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Assessment of Genetic Diversity and Stability Performance of Selected Soybean (Glycine max (L.) Merrill) Genotypes

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ABSTRACT

Despite soybean high economic value in many countries of Africa, the crop has received little attention with respect to genetic diversity and yield stability. Hence, inadequate production of soybean in Nigeria occasioned by lack of high-yielding improved varieties and unstable yields among others need to be investigated. This study assessed the diversity and yield stability in soybean genotypes for appropriate selection for improvement programme. Twenty-four soybean genotypes obtained from the International Institute of Tropical Agriculture, Ibadan were grown at the Teaching and Research Farms of the Federal University of Agriculture, Abeokuta (Latitude 7°15′N and Longitude 3°25′E), Institute of Agriculture Research and Training, Ibadan, Oyo State (Latitude 7°23′N and Longitude 3°27′E) and Lagos State Polytechnic, Ikorodu, Lagos State (Latitude 6°37′N and Longitude 3°30′E). Plantings were done in Abeokuta in May, 2017, Lagos and Ibadan in May and June, 2018, respectively. The experiments were laid out in a Randomized Complete Block Design with three replicates across the three locations. Data collected were subjected to Statistical Analysis. Results showed that the genotypes evaluated differed significantly ($p<0.05$) for agronomic characters, indicating the possibility of selecting soybean genotypes with superior seed yield characters. Dendrogram generated from Ward Linkage Clustering grouped the twenty-four soybean genotypes into five clusters, indicating genetic similarity and diversity among the genotypes. The AMMI analysis revealed that the total variance in soybean grain yield accounted for, by genotypes (G), environment (E) and genotype x environment interaction, with values of 43.00, 28.18 and 28.81%, respectively. Genotype TGx2004-10F was unstable across environments, but had high seed yield in Lagos. Genotype Selection Index (GSI), which combines both AMMI Stability Value and mean seed yield, revealed genotypes TGx1990-3F, TGx2010-11F, TGx1990-80F, TGx1991-10F and TGx1987-62F were stable with higher seed yield across the tested environments. These genotypes are therefore suitable for cultivation across the environments and are thus recommended.

Keywords

Genotype x environment interaction, Genetic diversity, Additive Main effect and Multiplicative Interaction (AMMI), Stability and seed yield.

Introduction

Soybean crop is of great economic and social importance worldwide. It provides about 64 percent of the world's oilseed meal supply and is one of the major sources of oil, accounting for about 28 percent of total oil production [1]. Also, world soybean production has been continuously increasing at a remarkable rate for several decades, it reached 265 million tons in 2010 from 30 million tons in 1970 [2]. Nigeria is the largest producer and consumer of soybean in Sub-Saharan Africa with production of 510,000 metric tonnes per annum [3]. The renewed interest in soybean production is as a result of its high nutritional qualities which include protein 35%, oil 19%, carbohydrate 35%, minerals 5% and vitamins [5,6]. Nutritional values from soybeans are important to human being especially resource-poor people of Africa, who cannot afford expensive sources of protein such as meat, fish and eggs

[6]. Therefore, demand for soybean oil and protein is increasing annually to match the growing world population [7].

Genotype × environment (G × E) interaction and yield-stability analysis has continued to be important in measuring varietal stability and suitability for cultivation across seasons and ecological zones. The analysis of genotype × environment has focused on the identification of stable genotypes for cultivation.

Additive Main Effects and Multiplicative Interaction (AMMI)

The additive main effect and multiplicative interaction (AMMI) method integrates analysis of variance and principal components analysis into a unified approach [8,9]. The AMMI method is used to summarize the patterns and relationships of genotypes and environments [9]. Moreover, it combines the analysis of variance for the genotype and environment main effects with principal components analysis of the genotype environment interaction [10]. It has proven useful for understanding complex GEI. The results can be graphed in a useful biplot that shows both main and interaction effects for both the genotypes and environments. AMMI combines analysis of variance into a single model with additive and multiplicative parameters [11]. The combination of analysis of variance and principal components analysis in the AMMI model, along with prediction assessment, is a valuable approach for understanding GEI and obtaining better yield estimates [11,12]. The interaction is explained in the form of a biplot display where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the GEI components. Integrating biplot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance across diverse environments.

GGE Biplot: The concept GGE biplot Methodology

The GGE-biplot methodology consists of two concepts: biplot and 'GGE'. The concept of GGE originates from analysis of mega environment trials (MET) of crop cultivars. The yield of a cultivar (or any other measure of cultivar performance) in an environment is a mixed effect of genotype main effect (G), environment main effect (E), and genotype by environment interaction (G × E). In normal METs, E accounts for 80% of the total yield variation, and G and GE each account for about 10% [13,14]. For the purpose of cultivar evaluation, however, only G and GE are relevant [15].

Furthermore, both G and GE must be considered in cultivar evaluation, thus the term GGE [16]. The GGE biplot is a biplot that displays the GGE part of MET data. The recently developed GGE biplot method provides a more elegant and useful display of mega environment trials data. It effectively addresses both the issue of mega environment differentiation and the issue of genotype selection for a given mega environment based on mean yield and stability. It also allows environments to be evaluated just as well as genotypes.

