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Stability and Adaptability of Soybean [*Glycine max* (L.) Merrill] Genotypes for Yield, Protein and Oil Content using AMMI analysis in Kenya

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ABSTRACT

Stability analysis helps to identify superior genotypes suited to specific agro-ecological zones. The objective of the study was to determine stability and adaptability of fifteen soybean genotypes for seed yield, protein and oil contents by additive main effects and multiplicative interaction (AMMI) analysis. The research was conducted at Eldoret, Lanet, Nakuru West and Njoro. AMMI analysis identified genotypes DPSB 8 and SBH 7/1/1 as most stable for seed yield with means above the trial mean of 1267 kg ha^{-1}. Genotypes SBH 4/4/4, SBH 7/1/1, SBH 1/12/19 and Gazelle were stable for seed yield and oil content. Genotype DPSB 19 had high and stable protein content (402.8 g kg^{-1}) with low seed yield. Genotypes SBH 4/4/4 and EAI 3600 were stable for pods plant^{-1} and 100-seed weight. Either GGE or AMMI analysis maybe employed to identify stable soybean genotypes for production across environments and adaptable genotypes for specific environments.

Key words: AMMI, GGE, Protein, Soybean, Stability, Yield.

INTRODUCTION

Stability analysis of genotypes is a valuable and important tool for agronomists and breeders. Identification of adapted and stable genotypes translates to increased profitability (Modali, 2004). Stability analysis helps to identify and make choice of superior performing genotypes for a given set of agro-ecological zones Jadong *et al.* (2011). Additive main effects and multiplicative interaction analysis (AMMI) combines additive components for the principal genotype effects and environments, with multiplicative components for the effects that involve G × E interactions Oliveira *et al.* (2006). A genotype and genotype by environment (GGE) biplot method by Yan *et al.* (2000) emphasizes that although measured yield is the combined effect of genotype (G), environment (E) and genotype by environment interaction (G×E), only (G) and GE are relevant to and must be considered simultaneously, in cultivar evaluation (Yan and Rajcan 2002). A genotype should have a high PC1 score indicating high yield ability and a small (absolute) PC2 score indicating high stability Ullah *et al.* (2011). Biplot analysis has been utilized to identify cultivar performance in an environment, identification of mega environments, selection of superior cultivars and test environments for a given mega environment and identification of stable cultivars (Yan and Rajcan, 2002).

Soybean [*Glycine max* (L.) Merrill] is an important food and cash crop in the tropics due to its nutritional qualities and adaptability to diverse environments (McKevith, 2005). The crop is an important source of oil (20%) and protein (40%), useful in maximizing dietary protein and oil gap for the masses Gunjan *et al*. (2016). Soybean benefits the soil through biological nitrogen fixation, revitalizing and maintaining soil fertility Ngalamu *et al.* (2013). Evaluation of genotypes under different environments for their stability in yield, oil and protein content should be a priority in soybean breeding programs.

The objective of the study was to identify adaptable and high yielding genotypes for specific environments and stable genotypes in yield, oil and protein contents for diverse environments.

MATERIALS AND METHODS

The study was conducted at Njoro (0° 20′S, 35° 56′E) for two seasons (Njoro I and Njoro II), Eldoret (0°35′N, 35°18′E), Nakuru West (0°33′S, 360 0'E) and Lanet (0°18′S, 36°09′E). Njoro in Nakuru County is at an altitude of 2185 m above sea level (m.a.s.l.) and experiences daily temperature range of 9.5°C-24.2°C with a mean rainfall of 1032 mm. The soils are mollic andosols Jaetzold *et al.* (2010). Eldoret (2154 m.a.s.l.) is in Uasin Gishu County where soils are largely

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acidic (pH 4.7) rhodic ferrasols, low in organic matter. Lanet is located in Nakuru County at an altitude of 1920 m.a.s.l. Lanet experiences a bimodal rainfall pattern with an annual mean of 800 mm and temperature range of 10°C to 26°C. The soils are well drained, deep, friable, sandy clay loam to sandy clay with a humic top soil Jaetzold *et al.* (2010). Nakuru West is at an altitude of 2003 m.a.s.l. with well drained, moderately deep, dark brown clay loams Jaetzold *et al.* (2010).

