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Studies on Genotype by Environment Interaction (GEI) and Stability Performances of 43 Accessions of Tropical Soybean (*Glycine max* (L.) Merrill)

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ABSTRACT

Soybean is the one most important oil-producing crop in Nigeria and the world. Genotype by environment interaction has been a major hindrance to effective selection and production. This study was conducted to determine the response of 43 soybean accessions to three environments to identify accessions that are adapted to the specific location and those that have wide adaptation. The 43 accessions were collected from the International Institute for Tropical Agriculture (IITA), Ibadan, Nigeria, and tested during the growing seasons of the years 2013, 2014, and 2015 in Ibadan. The data were analyzed using the additive main effects and multiplicative interaction (AMMI) and genotype main effect plus genotype-by-environment interaction (GGE) biplot methods. The AMMI analysis showed significant G x E interaction and identified accessions TGm-107, TGm-1200, and TGm-802 as the most desirable genotypes, whereas, TGm-868 and TGm-1209 were the least stable. The first two PC of the GGE analysis were able to capture 88.8% of the total variability due to G x E interaction. Accessions TGm-107, TGm-1200, and TGm-802 were the best performing and stable accessions due to their shortest projections in GGE biplot.

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INTRODUCTION

Soybean is one of the leading oil crops in the world, which produces significantly higher protein per hectare when compared to many other crops. Nigeria ranks second among

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soybean-producing countries in sub-Saharan Africa. In 2014, Nigeria recorded production of 679,000 metric tons (Food and Agriculture Organization [FAO], 2016). It is cultivated by small- and large-scale farmers majorly for human consumption and livestock feed in various agro-ecological zones in Nigeria. Changes in climate can have a strong impact on agriculture, i.e. climatic conditions determine not only crop growth but also yield, so even little change of climatic conditions required for production can seriously reduce yield (Kang et al., 2009). Therefore, it is important to understand the effect of environmental factors on crop growth and development. This knowledge would reduce the G × E interactions and improve the selection of genotypes for specific and wide adaptations in the target environments. The genotypic performance of soybean germplasm in many environments and seasons can assess the stability and adaptations of genotypes (Gedif et al., 2014). Interaction between genotype and environment interaction (GEI) complicates evaluations/trials, selection, and release and recommendation decisions of superior and improved genotypes, and consequently, reduces genetic progress from the selection because breeders need to identify different genotypes from the evaluation (Rincent et al., 2017; Tariku, 2017). As a result, GEI alters the genotype rankings from one environment to the other, and genotypes selected from one environment may not do well in another environment. Hence, there is a need to conduct trials over a wide range of environments to ascertain the selection of superior and stable genotypes. To this end, breeders usually conduct multi-environmental trials (MET) to identify high yielding and stable genotypes.

Many statistical models have been employed to detect and quantify the GEI. Currently, additive main effects and multiplicative interaction (AMMI) analysis models developed by Gauch (1992) and Zobel et al. (1988); and genotype main effect plus genotype-by-environment interaction (GGE) biplot developed by Yan and Kang (2003) and Yan and Rajcan (2002) are the most frequently used statistical models. However, before the advent of the two models mentioned above, breeders also used principal component analysis (PCA) developed by Hill and Godchild (1981), joint regression analysis developed by Eberhart and Russel (1966) as well as Finlay and Wilkinson (1963), and ANOVA developed by Snedecor and Cochran (1980).

Several studies reported on stability studies that focused on soybean. Cucolotto et al. (2007) found four cultivars out of thirty that combined good adaptation and stability, while Gurmu et al. (2009) reported that high yielding cultivars were more likely to have lower stability and *vice versa*. Jandong et al. (2011) examined seven genotypes grown in six different soil pH regimes for adaptability and stability and observed specific adaptation, implying that each genotype had specific soil requirements. Therefore, the main objective of the study was to evaluate Genotype × Environment Interaction (GEI) and the level of yield stability of the 43 accessions of soybean.