The main objective in plant breeding is to match genotypes to specific environments in such a way that the response is optimized. Some genotypes can do well across most conditions. However, there are some genotypes that do better (or worse) than others exclusively under a specific set of environmental conditions or managements, this adaptation is related to an interaction denominated by genotype × environment [17]. It is important to identify the most stable and adapted genotypes as environmental conditions such as soil and climatic conditions play a critical role in soybean production. These environmental conditions have the ability to influence the reproductive development of a particular genotype either to boost the production or retard its development. There are various degrees in which these factors affect the plant and it also depends on the genetic makeup of the plant. Thus, obtaining information on genetic diversity and heritable traits in soybean genotypes to make selection for improvement programme is necessary.

Materials and Methods

Twenty-four (24) genotypes of soybean used for this experiment were sourced from International Institute of Tropical Agriculture (IITA), Ibadan. The experiment was carried out at three different locations; Location 1: Teaching and Research Farm, Federal University of Agriculture, Abeokuta, Ogun State (Lat. 7°15′N and Long. 3°25′E) altitude 144m above sea level. Location 2: Institute of Agriculture Research and Training (IAR&T) Ibadan, Oyo State (Lat. 7°23′N and Long. 3°27′E) and Location 3: Teaching and Research Farm, Lagos State Polytechnic, Ikorodu, Lagos State (Lat. 6°37′N and Long. 3°30′E).

Across the three locations, the experimental field was ploughed and harrowed. Planting was done in Abeokuta in May, 2017 while planting was done in Lagos and Ibadan in May and June, 2018, respectively. The experiment was laid out in a randomized complete block design with three replicates. Sixty (60) seeds of each genotype were sown on a single row plot of 3 m long, with 0.05 m x 0.75 m; intra and inter row spacing. Two seeds per hole were sown and later thinned to one plant per stand at two weeks after planting (WAP). Weeding was done manually at three weeks interval, while 40 ml of Cypermethrin in 15 liters of water was sprayed to control insect pest at 5 WAP. Harvesting was done manually at maturity across the three locations and data were collected on the following agronomic characters;

Number of days to 50% emergence: This was recorded as the number of days from sowing until 50% of the plants emerged from the soil.

Number of days to 50% flowering: This was taken from the date of sowing to the day at which 50% of the plants had flowered.

Plant height at flowering (cm): This was measured from the soil base to tip of the plant using a measuring tape.

Number of days to 50% maturity: Number of days taken from date of sowing to physiological maturity of the plants was recorded as days to 50% maturity.

Number of days to 50% pod formation: This was recorded as the number of days from sowing to 50% of the plant showed pod formation.

Pod length (cm): The length of the pods from ten randomly selected plants were taken using a measuring tape and recorded.

Number of pods per plant: This was determined by counting the

number of pods present on main stem and branches on each plant and recorded.

Number of seeds per pod: seeds from ten randomly selected pods were counted and recorded.

Number of seeds per plant: The total number of seeds from randomly selected plants were counted and recorded.

Pod width (cm): The width of ten randomly selected pods was determined using digital vernier caliper.

100 seed weight (g): This was computed by weighing 100 seeds, which was randomly selected and was recorded in grams using a weighing balance.

Yield per plant (g): The seed yield per plant was measured using a weighing balance by averaging value of the total weight of harvested seeds from sampled plant and was recorded.

Statistical Analysis

Data collected were subjected to combined analysis of variance (ANOVA) to determine the effects of Genotypes (G), Environment (E), and their interaction. Single linkage cluster analysis (SLCA) was done to determine the level of relatedness among the twenty-four soybean genotypes. Morphological dendrogram was drawn from the single linkage cluster analysis.

Yield stability and superior genotypes with respect to seed yield was determined using Additive Main effect and Multiplicative Interaction (AMMI) model according to Gauch and Zobel [18]:

$$Y_{ij} = \mu + g_i + e_i \qquad \lambda_n \alpha_{in} \gamma_{jn} + \rho_{ge} + \varepsilon_{ij}$$

The stability of each genotype measured by the Ammi Stability Value (ASV) is based on the weighted Interaction Principal Component Axis (IPCA1 and IPCA2) to the interaction sum of squares SS according to Purchase et al., (2000):

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

Summation of rankings based on the ASV and mean seed yield across environments result in Genotype Selection Index (GSI), which is calculated as follows:

$GSI_i = RIPCA_i + RY_i$

The Genotype and Genotype x Environment (GGE) biplot methodology which is composed of two concepts: biplot concept and Genotype and Genotype x Environment (GGE) concept [19,20] was applied to visually analyze and identify the genotypes relative to the test with the yielding performance.

$$Y_{ij} = \mu + \alpha_i + \beta_j + \theta_y$$

Results

The means and standard deviation (SD) of agronomic characters of 24 soybean genotypes using Ward Linkage clustering procedure are presented Table 1. Cluster I comprises of four genotypes, while cluster II had ten genotypes; these genotypes could be selected for pod length and number of seeds per pod. Cluster III consist of four genotypes, the cluster produced the highest number of pods per plant, number of seeds per plant, 100 seed weight and seed yield per plant. Three genotypes were grouped in cluster IV with highest number of plant height at flowering and pod width. Cluster five had three genotypes with the highest number of days to 50% emergence, days to flowering, days to pod formation and days to maturity.