Soybean genotypes for the study were early (DPSB 19, SBH 3/8/4/1, SBH 10/5/6, SBH 6/6/6/2, SBH 1/12/9, SBH 4/4/4, SBH 10/2/3, SBH 4/6/6, EAI 3600), medium (SBH 7/1/1, Nyala, Gazelle) and late maturing (DPSB 8, 931/5/34, DPSB 3). The trial was laid out in June and July of 2011 in the selected sites on a mechanically prepared seedbed. The design was a randomized complete block design (RCBD) replicated thrice. Plot area was 8.1 m^2 which consisted of 6 rows, 3 m long and 0.45 m apart and intra-row spacing was 0.1 m. A seed rate of 75 kg ha^{-1} was used and Diamonium phosphate (DAP) fertilizer applied to supply 22 kg of N ha^{-1} and 57.5 kg of P ha^{-1}. Weed control was by application of Metribuzin at a rate of 360 g ha^{-1}. Foliar fungal diseases were controlled by weekly application of Tebuconazole at the rate of 250 g ha^{-1}.

Yield was estimated by weight of seed from four center rows of each plot. Oil and protein content were estimated using near-infrared reflectance whole grain analyzer (Infratec™ 1241 Grain Analyzer ISW 3.20: Foss Analytical AB, SE-2632 21 Hoganas, Sweden). Seed yield, protein and oil content stability and adaptability were analyzed using an additive main effects and multiplicative interaction (AMMI) model and GGE biplots in GenStat 13th edition statistical software (VSN international, Ltd 2010). Combined data analysis was done using SAS statistical software version 8.1. The AMMI model used was

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$$

Where; Y_{ij} is the yield of i^{th} genotype in the j^{th} environment; μ is the grand mean; g_i and e_j are the genotype and environment deviations from the grand mean, respectively; λ_n is the eigenvalue of the PC analysis axis n; γ_{in} and δ_{jn} are the genotype and environment principal component scores for axis *n*; *n* is the number of principal components retained in the model and ρ_{ij} is the error term Sabaghnia *et al.* (2008). The number of PCA axes retained is determined by consideration of F-test of significance (Gauch 1988).

RESULTS AND DISCUSSION

Variety adaptability and yield stability

Analysis of variance indicated that specific genotype and environment combinations were significantly ($P < 0.01$) different (Table 1). The AMMI analysis divided the main effects of treatments into genotype, environment and G × E interactions (Table 1). There were significant ($P < 0.01$) differences among the components. Environmental effects accounted for 37.13% of the total variation while the genotypes (G) and the G × E interaction accounted for 23.68% and 23.54%, respectively. Anuradha *et al.* (2017) observed comparable significant results while evaluating 36 soybean genotypes in three environments. The first and second interaction principal component axis (IPCA) explained 18.76% (IPCA1-9.8%; IPCA2-8.96%) of the interaction. The IPCA1 score indicated that about 66% of the genotypes were highly interactive (Table 4). The most interactive genotypes were DPSB 3 (-28.8) and Nyala (17.23). The least interactive genotype based on first IPCA was DPSB 8 (0.49). Genotype by environment interaction makes it difficult for breeders to make genotype selections and variety recommendations Cucolotto *et al.* (2007). Prediction of performance or selection of elite genotypes based on seed yield is better achieved by use of multi-environment trials Yan *et al.* (2010). The high yielding genotypes were Nyala, SBH 7/1/1, SBH 1/12/19 and DPSB 8 [Table 4 and Fig 1(a)]. The highest seed yielding genotype (Nyala) was unstable Fig 1(b). Low yielding genotypes (DPSB 3) had high IPCA1 scores (Table 4) and DPSB 19 in Fig 1 (b) denoting that either high yielding or low yielding genotypes maybe unstable. Selection of genotypes based on seed yield may result in selection of unstable genotypes.

Table 1: AMMI analysis for yield of 15 soybean genotypes evaluated across five environments in 2011.

