for each new breeding cycle, that have higher additive breeding value than the previous generation is critical and optimizes the genetic gain [27]. This approach enhances rapid increase in the frequency of favourable alleles, which become fixed in the gene pool. Appreciable rates of genetic gain have been observed in many breeding programs through the application of elite × elite crossing strategy [28]. Essentially, this strategy can drive the competitiveness of the soybean breeding program in the region. It is recommended to evaluate the historical data and use it to create and assemble a core set of high performing lines, such as the top four genotypes that were identified in the current study. The inconsistent utilization of the elite × elite crossing strategy partly explains why some older genotypes outperformed some recently released genotypes. Integration of resistance to new diseases, such as soybean rust, without a good background check could have compromised mean performance of new genotypes that were released in the 2010–2013 period.

As a generalization, AMMI analysis showed that 61.9% of the genotypes obtained IPCA values between −10 and 10, possibly indicating average stability across environments. This suggested that stability was accumulated over time through breeding, extensive evaluation and selection. This was affirmed further by the observation that the founder genotype (G2 which was released in 1966) showed poor stability (IPCA score about 30) in comparison with G28 (which was released in 2006 and IPCA value close to zero). Since yield stability is heritable and conditioned by additive gene action, simple selection methods could be applied in breeding programs to advance yield stability and plasticity for cultivation over a wide range of environments [29,30].

This study was different from previous ones in that it considered the implication of soybean genotypic age (i.e., when a genotype was released) for both productivity and stability, both of which can impact on recommendation of genotypes to growers as well as the breeding and selection of new ones in the region. In addition, the conventional breeders in the region have not been using modern stability models (AMMI and GSI) to identify genotypes that combine both high productivity and stability. Instead, they have been using rank analysis based on the simple arithmetic mean to select and advance new genotypes. The application of modern tools will help to improve selection accuracy and identify genotypes that combine both high productivity and stability which is desired in a region with high levels of variability across sites and seasons. In addition, the information generated in this study will be useful to soybean breeders aiming to develop sustainable genotypes adapted to target environments in the region and possibly using the identified genotypes as reference genotypes in the selection process. Moreover, the stable genotypes that were identified in this study provided insights into future studies aimed at identifying the genomic regions that are associated with stability. For instance, a recent study reported that seven genomic regions in six chromosomes of soybean were associated with genotype-by-environment interactions thus opening a novel frontier of genomic assisted breeding aimed at achieving stable performance of soybean [31].

5. Conclusions

The results of this study showed that both new and old genotypes were among the top four which displayed a combination of high yield potential (>5.0 t ha^{-1}), dynamic stability and GSI. These findings have important implications for soybean genotype recommendations, breeding progress and breeding strategy for the region. These results suggested that grain yield in soybean could be maximized through selecting genotypes showing consistently high yield performance across heterogeneous growing environments. The AMMI analysis revealed the relative magnitude and significance of GEI effects and its interaction terms in relation to genotype and environmental effects. The results also showed that GEI was a vital component of soybean yield variation and the biplots provided a good visualization of the response patterns of genotypes and environments. Two genotypes from both the AMMI and GSI analysis were classified under the high yielding category. Overall, the stability measurements demonstrated that >60.0% of the genotypes were, on average, stable across the 13 test environments while the rest were unstable but suitable for specific environments. Considering the two analytical methods (AMMI and GSI), two genotypes (G1 and G25) were among the best and thus could be recommended for cultivation across the three countries and utilization as breeding stocks in programs that aim to improve both stability and productivity of soybean.

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