The dendrogram from the single linkage cluster analysis is presented in Figure 1. It was observed from the result that at 100% level of similarity, all the soybean genotypes had formed a single cluster, meaning that the genotypes were distinct at 100% level of similarity. Also, three distinct clusters were formed at 80% level of similarity. The dendrogram revealed five distinct clusters of the soybean genotypes at 40%, grouping TGx1835-10E, TGx2007-8F, TGx1989-49FN and TGX1990-80F into cluster 1. TGx1989-40F, TGx2008-4F and TGx2006-3F formed cluster 2. TGx1993-4FN, TGx2004-13F and TGX1448-2E made up cluster 3. Cluster

Table 1: Means and Standard Deviation (SD) of agronomic characters of 24 soybean genotypes using Ward Linkage clustering procedure.

Clusters					
Character	**I**	**II**	**III**	**IV**	**V**
	TGx1448-2E TGx1990-95F TGx1991-10F TGx2010-3F	TGx1835-10E TGx1951-3F TGx1989-20F TGx1989-21F TGx1989-49FN TGx1990-3F TGx1990-8F TGx1993-4FN TGx2004-13F TGx2007-8F	TGx1987-10F TGx1987-62F TGx1990-21F TGx2010-	TGx1989-40F TGx2006-3F TGX2008-4F	TGx1989-45F TGx2004-10F TGx2010-12F
D50E	6.16 ± 1.26	5.80 ± 0.55	5.66 ± 0.39	5.78 ± 0.39	9.11 ± 1.90
D50FLW	50.70 ± 1.24	50.90 ± 1.33	51.64 ± 1.98	50.56 ± 0.87	55.37 ± 0.57
PH50FLW	53.62 ± 1.98	52.96 ± 3.70	54.77 ± 2.15	60.57 ± 1.94	54.55 ± 3.80
D50POD	57.5 ± 1.36	57.70 ± 1.59	58.51 ± 1.95	57.41 ± 0.94	62.13 ± 0.73
D50MAT	99.39 ± 3.81	98.80 ± 1.20	98.72 ± 1.54	97.63 ± 1.09	104.33 ± 0.91
P.LGT	3.78 ± 0.19	4.07 ± 0.18	3.64 ± 0.13	4.02 ± 0.33	3.84 ± 0.19
P.WDT	5.88 ± 0.12	6.28 ± 0.28	5.95 ± 0.29	6.34 ± 0.42	6.10 ± 0.28
P/PLT	83.19 ± 10.60	70.34 ± 12.99	98.44 ± 17.14	51.77 ± 6.80	75.53 ± 1.87
S/PD	2.18 ± 0.10	2.40 ± 0.12	2.38 ± 0.09	2.25 ± 0.11	2.32 ± 0.05
S/PLT	192.87 ± 35.55	185.51 ± 35.21	233.50 ± 42.95	118.17 ± 18.76	222.42 ± 29.32
100SW	13.14 ± 1.78	15.00 ± 0.93	15.26 ± 1.08	15.23 ± 1.51	13.71 ± 1.77
Y/PLT	25.87 ± 3.60	28.23 ± 6.02	34.85 ± 5.36	20.70 ± 2.75	31.40 ± 11.26