Source	df	Sum of squares	Mean square	% of sum squares
Treatments	74	46028296	622004**	84.35
Genotype	14	12923694	923121**	23.68
Environments	4	20260360	5065090**	37.13
Block	10	1011410	101141	1.85
Interactions	56	12844216	229361**	23.54
IPCA1	17	5354677	314981**	9.81
IPCA2	15	4888590	325906**	8.96
IPCA3	13	1529632	117664**	2.80
Residuals	11	1071323	97393	1.96
Error	140	7530320	53788	13.80
Total	224	54569984	243616	123.54

**Significant at P=0.01.

However, genotypes identified as seed yield stable were medium yielding [Table 4 and Fig 1(b)] with yields 1.8-21.8% higher than the mean yield of 1267 Kg ha^{-1}.

Analysis by AMMI determined the best four high yielding genotypes per environment [Table 2 (a)]. The check genotype (EAI 3600) was placed second in two out of the five environments. The best yielding genotype (Nyala) outperformed the check by 16.4%.

The GGE biplot showed genotypes that were stable in yield and adaptable [Fig 1(b) and (c)]. The first principal component is represented on the x-axis and the higher the value along its length on Fig 1(a), the higher the genotype yield. The first principal component accounted for 52.25% of the variation in stability and the two principal components explained 71.8% of the variation. The 2nd principal component is represented on the y-axis and the further from the average environment axis (AEA) line the genotype is placed, the lower the stability in yield on Fig 1(b).

The stability analysis showed that genotype SBH 4/4/4 as most stable in seed yield while genotype 931/5/34 had longest vector suggesting that it was the least stable [Fig 1(b)]. The GGE biplot indicated two potential main-environments [Fig 1(c)]. The polygon view of the GGE biplot had five sectors that identified wining genotypes for the four sectors [Fig 1(c)].

Genotype adaptability and stability based on oil content

Analysis of variance indicated significant ($P < 0.01$) genotype differences for their seed oil content across environments (Table 3). The effects due to genotypes, environments and G × E interactions were significant ($P < 0.01$) among the components. The environment component contributed

Table 2: The first four AMMI selections of soybean genotypes per environment based on (a) yield (b) oil content and (c) protein content in five environments.

Environment		Score	1	2	3	4
(a) Seed yield (kg ha^{-1})						
Lanet	1754	6.32	Gazelle	EAI 3600	SBH 7/1/1	Nyala
Njoro II	1435	29.04	Nyala	SBH 7/1/1	SBH 6/6/6/2	SBH 1/12/9
Njoro I	1119	-7.29	DPSB 8	931/5/34	SBH 7/1/1	SBH 1/12/9
Eldoret	1107	-15.69	SBH 7/1/1	EAI 3600	Nyala	SBH 10/5/6
Nakuru west	896	-12.38	Nyala	SBH 7/1/1	EAI 3600	Gazelle
(b) Oil content (g Kg^{-1})						
Njoro I	182.0	0.69	931/5/34	SBH 7/1/1	SBH 4/4/4	SBH 10/5/6
Lanet	192.9	0.46	931/5/34	SBH 7/1/1	SBH 4/4/4	SBH 10/5/6
Nakuru West	223.0	0.19	931/5/34	Gazelle	SBH 1/12/9	SBH 4/4/4
Njoro II	179.4	0.16	931/5/34	SBH 10/5/6	SBH 7/1/1	SBH 4/4/4
Eldoret	193.0	-1.50	931/5/34	SBH 10/5/6	SBH 4/6/6	SBH10 /2/3
(c) Protein content (g Kg^{-1})						
Nakuru West	311.3	1.35	SBH 1/12/9	DPSB 19	SBH 4/6/6	DPSB 8
Eldoret	381.5	1.10	DPSB 3	DPSB 19	Nyala	SBH3/8/4/1
Lanet	383.7	-0.13	DPSB 19	SBH 3/8/4/1	DPSB 3	SBH 10/2/3
Njoro II	401.4	-0.61	DPSB 19	SBH 10/2/3	SBH 4/6/6	SBH3/8/4/1
Njoro I	405.3	-1.71	DPSB 19	SBH 3/8/4/1	SBH 10/2/3	DPSB 3

Table 3: Sum of squares and mean squares for oil and protein contents of 15 soybean genotypes evaluated across five environments in 2011.