MATERIALS AND METHODS

Forty-three (43) soybean accessions collected from the Genetic Resources Center, International Institute for Tropical Agriculture (IITA) (Table 1), Nigeria were evaluated during the three years of 2013, 2014, and 2015. The trials were laid out in the research farms of the Department of Seed GenBank Unit, National Center for Genetic Resources and Biotechnology (NACGRAB), Ibadan (7.23 ′47″N 3.55 ′0″ E) in 2013 and 2014; and International Institute of Agriculture (IIA) (8.0'N 4.0'E), Ibadan, Nigeria in 2015, respectively. NACGRAB is situated at moor plantation, Apata along Abeokuta Ogun State, Nigeria while IITA is situated at Moniya along Oyo town in Oyo State, Nigeria. The meteorological data of the three years are shown as appendix I, II, and III. The 43 accessions were planted in single-row plots with 60 cm between-row and 5 cm within-row spacing, with three replications using a 1-m alley between blocks in a randomized complete block design. Data were collected on five yield characters: number of days to 50% flowering, number of days to maturity, number of pods per plant, 100 seed weight (gm), and seed yield per plant (g). They were analyzed using AMMI analysis, MATMODEL version 2.0 (Gauch & Zobel, 1996). In this analysis, each planting season was considered an environment. Thus, there were three environments in this study. The analysis was done to estimate the magnitude of the GE interaction.

The AMMI statistical model equation used was:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \Sigma\lambda_n\, y_{gn}\, \delta_{en} + P_{ge} + \epsilon_{ger}$$

AMMI's Stability Value (ASV) was also estimated by using the formula of Purchase (1997):

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}\left(IPCA1_{score}\right)\right]^2 + \left(IPCA2_{score}\right)^2}$$

ASV = AMMI's stability value, SS = sum of squares, IPCA = interaction principal component axis.

Likewise, Yield Stability index (YSi) was also calculated by adding up the ranks obtained from ASV and mean yield according to Farshadfar et al. (2011):

YSi = RASVi + RGYi

where; RASVi = rank of AMMI stability value of the ith genotype and RYGi = rank of the mean of seed yield of the ith genotype. The collected data also underwent a GGE biplot analysis to view the GEI. This analysis was carried out according to Mandel's site regression model ($SREG_{m+1}$ biplot) for MET data (Yan et al., 2001). In this biplot, the genotype main effect is the primary effect. The secondary effect comes from the first principal component (PC1) that comes from applying singular value decomposition (SVD) of the environment-centered data to the residual (Mandel, 1961).

According to Mandel (1961), the following model was used for the analysis:

$$Y_{ij} - \beta_j = b_j\alpha_i + \lambda_1\eta_{j1} + \Sigma_{ij}$$

GGE biplots were used to compare and

contrast among the performances of different genotypes in an environment as well as a genotype in different environments. It identifies the highest yielding genotypes at the different mega-environments and identifies ideal genotypes and test locations.

Table 1
The accession names and origin of 43 genotypes of soybean

S/N	Accession	Origin
1	TGm-107	Nigeria
2	TGm-109	Nigeria
3	TGm-1106	Taiwan
4	TGm-1200	Burkina Faso
5	TGm-1209	Burkina Faso
6	TGm-1215	Nigeria
7	TGm-136	Nigeria
8	TGm-138	Uganda
9	TGm-14	Nigeria
10	TGm-142	Uganda
11	TGm-150	Uganda
12	TGm-27	Nigeria
13	TGm-553	Nigeria
14	TGm-569	Nigeria
15	TGm-570	Nigeria
16	TGm-574	Nigeria
17	TGm-577	Nigeria
18	TGm-579	Nigeria
19	TGm-584	Taiwan
20	TGm-658	Indonesia
21	TGm-669	Indonesia
22	TGm-682	Indonesia
23	TGm-686	Indonesia
24	TGm-802	Burkina Faso
25	TGm-861	Taiwan
26	TGm-863	Taiwan
27	TGm-864	Taiwan
28	TGm-865	Taiwan
29	TGm-866	Taiwan
30	TGm-867	Taiwan
31	TGm-868	Taiwan
32	TGm-869	Taiwan
33	TGm-93	Nigeria
34	TGm-94	Nigeria
35	TGm-947	Nigeria
36	TGm-948	Nigeria
37	TGm-95	Nigeria
38	TGm-96	Nigeria
39	TGm-961	Nigeria
40	TGm-97	Nigeria
41	TGm-98	Nigeria
42	TGm-99	Nigeria
43	TGm-946	Nigeria