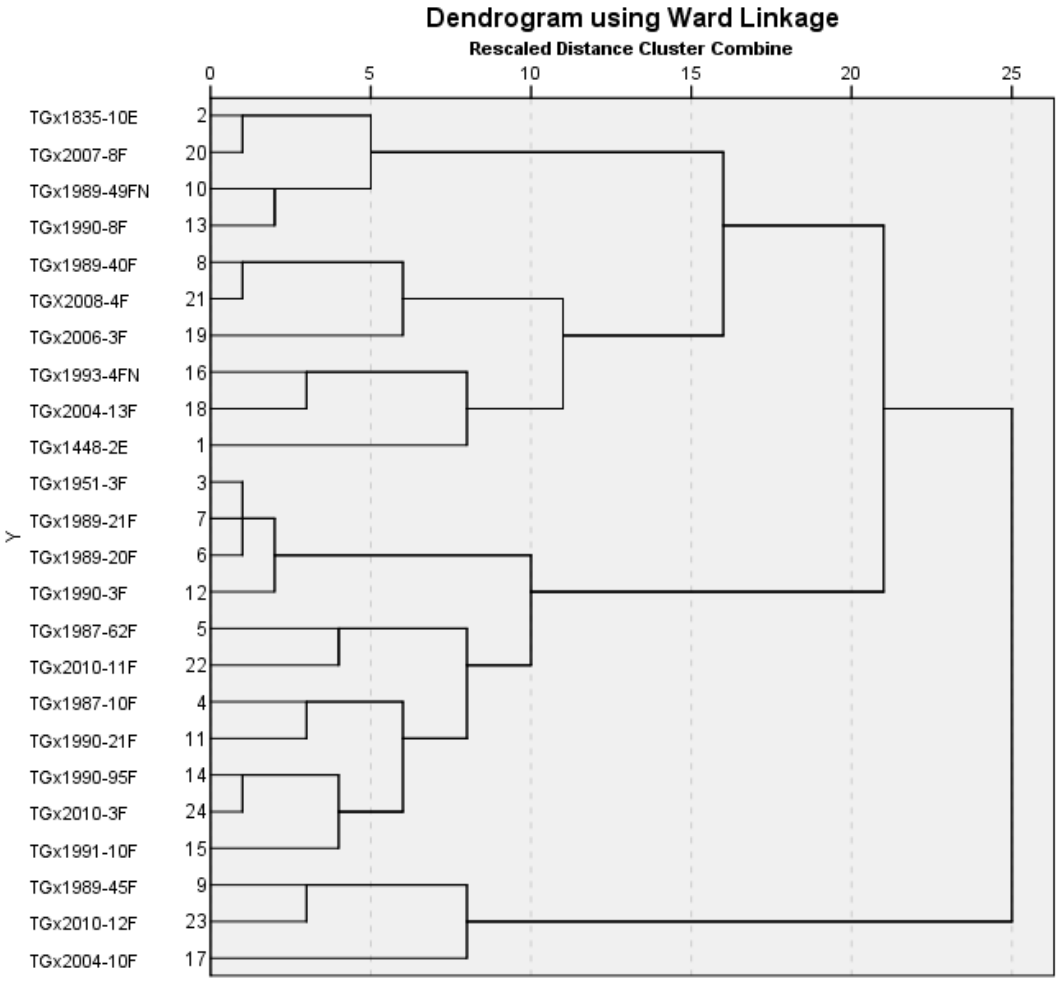

Figure 1: Dendrogram resulting from single linkage cluster analysis of 24 soybean genotypes.

Coefficient of similarity

Table 2: AMMI Analysis of variance for 24 soybean genotypes tested in three environments.

SV	DF	SS	MS	% Treatment SS	% Interaction
Total	215	30465	141.7		
Treatments	71	23391	329.4**		
Genotypes	23	10059	437.4**	43.00%	
Environments	2	6592	3295.8**	28.18%	
Blocks	6	796	132.7**		
Interactions	46	6740	146.5**	28.81%	
IPCA1	24	6727	280.3**		99.81%
IPCA2	22	12	0.6		
Residual	0	0	-		
Error	138	6278	45.5		

** = highly significant (P<0.01)

4 had TGx1989-45F, TGx2010-12F and TGx2010-10F, while the remaining genotypes formed cluster five (5).

The AMMI analysis of variance for grain yield (g/plt) of 24 soybean genotypes tested in three (3) environments is presented in Table 2. The analysis showed that the soybean grain yield was significantly (P<0.01) affected by genotypes, environment and genotype x environment interaction. Genotype accounted for 43.00% of the total variation while the environments and genotype x environment interactions accounted for 28.18 and 28.81%, respectively. Only the first interaction PCA was significant and accounted for 99.81% of the sum of square due G × E interaction.

Table 3 presents the ranking of 24 soybean genotypes by mean performance, AMMI stability value and genotype selection index for seed yield evaluated in three environments. The result show

Table 3: Ranking of 24 soybean genotypes by mean performance, AMMI stability value and genotype selection index for seed yield evaluated in three environments.

Genotypes	GM	Rank	IPCAg[1]	IPCAg[2]	ASV	Rank	GSI	Rank
TGx 2006-3F	23.69	17	0.01	0.50	1.91	1	18	6
TGx 2008-4F	18.27	24	1.47	-0.01	823.47	18	42	24
TGx 2010-12F	27.51	13	-1.63	-0.40	910.66	22	35	21
TGx 2004-13F	19.14	23	0.48	0.18	268.22	7	30	16
TGx 1448-2E	20.53	19	0.13	-0.63	75.32	4	23	10
TGx 2010-11F	36.38	3	-0.58	0.37	326.02	10	13	2
TGx 1989-45F	22.6	18	1.18	-0.42	658.47	14	32	18
TGx 1987-62F	35.22	4	0.61	-0.12	344.11	11	15	5
TGx 2010-3F	27.02	16	0.51	-0.59	287.45	8	24	11
TGx 1990-3F	32.74	7	0.21	0.17	114.61	5	12	1
TGx 1989-20F	33.74	5	1.12	0.30	626.61	13	18	6
TGx 1989-21F	32.67	9	-1.52	0.22	853.55	19	28	15
TGx 1990-95F	27.51	13	-1.54	-0.14	862.09	20	33	20
TGx 1987-10F	40.29	2	-1.33	0.03	745.87	16	18	6
TGx 1835-10E	29.36	10	1.20	-0.25	672.94	15	25	13
TGx 1990-21F	27.5	15	2.52	0.32	1410.97	23	38	23
TGx 2004-10F	44.09	1	-4.29	0.10	2403.57	24	25	13
TGx 1989-40F	20.13	21	-0.04	-0.05	21.54	3	24	11
TGx 2007-8F	20.36	20	1.34	-0.12	749.25	17	37	22
TGx 1989-49FN	28.71	11	1.62	0.31	908.09	21	32	18
TGx 1990-80F	32.39	8	0.24	-0.08	136.89	6	14	3
TGx 1991-10F	28.39	12	-0.02	0.11	10.52	2	14	3
TGx 1951-3F	33.23	6	-1.12	0.09	629.36	12	18	6
TGx 1993-4FN	20	22	-0.56	0.12	315.06	9	31	17