		Oil content			Protein content		
Source	df	Sum of squares	Mean squares	% of sum squares	Sum of squares	Mean squares	% of sum squares
Treatments	74	970.14	13.11**	93.95	3225.66	43.59**	86.75
Genotype	14	377.72	26.98**	36.57	368.34	26.31**	9.90
Environments	4	538.72	134.68**	52.17	2597.36	649.34**	69.85
Block	10	8.1	0.81	0.78	68.8	6.88	1.85
Interactions	56	54.32	0.97**	5.26	260.4	4.65**	7.00
IPCA 1	17	27.7	1.60**	2.68	119.51	7.03**	3.21
IPCA 2	15	17.7	1.18**	1.71	99.9	6.66	2.68
Residuals	24	9.12	0.38	0.88	40.56	1.69	1.09
Error	140	54.6	0.39	5.29	422.8	3.02	11.37
Total	224	1032.64	4.61	-	3718.4	16.60	-

Table 4: Mean oil, protein content and interaction scores of 15 soybean genotypes across five environments.

Genotype	Mean yield (kg ha^{-1})	IPCA 1	IPCA 2	IPCA 3	Mean oil content (g kg^{-1})	IPCA 1	IPCA 2	Mean Seed Protein (g kg^{-1})	IPCA 1	IPCA 2
SBH 10/5/6	1303	-6.6448	-5.4367	0.8741	204.7	-0.74932	0.31025	365.8	0.24702	0.80337
SBH 6/6/6/2	1198	6.7862	8.4653	6.5740	192.1	-0.47153	-0.40684	378.5	-0.74272	0.53584
DPSB 8	1415	0.4982	-19.2481	8.0822	179.6	0.24843	0.67095	380.3	0.23320	-0.27976
DPSB 19	808	2.5775	15.4596	4.2702	170.1	0.35654	0.27518	402.8	-0.93528	-0.75098
931/5/34	1323	-5.2747	-14.7096	-5.5063	218.8	0.19607	-0.91206	352.1	0.39008	1.09580
DPSB 3	660	-28.8156	11.3142	6.0144	165.9	0.41718	-0.91206	391.7	0.02848	-1.05209
SBH 3/8/4/1	1243	6.5759	2.3849	-1.7210	191.8	0.08556	-0.22194	389.8	-0.74992	-0.45292
SBH 1/12/19	1435	1.4815	-7.1336	1.1503	196.3	0.48386	-0.55802	370.3	0.41640	0.51761
SBH 7/1/1	1544	1.0449	-5.4754	2.5177	201.3	0.42027	0.26914	367.7	1.11370	-0.36843
Gazelle	1308	3.3330	9.3407	-17.0816	198.9	0.14682	-0.37258	360.9	0.44126	0.54953
SBH 4/4/4	1302	1.0057	1.5485	4.9685	202.6	-0.12200	0.14907	368.5	0.90524	-0.46034
SBH 10/2/3	1125	3.9994	-2.8099	-6.1595	196.6	-0.66762	-0.01531	387.7	-0.82979	0.05189
SBH 4/6/6	1290	-1.0609	-0.2970	-5.4123	197.3	-0.63256	0.01009	384.1	-0.70330	0.48243
Nyala	1601	17.2451	6.0809	8.6099	194.8	0.63476	0.24594	372.0	0.55536	-0.72622
EAI 3600	1375	-2.7518	0.5162	-7.1808	200.2	-0.34646	0.24686	377.6	-0.36974	0.05428
Grand mean	1267	-	-	-	194.1	-	-	376.7	-	-