RESULTS AND DISCUSSION

The AMMI analysis results are presented in Table 2. The treatments (accessions + environments + interactions) accounted for 81.23% of the total sums of squares using approximately 33.16% of the total degrees of freedom. The accessions captured 38.39% of the total sums of squares explained and 47.26% of the total sum of treatment explained, while the environments explained 8.1% of the total sums of squares and 10.0% of the treatment sums of squares. The interactions explained 34.73% of the total sums of squares and 42.75% of the sums of squares for treatment (Table 2). Therefore, the accessions accounted for more variation, followed by the interactions

Table 2
Analysis of Variance for AMMI model

Source	df	SS	MS	% interaction explained	F	% total SS explained	% total treatment explained
Treatments	128	30034	234.6		9.29**	81.23	
Accessions	42	14193	337.9		13.38**	38.39	47.26
Environments	2	3000	1499.8		15.61**	8.1	10
Block	6	576	96.1		3.80**		
Interactions	84	12841	152.9		6.05**	34.73	42.75
IPCA	43	9792	227.7	76.26	9.02**		
IPCA	41	3049	74.4	23.74	2.95**		
Residuals	0	0					
Error	252	6363	25.3				
Total	386	36973	95.8				

Note. *, ** significant at 5% and 1% levels, respectively.
df = degrees of freedom; SS = sum of squares; MS = mean squares

and the environment captured the least variation. These results suggest that the 43 accessions and the three environments used were significantly different from each other. The significant differences showed for genotype by environment interaction indicated that the 43 accessions responded to the 3 environments differently. Furthermore, the results revealed that the accession component had more influence on the performance of soybean accessions, indicating less environmental influence for the test years and also showed that the largest source of variation observed was mainly due to genetic component probably because the genotypes are evaluated in the same geographical locations through different years.

The seed yield, environment, year, and first IPCA scores are shown in Table 3. The range of genotype mean yields was between 12.32 g in TGm-14 and 39.15 g in TGm-868. The environment means ranged from 21.62 g in environment 1 to 27.67 g in environment 3. Genotype TGm-868 recorded the largest IPCA score of 3.01 while genotype TGm-107 recorded the lowest IPCA1 score of –0.05. However, the largest environmental IPCA1 score was observed in environment 3 (6.07), while the lowest was recorded for environment 2 (–2.09). Accessions with IPCA1 scores close to zero had less interaction across the environments. It follows that out of the 43 accessions considered, TGm-1200 = G4 (0.10), TGm-570 = G15 (–0.07), TGm-579 = G18 (0.31), TGm-686 = G23 (0.16), TGm-802 = G24 (–0.06), TGm-865 = G28 (0.42) and TGm-869 = G32 (0.40) had negligible interaction with the test environments. All the remaining 36 accessions had high IPCA1 scores and were highly interactive with the environments.

The AMMI biplot for the 43 accessions of soybean is presented in Figure 1. In AMMI analysis, the IPCA scores of a genotype either positive or negative suggest its stability. The higher the IPCA score, the more adapted The IPCA scores of genotypes in the AMMI analysis indicate the stability of a genotype over environments. The greater the IPCA score of a genotype, either positive or negative, the more specifically adapted that genotype is to a specific environment. Also, the closer an IPCA score is to zero, the more stable the genotype is over all environments (Gauch & Zobel, 1996). Figure 1 indicates that G31 (TGm-868) gave the highest yield followed by G26 (TGm-863) and G1 (TGm-107). The lowest yielding among the 43 accessions was G9 (TGm-14) due to its placement on the top left corner in the biplot. Accessions G1 (TGm-107), G4 (TGm-1200), and G24 (TGm-802) were most stable and high yielding considering their IPCA score being the closest to zero and can be considered adaptable to all the environments.

On the other hand, G31 (TGm-868) was the least stable as it was the farthest from the IPCA1 score of zero, however, due to its high mean seed yield, it can be considered a responsive accession for a specific environment. The most undesirable accession was G9 (TGm-14) as it combined low yield with instability. Accession G1 (TGm-107) was considered the most desirable.