that average seed yield ranged from 18.27g/plant for TGx2008-4F to 44.09g/plant for TGx2004-10F. Only ten of the genotypes (TGx2010-11F, TGx1987-62F, TGx1990-3F, TGx1989-20F, TGx1989-21F, TGx1978-10F, TGx1835-10E, TGx2004-10F, TGx1989-49FN, TGx1990-80F, TGx1991-10F and TGx1951-3F) yielded above average. Genotypes ranking based on genotype selection index (GSI), which combines both AMMI stability value (ASV) and mean seed yield performance rankings, revealed that genotypes TGx1990-3F, TGx2010-11F, TGx1990-80F, TGx1991-10F and TGx1987-62F were stable and performed well above average across the environments. Considering the ASV alone, three genotypes; TGx2006-3F, TGx1991-10 and TGx1985-40F had the relatively lowest ASV value, representing the genotypes that were stable for seed yield. Environment 3 produced the highest yield of 32.64 g/plant (Appendix 7), followed by environment 2, with the yield of 31.95 g/plant, while environment 1 produced the lowest yield 20.59 g/plant during the study.

Biplot of the AMMI result is presented Figure 5. Genotypes TGx1989-40F (19), TGx1448-2E (5), TGx2006-3F (1), TGx1991-10F (23), TGx1990-80F (22) and TGx1990-3F (10) were close to origin of the biplot, which indicated that, they were stable across the tested environments. TGx2004-10F (17), TGx1990-21F (16), TGx1989-49FN (21), TGx2008-4F (2), TGx2007-8F (20), TGx2010-12F (3), TGx1990-95F (13), TGx1989-21F (12) and TGx1989-20F (11) were farther away from origin. In terms of yield performance, TGx2010-11F (6), TGx1951-3F (24), TGx1987-62F (8), TGx1989-21F (12), TGx1978-10F (14) and TGx2004-10F (17) were above average in their performance. TGx2004-10F (17) had the highest yield but highly unstable and was closely followed by TGx1978-10F (14). However, only TGx1990-80F (22) and TGx1990-3F (10) were stable and also high yielding. TGx1990-80F (22), TGx1990-3F (10), TGx1987-62F (8) and TGx2010-11F (6) were well adapted to Ibadan. Also, TGX2004-10F (17) being a high yielding genotype was adapted to Lagos, while TGx2008-4F (2), TGx2007-8F (20) and TGx1990-21F (21) were well adapted to Abeokuta.

The polygon view of a GGE – biplot which displays the which – won – where pattern for twenty four soybean genotypes evaluated in three environments with respect to seed yield is presented in Figure 3. The convex hull in the graph is drawn on genotype relative position from the biplot origin in order that all other genotypes are contained within the convex hull. The biplot contains a set of lines perpendicular to each sides of the convex. These lines divide the biplot into six sectors and the environments fall into two of them. E1 (environment 1) fell into a sector with the vertex genotype TGx1989-20F (G11), while E2 and E3 (environment 2 and 3) fell into the same sector where TGx2004-13F (G4) and TGx2004-10F (G17) were the vertex genotypes. Conversely, TGx1989-49FN, TGx1990-21F, TGx1448-2E and TGx2007-8F were poor yielding genotypes and so they were not captured in any of the three environments. The biplot also divides the environments into two mega environments. E1 was identified as one mega environment while E2 and E3 were grouped as another mega environment.