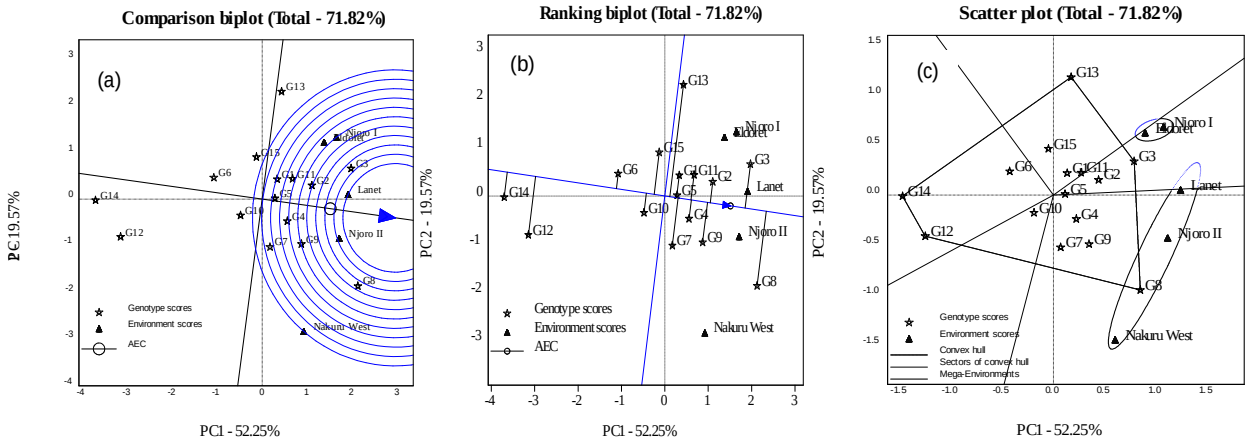


Fig 1: GGE biplots showing (a) genotype ranking (b) stability and (c) main-environments and their winning genotypes based on seed yield data. The Genotypes are G1-SBH 10/5/6; G2-SBH 1/12/9; G3-SBH 7/1/1; G4 Gazelle; G5-SBH 4/4/4; G6- SBH 10/2/3; G7-SBH 4/6/6; G8-Nyala; G9-EAI 3600; G10 SBH 6/6/6/2; G11-DPSB 8; G12-DPSB 19; G13- 931/5/34; G14-DPSB 3; G15-SBH 3/8/4/1.

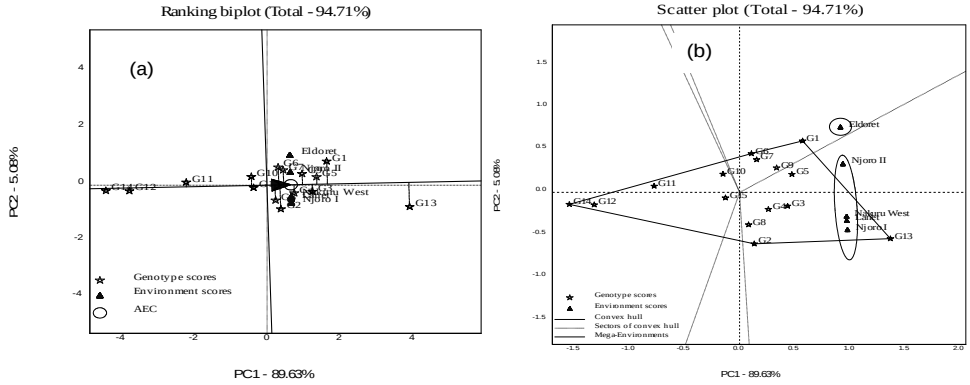


Fig 2: GGE biplots showing (a) stability and (b) main-environments and winning soybean genotypes based on oil content in g kg^{-1}. The genotype codes are G1-SBH 10/5/6; G2-SBH 1/12/9; G3-SBH 7/1/1; G4 Gazelle; G5-SBH 4/4/4; G6- SBH 10/2/3; G7-SBH 4/6/6; G8-Nyala; G9-EAI 3600; G10 SBH 6/6/6/2; G11-DPSB 8; G12-DPSB 19; G13 931/5/34; G14-DPSB 3; G15-SBH 3/8/4/1.

52.17% to the total sum of squares while the genotypes contributed 36.57% and the G × E interaction contributed 5.26%. The IPCA1 explained 2.68% of the variation while IPCA 2 explained 1.71%. The mean oil content was highest at Nakuru west (223 g kg^{-1}) and least at Njoro II (179 g kg^{-1}) [Table 2 (b)]. Genotypes SBH 4/4/4, 931/5/34 and Gazelle were the most stable genotypes for oil content based on AMMI analysis and genotypes SBH 4/4/4, Gazelle and SBH 7/1/1 based on GGE biplot analysis [Table 4; Fig 2 (a)]. The choice of stable varieties by both methods of analysis were similar but there were differences in the ranking. Tubic *et al.* (2011) while evaluating thirteen soybean genotypes observed small differences in oil content stability. Genotype by environment interactions observed in AMMI analysis could be attributed to weather and edaphic factors as was suggested by Tukamuhabwa *et al.* (2012).