Table 3

Seed yield of forty-three (43) soybean accessions grown in three environments, mean values and the first PCA scores

Genotype	code	E1	E2	E3	GM (g)	IPCA 1
TGm-107	G1	34.51	35.44	40.30	36.75	–0.05
TGm-109	G2	14.83	17.33	34.40	22.19	1.36
TGm-1106	G3	25.14	19.00	36.13	26.76	0.76
TGm-1200	G4	21.13	32.67	31.97	28.59	0.10
TGm-1209	G5	29.59	18.67	6.90	18.39	–2.64
TGm-1215	G6	16.21	20.67	16.37	17.75	–0.78
TGm-136	G7	27.28	26.00	14.47	22.58	–1.95
TGm-138	G8	19.55	30.67	32.40	27.54	0.33
TGm-14	G9	17.17	14.63	5.17	12.32	–1.82
TGm-142	G10	18.37	24.33	21.57	21.42	–0.51
TGm-150	G11	24.14	16.00	6.50	15.55	–2.21
TGm-27	G12	22.48	20.92	29.67	24.36	0.19
TGm-553	G13	20.61	**35.67**	36.57	30.95	0.51

Table 3 *(Continued)*

Genotype	code	E1	E2	E3	GM (g)	IPCA 1
TGm-569	G14	21.75	14.60	11.10	15.82	–1.50
TGm-570	G15	15.63	13.14	20.07	16.28	–0.07
TGm-574	G16	24.43	22.36	32.20	26.33	0.27
TGm-577	G17	**38.09**	27.67	23.37	29.71	-1.82
TGm-579	G18	16.07	27.00	28.73	23.94	0.31
TGm-584	G19	20.76	18.97	37.47	25.73	1.21
TGm-658	G20	18.75	20.67	29.83	23.08	0.48
TGm-669	G21	17.78	24.07	31.30	24.38	0.57
TGm-682	G22	17.79	19.67	34.67	24.04	1.10
TGm-686	G23	23.73	21.38	30.40	25.17	0.16
TGm-802	G24	35.48	17.00	34.47	28.98	–0.06
TGm-861	G25	23.67	17.67	24.00	21.78	–0.38
TGm-863	G26	35.69	31.00	46.83	37.84	0.72
TGm-864	G27	15.99	15.67	31.13	20.93	0.99
TGm-865	G28	12.02	16.00	23.27	17.10	0.42
TGm-866	G29	22.83	14.33	31.00	22.72	0.55
TGm-867	G30	18.88	16.15	15.00	16.68	–0.94
TGm-868	G31	22.09	34.67	**60.70**	39.15	3.01
TGm-869	G32	20.24	15.67	28.37	21.42	0.40
TGm-93	G33	16.46	17.67	31.97	22.03	0.97
TGm-94	G34	15.48	24.00	41.33	26.94	1.80
TGm-946	G35	22.11	22.97	22.13	22.40	–0.66
TGm-947	G36	10.79	15.87	11.83	12.83	–0.71
TGm-948	G37	23.48	14.97	31.40	23.28	0.52
TGm-95	G38	18.25	21.33	30.27	23.28	0.53
TGm-96	G39	27.73	24.67	38.33	30.24	0.61
TGm-961	G40	25.48	34.67	15.30	25.15	–2.05
TGm-97	G41	13.27	22.97	10.53	15.59	–1.28
TGm-98	G42	16.14	18.01	32.33	22.16	1.02
TGm-99	G43	27.70	25.78	38.03	30.51	0.54
Mean		21.62	21.92	27.67		
PCA 1 score		–3.98	–2.09	6.07		

Note. E 1(NACGRAB) = 2013; E 2 (NACGRAB) = 2014; E 3 (IITA) = 2015; GM = grand mean; IPCA = interaction principal component axis