The biplot of stability and mean performance of twenty-four soybean genotypes evaluated across three environments is presented in Figure 4. The small circle indicates the average

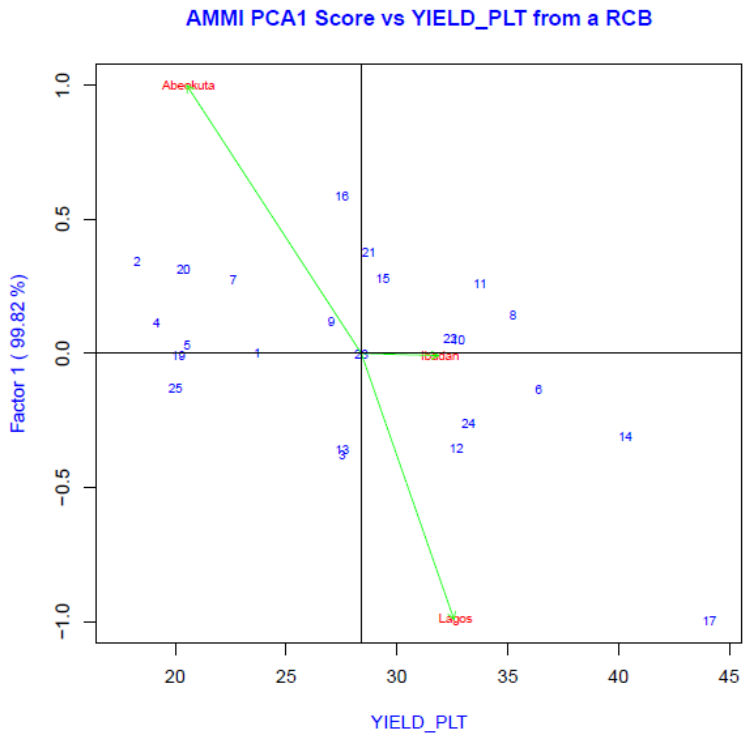

Figure 2: Biplot of the AMMI model for soybean trial with 24 genotypes grown in three locations.

1=TGx 2006-3F, 2=TGx 2008-4F, 3=TGx 2010-12F, 4=TGx2004-13F, 5=TGx 1448-2E, 6=TGx 2010-11F, 7=TGx 1989-45F, 8=TGx1987-62F, 9=TGx 2010-3F, 10=TGx 1990-3F, 11=TGx 1989-20F, 12=TGx 1989-21F, 13=TGx 1990-95F, 14=TGx 1987-10F, 15=TGx 1835-10E, 16=TGx 1990-21F, 17=TGx 2004-10F, 19=TGx 1989-40F, 20=TGx 2007-8F, 21=TGx 1989-49FN, 22=TGx 1990-80F, 23=TGx 1991-10F, 24=TGx 1951-3F, 25=TGx 1993-4FN.

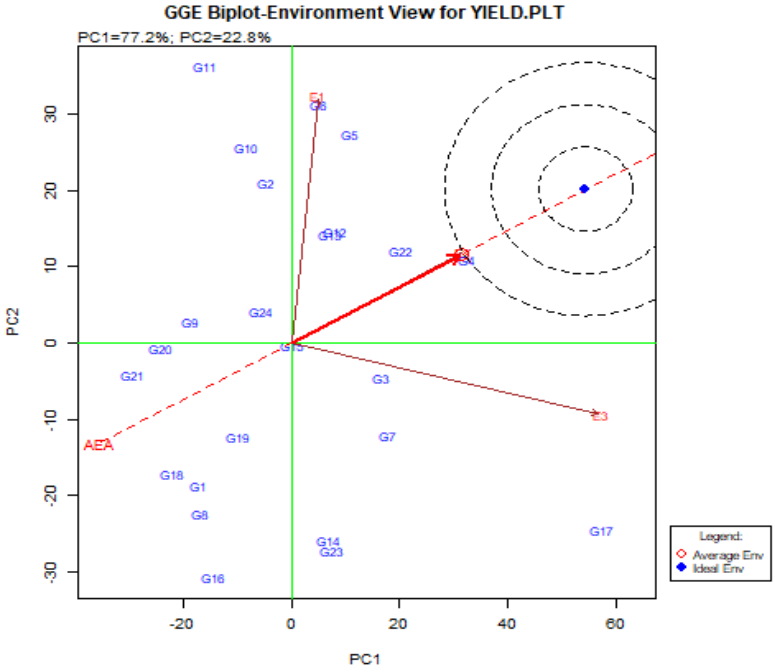

Figure 3: Polygon view of the GGE biplot of seed yield character of 24 soybean genotypes evaluated across three environments.