All the genotypes were relatively stable for oil content as they had absolute IPCA1 scores of < 1 (Table 4). Genotypes DPSB 3, DPSB 19, DPSB 8, SBH 6/6/6/2 and SBH 3/8/4/1 were stable but had oil contents lower than the overall mean of 194.1 g kg^{-1}.

The GGE biplot analysis explained 94.71% of the genotypic variation in stability for oil content [Fig 2 (a)]. The most stable genotype was DPSB 3 while SBH 931/5/34 was the least stable for its oil content. The polygon view GGE biplot for oil content indicated the best or worst genotypes in each environment and groups of environments [Fig 2 (b)]. The best genotypes were located at the vertex of the polygon. Genotype 931/5/34 was the best in oil production in all environments. There were two main-environments that were delineated in the GGE biplot [Fig 2 (b)].

Genotype adaptability and stability based on protein content

Analysis of variance for protein content indicated significant ($P < 0.01$) genotype and environment interactions (Table 3). Genotypes, environments and genotype by environment interactions accounted for 9.9%, 69.85% and 7% of the variation, respectively. This implied that specific environments were better placed for production of soybean with higher protein content. Fehr (2003) analyzed protein content and found that genotype × environment interaction had no

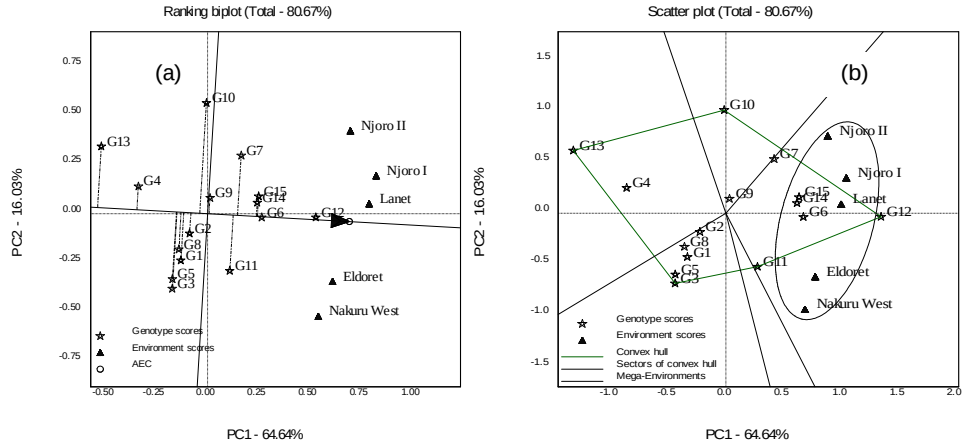


Fig 3: GGE biplot showing (a) stability and (b) main-environment winning genotypes based on protein content. The genotype codes are G1-SBH 10/5/6; G2-SBH 1/12/9; G3-SBH 7/1/1; G4 Gazelle; G5-SBH 4/4/4; G6- SBH 10/2/3; G7-SBH 4/6/6; G8-Nyala; G9-EAI 3600; G10 SBH 6/6/6/2; G11-DPSB 8; G12-DPSB 19; G13 931/5/34; G14-DPSB 3; G15-SBH 3/8/4/1.