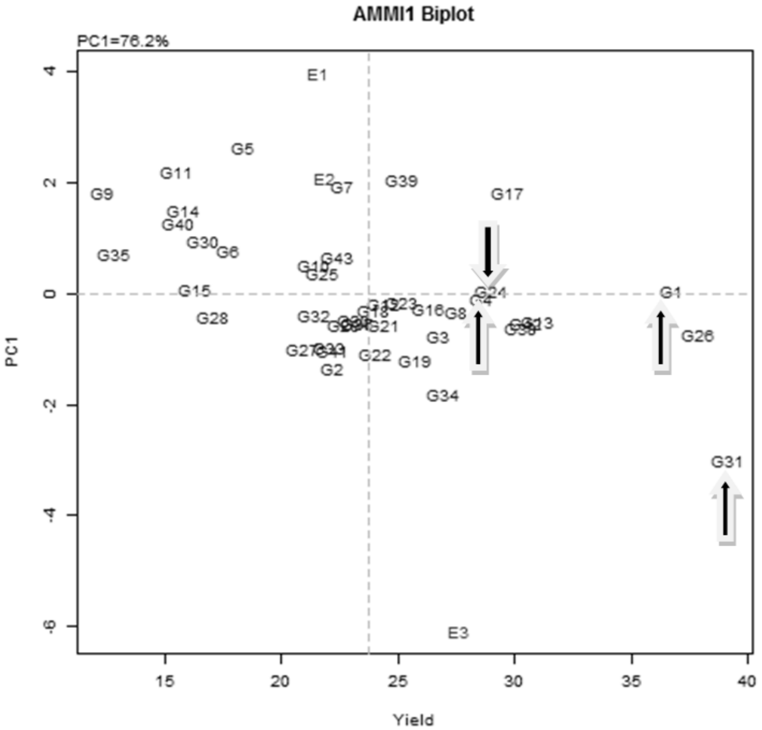


Figure 1. AMMI biplot of yield for 43 soybean accessions in three environments

Therefore, AMMI revealed that TGm-107 (G1), TGm-1200 (G4), TGm-802 (G24), TGm-138 (G8), TGm-686 (G23), TGm-553 (G13), TGm-869 (G32), and TGm-574 (G16) were the most desirable as they combine stability with high yield. This made them the most suitable variety for cultivation across seasons. However, accessions TGm-868 (G31), TGm-1209 (G5), and TGm-150 (G11) had high IPCA values indicating that they were responsive to changes in environments, a sign of high interaction with environments. The accessions that had more interaction with environments were found to be unpredictable in performance (unstable) and hence could be recommended for specific adaptation. Mohammadi et al. (2009) described a genotype exhibiting dynamic stability as one that responded to improved conditions and management practices with increased yield. Therefore, it would not be logical to recommend it for growing across environments. However, it would be better to recommend it for production in optimum growing conditions or environments. The differences among the test environments could be explained by climatic conditions, season length, and seasonal effects. Environment 1 (2013) was the least in terms of yield while environment 2 was the best in terms of stability in this study and therefore had little interaction effect with the 43 accessions studied. These results were consistent with numerous studies (Gurmu et al., 2009; Rao et al., 2002; Yothasiri & Somwang, 2000). Accession TGm-868 (G31) was identified to be the highest yielding and most unstable accession and therefore not reliable while TGm-107 (G1) was the best candidate in terms of stability and yield. These results were in agreement with the reports of Mut et al. (2009). Studies have shown that seed yield is heritable and conditioned by additive gene action (Spehar, 1999). Thus, simple selection methods could be applied to advance yield stability and plasticity for cultivation over a wide range of environments. These results suggested that seed yield could be maximized through selecting accessions showing consistently high yield performance across heterogeneous growing environments.

The AMMI stability value (ASV) and yield stability index (YSi) are presented in Table 4. The genotypes with a larger ASV score, either positive or negative will be better adapted to a specific environment while those with a smaller ASV score indicate a more stable genotype across environments. Accordingly, TGm-107 with the lowest ASV (0.020 followed by TGm-570 (0.08) and TGm-686 (0.20) were the most stable accessions, whereas, TGm-868 (47.10) followed by TGm-1209 (36.27) and TGm-150 (25.35) were identified as more adapted and sensitive to environmental changes. Yield stability Index (YSi) (Farshadfar et al, 2011) measures stability and can be calculated by summing of genotype rank of mean seed yield across environments and rank of AMMI stability value of genotypes. The genotypes with the lowest value are desirable genotypes with high mean grain yield and stability. Hence, YSi identified TGm 107 and TGm 1200 as the most desirable accessions among all the 43 accessions of soybean.

Table 4

Ranking of 43 accessions of soya bean by AMMI stability value (ASV) and yield stability index (YSi)

Accession	Code	MY	RANK	ASV	RANK	YSi
TGm-107	G1	36.75	3	0.02	1	4
TGm-109	G2	22.19	27	9.54	33	60
TGm-1107	G3	26.76	12	3.48	26	38
TGm-1200	G4	28.59	9	1.05	8	17
TGm-1209	G5	18.39	35	36.27	42	77
TGm-1215	G6	17.75	34	3.40	25	59
TGm-136	G7	22.58	25	19.66	39	64
TGm-138	G8	27.54	10	1.41	12	22
TGm-14	G9	12.32	43	17.09	37	80
TGm-142	G10	21.42	32	1.69	15	47
TGm-150	G11	15.55	41	25.35	41	82