E1: Abeokuta
E2: Ibadan
E3: Lagos

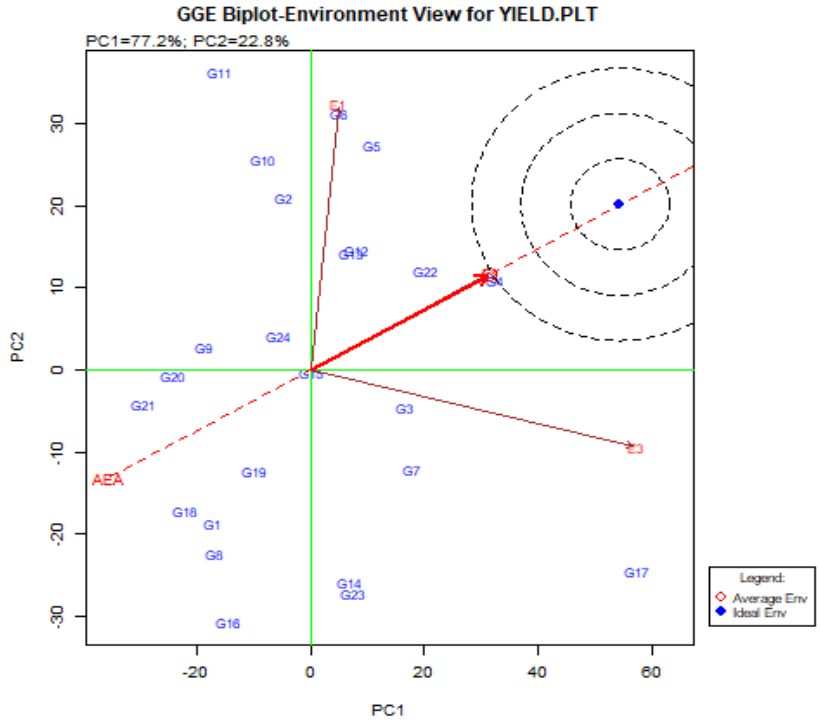

Figure 4: GGE biplot of stability and mean performance of 24 soybean genotypes evaluated over three environments.

G1=TGX 2006-3F, G2=TGX 2008-4F, G3=TGX 2010-12F, G4=TGX2004-13F, G5=TGX 1448-2E, G6=TGX 2010-11F, G7=TGX 1989-45F, G8=TGX1987-62F, G9=TGX 2010-3F, G10=TGX 1990-3F, G11=TGX 1989-20F, G12=TGX 1989-21F, G13=TGX 1990-95F, G14=TGX 1987-10F, G15=TGX 1835-10E, G16=TGX 1990-21F, G17=TGX 2004-10F, G18=TGX 1989-40F, G19=TGX 2007-8F, G20=TGX 1989-49FN, G21=TGX 1990-80F, G22=TGX 1991-10F, G23=TGX 1951-3F, G24=TGX 1993-4FN.

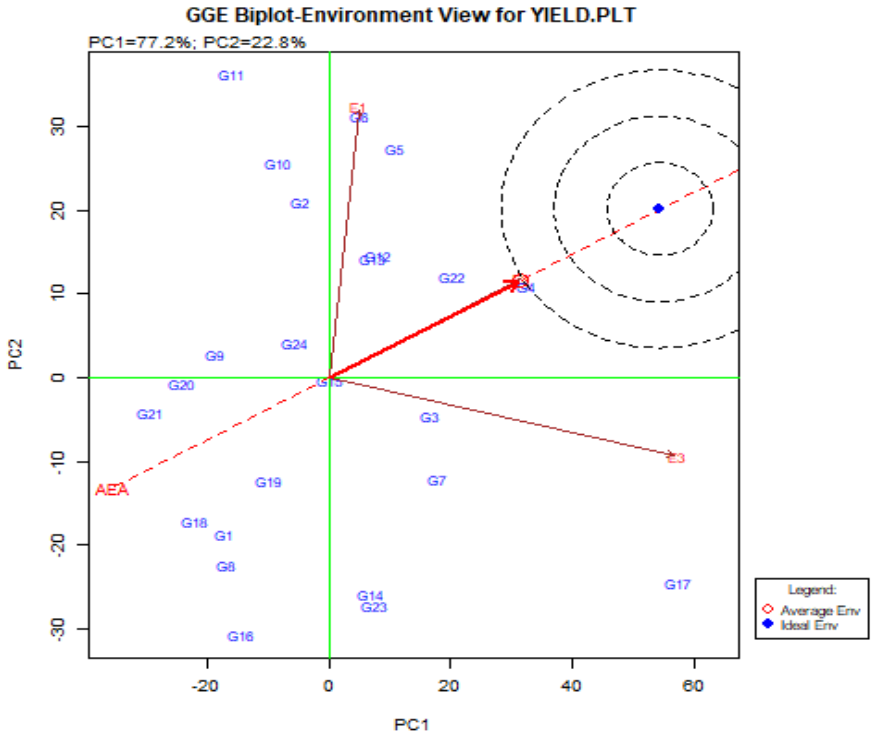

Figure 5: GGE biplot displaying the representativeness and discriminating ability of the tested environments.

environment which was defined by the interception of PC1 and PC2 scores of the environment. The line that passed through the biplot origin and the average environment with single arrow is called the average environment axis (AEA) is the ordinate. The line with double arrow heads is called the abscissa. Projections of genotype markers onto the average environment axis approximate the mean yield of genotypes. The genotypes were ranked along the ordinate. Genotype TGx2004-10F (G17) was the highest yielding genotype, followed by genotypes TGx2004-13F (G4) and TGx1991-10F (G22). The average environment coordinates (AEC) ordinate is the double arrowed line that passed through the biplot origin and is perpendicular to the average environment coordinates (AEC) abscissa. The AEC ordinate approximates the G × E interaction associated with each genotype and this is a measure of variability or instability of the genotypes. longer projection onto AEC aordinate, means higher instability. So, genotypes TGx2004-10F (17), TGx1989-45F (G7), TGx2004-13F (G4), TGx1989-20F (G11), TGx1951-3F (G23) and TGx2010-12F (G3) were considered unstable. Genotypes TGx1989-21F (G12), TGx1991-10F (G22) and TGx1835-10E (G15) with shorter projections were relatively stable over the environments. TGx1989-21F (G12), TGx1448-2E (G5) and TGx1991-10F (G22) combined good performance with stability.