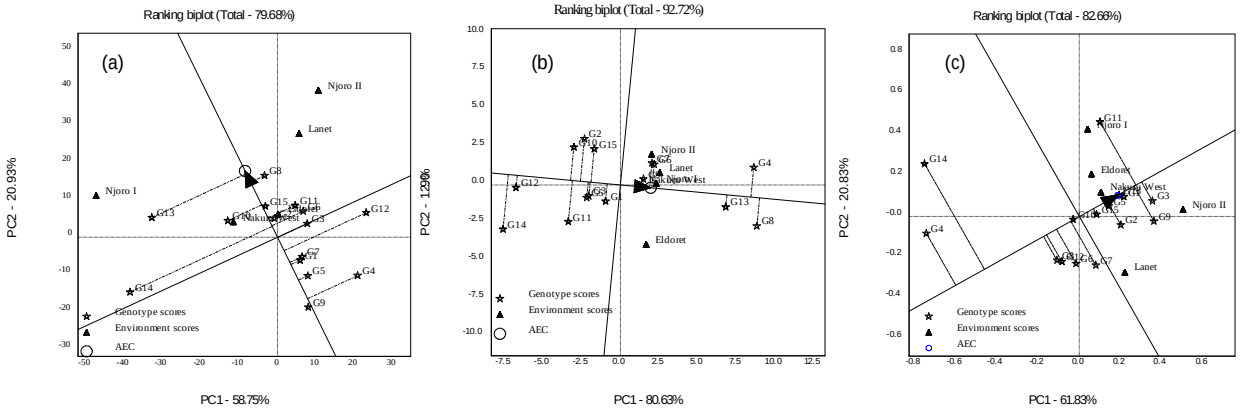


Fig 4: GGE biplots showing stability of soybean genotypes for (a) pods $plant^{-1}$ (b) 100-seed weight and (c) seeds pod^{-1}. Genotype codes G1-SBH 10/5/6; G2-SBH 1/12/9; G3-SBH 7/1/1; G4 Gazelle; G5-SBH 4/4/4; G6- SBH 10/2/3; G7-SBH 4/6/6; G8-Nyala; G9-EAI 3600; G10 SBH 6/6/6/2; G11-DPSB 8; G12-DPSB 19; G13 931/5/34; G14-DPSB 3; G15-SBH 3/8/4/1.

significant effects on soybean protein components. The first and second interaction principal components accounted for 5.89% of the interaction (IPCA1-3.21%; IPCA2-2.68%). High mean protein content was recorded on genotype DPSB 19 (402.8 g kg^{-1}) and least on genotype 931/5/34 [(352.1 g kg^{-1}) (Table 4)]. Interactive scores (Table 4) indicated genotype SBH 7/1/1(1.11) had low stability while DPSB 3 (0.02) had high stability. Ramana and Satyanarayana (2006) identified a genotype that was stable for seed yield $plant^{-1}$, oil and protein content. Studies have indicated that environmental factors have significant effects on protein and oil content in soybean (Ramana and Satyanarayana, 2006; Tubic *et al.* 2011). Environments fitted into one main-environment where DPSB 19 was the winning genotype [Fig 3 (b)].

Stability of important soybean yield components

Stability was highest on EAI 3600 on pods $plant^{-1}$ and least on DPSB 3 [Fig 4 (a)]. The principal components explained 79.68% of the variation in stability among genotypes. Genotype EAI 3600 had highest stability based on 100-seed weight [Fig 4.4 (b)]. The first principal component explained 80.63% of the variation while the second principal component explained 12.09% of the variation in stability of genotypes based on seed weight.

The principal components accounted for 82.66% of the variation in stability of the genotypes based on number of seeds pod^{-1}. Genotype SBH 6/6/6/2 was highly stable for seeds pod^{-1} while DPSB 3 was unstable for the trait [Fig 4.4 (c)]. In soybean, important yield components are pods $plant^{-1}$, seed size and seeds pod^{-1} (Khodadad, 2012). Genotype Gazelle was considered stable by GGE biplot analysis but the genotype had average stability for other yield components. This implies that there are more factors that contribute to stability of genotypes than the contribution by important yield components. Sujay *et al.* (2012) had observed that a genotype stable for one trait, may not be stable for other traits as each trait is governed by different sets of genes and influence of environment on the cumulative expression of different sets of genes vary considerably as indicated by variation in stability of genotypes for seed yield [Fig 1 (b)]. Yothasiri and Somawang (2006) observed that genotypes were above average in stability for 100-seed weight. However, stability in number of seeds pod^{-1} and number of pods $plant^{-1}$ was below and above average among the genotypes.

CONCLUSION AND ACKNOWLEDGEMENT

The AMMI method of genotype stability analysis can identify high yielding and stable genotypes. Identification of genotypes stable for seed yield is likely to include genotypes stable for oil and protein content. The oil and protein contents were least affected by G × E interaction but were significantly affected by the environment. Genotypes DPSB 8 and SBH 7/1/1 were high yielding and stable for seed yield and may be used as parental material for commercial production and breeding purposes. Genotype (EAI 3600) is recommended for continued commercial production. Genotypes SBH 4/4/4, SBH7/1/1, Gazelle and 931/5/34 may be recommended for inclusion in a breeding program where focus is on high oil content. Further research with higher number of environments is recommended.

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