Table 4 *(Continued)*

Accession	Code	MY	RANK	ASV	RANK	YSi
TGm-27	G12	24.36	18	0.23	4	22
TGm-553	G13	30.95	4	2.87	22	26
TGm-569	G14	15.82	39	11.78	35	74
TGm-570	G15	16.28	38	0.08	2	40
TGm-574	G16	26.33	13	0.44	5	18
TGm-577	G17	29.71	7	17.52	38	45
TGm-579	G18	23.94	20	1.32	11	31
TGm-584	G19	25.73	14	7.71	32	46
TGm-658	G20	23.08	23	1.19	10	33
TGm-669	G21	24.38	17	1.87	16	33
TGm-682	G22	24.04	19	6.32	31	50
TGm-686	G23	25.17	15	0.20	3	18
TGm-802	G24	28.98	8	2.83	21	29
TGm-861	G25	21.78	30	1.00	7	37
TGm-863	G26	37.84	2	3.00	24	26
TGm-864	G27	20.93	33	5.11	29	62
TGm-865	G28	17.10	36	0.98	6	42
TGm-866	G29	22.72	24	2.34	20	44
TGm-867	G30	16.68	37	4.57	27	64
TGm-868	G31	39.15	1	47.10	43	44
TGm-869	G32	21.42	31	1.08	9	40
TGm-93	G33	22.03	29	4.86	28	57
TGm-94	G34	26.94	11	16.90	36	47
TGm-946	G35	22.40	26	2.27	19	45
TGm-947	G36	12.83	42	2.90	23	65
TGm-948	G37	23.28	21	2.18	18	39
TGm-95	G38	23.28	22	1.48	13	35
TGm-96	G39	30.24	6	2.08	17	23
TGm-961	G40	25.15	16	22.99	40	56

Note. ASV = AMMI stability value; YSi = yield stability index; MY = mean yield

The GGE biplot was also constructed for the 43 accessions. One of the important characteristics of a GGE biplot is its ability to reveal top-performing genotypes in a specific environment and it can also display low yielding genotypes across environments. Figure 2 illustrates the association of the 43 accessions of soybean within the three test environments. Five sectors were displayed in the biplot, which were generated by the perpendicular line that originated from the center of the biplot and runs perpendicular to the side of the polygon. Among the five sectors displayed, two had environments included within them. Accession(s) that fall in sectors where the environment(s) are included indicate the association of the accession(s) with that specific environment(s). The accession at the various vertices of the polygon is expected to be responding well as they are the furthest from the origin. However, the responsive vertex accession is the best performing accession at the specific environments where it is found (Rakshit et al., 2012; Yan & Rajcan, 2002). Accession G17 (TGm-577) was the most suitable accession at E1 (2013) whereas accessions G26 (TGm-863), G1 (TGm-107), G31 (TGm-868), and G34 (TGm-94) were found to perform well in E2 (2014) and E3 (2015). However, G31 was the best performer and most suitable in E2 and E3.