Figure 5 displays the representativeness and discriminating ability of the tested environments. From the vector view of the biplot, the length of the environment vectors approximate the standard deviation within each environment. It is also the measure of their discriminating ability, and thus, environment 3 with the longest vector is the most discriminating environment, followed by environment 1 while environment 2 is the least discriminating environment. The centre of concentric circles is where an ideal environment is located, while the line that passed through the biplot origin and the average environment is the average environment coordinates (AEC). The angle between the vector of an environment and AEC axis is a measure of the representativeness of the environment. Thus, environment 2 was the most representative of the tested environments.

Discussion

The success in breeding program of any crop species depends greatly on variation that exists within the crop. The higher the genetic variability, the greater the chances of success to be achieved through selection processes. Result of the study showed that soybean genotypes evaluated differed significantly for all agronomic characters, indicating the possibility of selecting soybean genotypes with superior seed yield characters. The significant difference among the three locations provided opportunity to evaluate the response of soybean crop to different locations. Genetic diversity in soybean genotypes have been reported by several authors [21,22].

Cluster analysis was employed to observe the genetic relationship among the twenty-four genotypes. Knowledge of genetic similarity between genotypes is useful in any breeding program because it facilitates efficient sampling and utilization of germplasm resources. The breeder can use genetic similarity information to make informed decisions regarding the choice of genotypes to cross for the development of segregating populations or to facilitate the identification of diverse parents to cross in hybrid combinations in order to maximize the expression of heterosis [23]. TGx1835-10E, TGx2007-8F, TGx1989-49FN and TGx1990-80F clustered separately from other genotypes. This indicates the genetic differences of these genotypes from the other genotypes. Also, TGx1989-40F, TGx2008-4F and TGx2006-3F with another cluster differed from other genotypes.

The stability performance of the twenty-four soybean genotypes across the three locations as measured by seed yield was investigated by AMMI [13] and GGE biplot [20] in view of the fact they provided some proof as to the location effects and its interactions with the genotype on yield production [24]. The advantage of using AMMI is that it offers a remarkably cost effective strategy for increasing the accuracy of yield estimates and can assist plant breeders to investigate the G × E interactions [15]. GGE biplot is used for assessment of ideal genotype and test location in multi-environment data [14].

The AMMI model also explains the structural variation in the G×E interaction. The main effect treatments were partitioned into genotype (G), environment (E) and G×E interaction. The percentage contribution to the sum of square showed that the locations represented a contrasting environment for G×E analysis in soybean genotypes. A good cultivar should be high yielding and stable across environments [25], that is, an ideal genotype should have the highest mean performance and be absolutely stable [20]. Such an ideal genotype is defined by having the greatest vector length of the high-yielding genotypes and with zero GE (or highest stability). Gauch and Zobel [8] have found that AMMI analysis significantly improved the probability of successful selection in soybean. TGX2004-10F was the highest yielding genotype and performed above the average mean in E2 (Ibadan) and E3 (Lagos) but below average in E1 (Abeokuta). It is therefore recommended for cultivation in E2 (Ibadan) and E3 (Lagos), as it is well adapted to these environments. Also, TGX1987-10F performed well consistently across the tested environments.

In terms of stability, TGX1990-3F, TGX1990-80F, TGX2010-11F, TGX1987-62F, TGX1448-2E and TGX1989-40F were identified as stable genotypes across the environments. However, TGX1990-3F, TGX1990-80F, TGX2010-11F and TGX1987-62F were stable with high yielding and are therefore recommended for cultivation in any of the three environments. The genotypes with high environmental interaction are dynamic, unstable and responsive to changes in the environments. Any genotype that has large interaction with the environment cannot be predicted in performance, thus they can be cultivated in limited environments. However, ranking the genotypes based on mean performance alone was not consistent with stability performance for the trait. In view of this, Genotype Selection Index (GSI) which has previously been shown to be a reliable selection criterion for identifying consistently high performing genotypes across environments

[26,27]. Individual genotypes were classified as stable or unstable based on the GSI statistics, TGx1990-3F was identified as stable genotypes with mean value better than the population mean for seed yield. Genotypes TGx2010-11F, TGx1990-80F and TGX 1991-10F were also identified with best performance for seed yield. The present study identified TGx2006-3F as the most stable genotype for seed yield according to AMMI Stability Value (ASV). Conclusively, genotypes TGX1990-80F and TGX2010-11F were identified as high yielding and stable soybean genotypes by AMMI and GGE biplots are recommended for cultivation in any part of the tropics that have similar environment conditions in Nigeria.

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