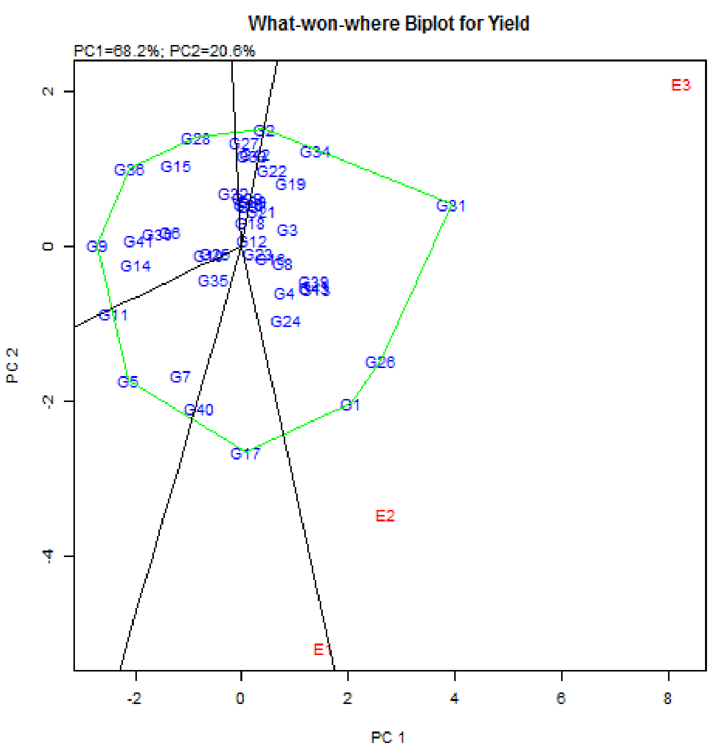


Figure 2. Which-won-where polygon view of the GGE biplot analysis

Figure 3 shows the biplot of stability and mean performance of the 43 accessions evaluated under three environments. The small circle indicates an average environment, which is defined by the mean IPC1 and IPC2 scores of the environments and the line that passes through the biplot and the average environment may be called the average axis (the ordinate). Projections of accession markers onto this axis approximate the mean yield of the accession. Thus, the accessions were ranked along the ordinate, with the arrow pointing to higher mean performance. Accession G31 was the highest yielding accession followed by G26. The abscissa is the double-arrowed line that passes through the biplot origin and is perpendicular to the ordinate (orthogonal). The double-arrowed line illustrates that a longer projection onto the abscissa, regardless of the direction, indicated greater instability. Given this, accessions G31 (TGm-868), G17 (TGm-577), and G34 (TGm-94) had the longest projections and were therefore the most variable across environments and less stable than others.

In contrast, accessions G4 (TGm-1200), G24 (TGm-802), and G1 (TGm-107) with shortest projections were relatively most stable over the three environments. Figure 4 shows the representativeness and

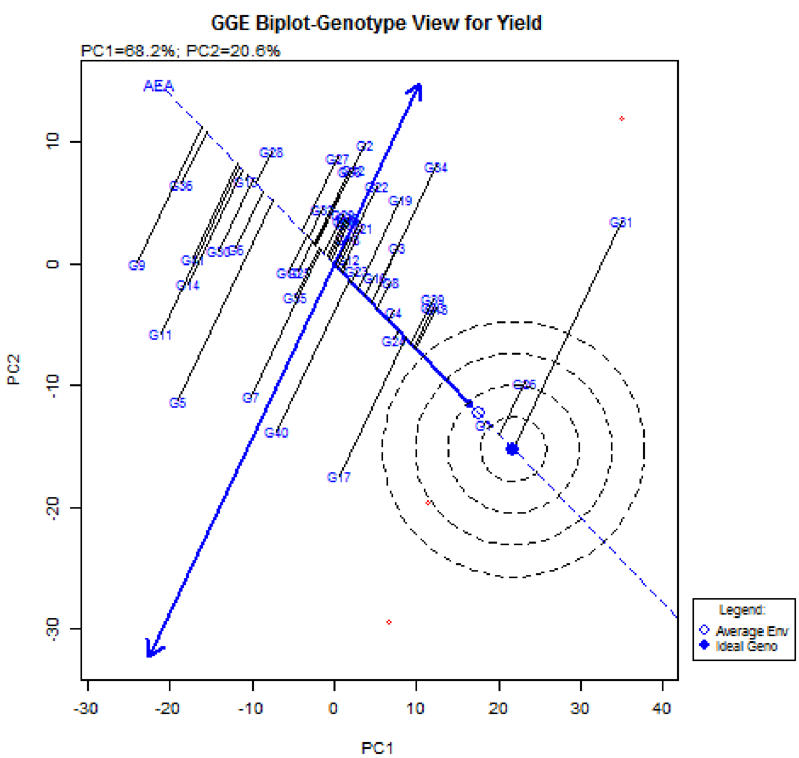
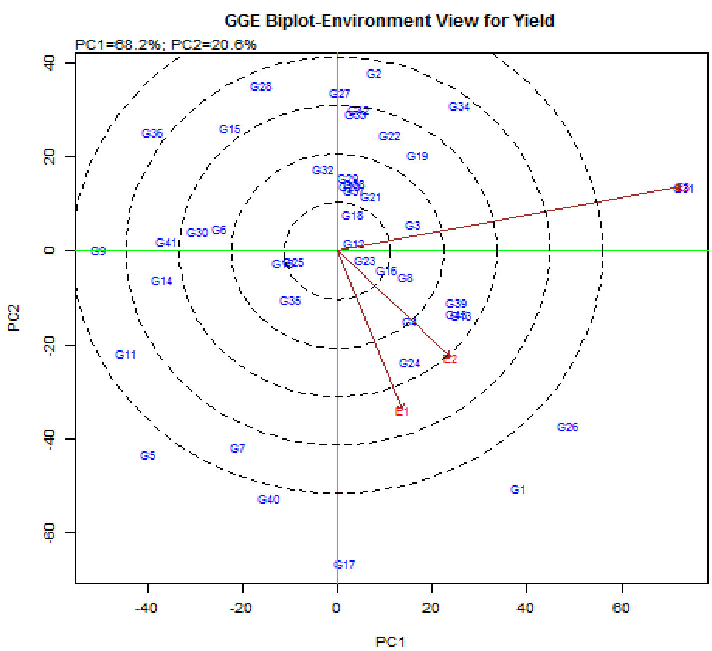


Figure 3. The mean performance and stability of the 43 genotypes of soybean across the three test environments

discriminating ability of the environments. The biplot explains 88.80% of the total variation. In a biplot analysis the vector length of an environment indicates its discriminating power; the longer the vector from the plot origin, the more discriminatory the environment. The longer the projection, the less representative the environment. Thus, E3 (2015) was the most discriminating environment due to its longest distance from the origin of the biplot while E2 (2014) was the least discriminating. Environments with small vector angles tend to have closer similarity and those with wide vector angles show a minimum association. Environments E1 and E2 were displayed close to each other as the association between them was small. However, the wider angle between E3 and E2; as well as E3 and E1 environments indicated the absence of association among them.

Similarly, accessions projected further from the ATC y-axis are considered less stable. The center of the concentric circle in a biplot is where an ideal accession should be. An ideal accession is considered as one with the highest yield and stable performance across test environments. Hence, the shorter the distance of accession to the ideal/virtual accession, the more suitable the accession (Yan & Kang, 2003). GGE also picked G31 (TGm-868) as the highest yielding in the E1 and E2 environments. The accessions that combined high yield with stability included G1 (TGm-107), G4 (TGm-1200), and G24 (TGm-802) because of their short projection on the genotype marker lines.



E = Environment, G = Genotype

Figure 4. Discriminating ability versus representativeness of the test environments

CONCLUSION

AMMI and GGE biplot revealed that accessions G1 (TGm-107), G4 (TGm-1200), and G24 (TGm-802) were the best and stable accessions across environments. This made them the most suitable variety for cultivation across the years. Among the environments, E3 (2015) was found to be the most discriminating, and E2 (2014) was found to be the most representative environment. Both AMMI and GGE agreed on the grouping of environment and the ideal test environment, as well on winner genotypes in this study, although, GGE biplot is believed to be superior to AMMI because it eliminates the environmental components in the analysis.

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APPENDIX

Appendix I

Monthly meteorological data for the year 2013 at NACGRAB, Ibadan

Month	Rainfall (mm)	No. of rain day	Temperature (°C)	Humidity (%)
January	0.0	NIL	27	70
Febuary	2.1	1	29	66
March	14.2	3	29	71
April	120.1	5	29	78
May	183.4	10	25.6	78
June	223.1	10	25.0	78
July	161.7	11	24.0	87
August	151.5	9	26	87
September	232.8	12	25	81
October	248.5	16	26.0	87
November	11.9	3	27.5	85
December	0.0	NIL	26.0	78

Appendix II

Monthly meteorological data for the year 2014 at NACGRAB, Ibadan

Month	Rainfall (mm)	No. of rain day	Temperature (°C)	Humidity (%)
January	15.3	2	28.0	60
Febuary	0.0	Nil	25.0	79
March	127.3	7	28.5	78
April	261.1	6	24.9	85
May	121.1	9	23.8	86
June	185.6	13	26.2	88
July	243	14	23.5	88
August	101	10	24.2	84
September	206.4	13	24.7	88
October	211.6	14	25.9	87
November	22.0	3	27.5	87
December	3.0	2	26.8	80

Appendix III

Monthly meteorological data for the year 2015 at IITA, Moniya

Month	Rainfall (mm)	No. of rain day	Temperature (^oC)	Humidity (%)
January	12.9	2	30	85
Febuary	23.2	3	27.5	83
March	90.3	6	27.4	83
April	115.6	7	28.1	83
May	117	10	26	84
June	85.3	7	25.2	85
July	462	19	26.6	86
August	154.8	5	24.6	87
September	345.9	18	24.3	88
October	324.1	18	25.8	87
November	43.4	3	27.4	82
December	0.0	NIL	26.1	83