Original Research Article

AMMI and GGE Biplot Analysis of Yield and related traits among selected mini-core Pigeonpea (*Cajanus cajan* L. Millsp.) Accessions

Abstract

Pigeonpea [*Canjanus cajan* (L.) Millsp.] is an orphan crop that has remained greatly unimproved in quality and quantity in Africa even though it has great potential of supplying food to the growing population. Its yield is affected by various biotic and abiotic factors and a lack of varieties with broad adaptability to a range of environments. It is therefore important to select accessionsthat are stable in different environments for yield and yield components. A randomized complete block design layout was used to carry out a multi-locational trial using 107 pigeonpea accessions. Data was taken for the total number of pods per plant at maturity, pod length, seed weight, seeds per pod, and seed yield per plant. Additive main effects and multiplicative interaction (AMMI) with genotype and genotype by environment interaction (GGE) biplot were used to interpret the data. The mean squares for the PCA explained by the first two principal components account for 100% of the G x E interaction. The results revealed that the differences in the yield and yield components across the three locations were mostly due to the genotypes of the pigeonpea and to some extent the genotype by environment interaction. Six accessions were observed to be high-yielding and stable across all three environments.

keywords: Pigeonpea, GE Interaction, GGE biplot, AMMI, stability, yield components

Introduction

Pigeonpea [*Canjanus cajan* (L.) Millsp.] has been reported to be an orphan crop that has remained greatly unimproved in quality and quantity in Africa even though it has great potential [1]. Its production in Nigeria has been at a subsistence level among small-scale farmers [2] but has recently been considered a cash crop for national income earnings [3]. This is not peculiar to only Nigeria or Africa, as pigeonpea production is distinguished from other major pulses in the world for being almost entirely produced by smallholder farmers [4].

This pulse is a rich source of 20-30% protein, especially sulfur-containing amino acids such as methionine and cysteine [5]. It also contains cajanin, cahanones 2-2 methyl cajanon, 2-hydroxy genistein, and isoflavones that confer antioxidant properties. It has been used generally for treating dysentery, jaundice, diabetes, skin irritations, sores, hepatitis, constipation, the expulsion of bladder stones, inducing lactation, and for stabilizing the menstrual period [6-9]. It is used for the production of noodles and confectionaries [10], improvement of soils, and as a national income earner, as India offered a hundred billion dollars to Nigeria to export pigeonpea and other legumes to India [11].

Pigeonpea cultivation in Nigeria is predominantly in the agroecological zones of the Guinea Savanna [2]. However, this region is presently the largest and most threatened agroecological zone [12] due to desert encroachment and its proximity to the Sudano-Sahelian region [13]. Similarly, there is a southward shift of the rainforest, creating a derived savanna, with a loss of forest biodiversity, and a change in agricultural practices [14]. The implication of this is that the crops being cultivated in the Guinea Savanna can now be cultivated in the derived savanna and the depleting rainforest region of Nigeria.

Currently, pigeonpea production in Nigeria is 3.52% of the world's 5.4 million hectare production area [15]. Its yield is affected by various biotic and abiotic factors ranging from moisture, altitude, temperature, photoperiodism, insect pests, mineral stresses, diseases, and a lack of varieties with broad adaptability to a range of environments [16-17]. In India, crop yield was reported to be 652 kg ha^{-1}, 1,268 kg ha^{-1} in Malawi, 921 kg ha^{-1} in Myanmar, 300-400 kg ha^{-1} in Mozambique, and 1,345 kg ha^{-1} in the guinea savanna of Nigeria, while global productivity is at 774 kg ha^{-1} [4, 18-19]. To mitigate against this gap in pigeonpea yield, varieties that are resistant to abiotic and biotic stresses need to be developed [20]. However, without multi-environment trials, the effects of genotypes by environment interaction (GEI) will result in inconsistencies in the performance of these varieties. It is therefore important to select genotypes that are stable in different environments for yield and yield components.

There are different components used for determining yield in pigeonpea hybrids. Seed yield per hectare, seeds per pod, pod length, 100 seed weight, seed yield per plant, and pods per plant are reported to be significantly associated with pigeonpea yield [21-22]. Since yield is not a monogenic trait, stability in these yield and yield components is therefore important when selecting pigeonpea for yield. Using multi-environment trials could become problematic to manipulate due to the large data generated. However, the additive main effects and multiplicative interaction (AMMI) analysis, with genotype and genotype by environment interaction (GGE) biplot models are some of the powerful means of interpreting this kind of data [23]. The AMMI model makes use of variance and principal component analysis to represent the GEI in several dimensions, while the GGE combines both genotype main effects and those of GEI for analysis [24-

25]. AMMI and GGE have been used to identify traits such as high yield performance and stability across rainfed environments in India [23], grain yield and stability in Malawi [26], yield stability of vegetable pigeonpea in Kenya [27], number of primary branches/plant, pod length, number of grains/pod, 100-seed weight, and seed yield/plant in Manipur, India [28]. However, no such information exists for pigeonpea in the guinea savanna agroecological zone of Nigeria. Hence, the objective of this study was to evaluate the yield stability and adaptability of Nigerian pigeonpea accessions using AMMI and GGE analyses.

Materials and Methods

Description of the study locations

This study was conducted at three locations which include Ejule (Kogi State), Ekpoma (Edo State), and the University of Lagos (Lagos State). Ejule is 369.6 m above sea level (m.a.s.l), in the Guinea Savannaagroecological zone where pigeonpea is cultivated [15]. Ekpoma is 256.6 m.a.s.l in the Derived Savannaagroecological zone and pigeonpea is cultivated there as well. Lagos is 7.3 m.a.s.l, in the humid forest, however, pigeonpea is not cultivated there.

Rainfall (mm) was recorded at Ekpoma and Ejule where crops were planted on the field, while temperature (°C) was recorded at all locations where the experiment was conducted. The average rainfall, and minimum and maximum temperatures throughout the research are presented in table 2. Soil samples were collected from both Ejule and Ekpoma fields before land preparation was carried out.

Description of plant samples

A total of 129 pigeonpea accessions were obtained from the regional genebank of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), located in Niamey, Niger Republic. The collections contained high, medium, and low-yielding accessions. These accessions were gathered from different parts of the world and kept in the genebank. The White accession is a local high-yielding genotype grown by many farmers in Kogi state, this was used as a local check, thereby, bringing the total accessions to 130.

Experimental design and planting

The 130 pigeonpea accessions were planted in a randomized complete Block design (RCBD). However, only 107 viable accessions germinated and were used for the multi-locational trials in the study (Table 1). Multi-locational trials were conducted at Ejule (Kogi State), Ekpoma (Edo State), and the University of Lagos (Lagos State). A 60 cm row-to-row and 20 cm plant-to-plant spacing was adopted for the sowing as described by Navneet [29] on ridges in Ejule and Ekpoma, while polyethene pots in the screen house were used in the University of Lagos. Accessions were thinned to a single plant per pot after three weeks of establishment. Five stands (replicates) per accession were used for the study. Normal agronomic practices were done throughout the duration of the study, including watering plants in the greenhouse every other day.

Collection of data

Data was as described by International Board for Plant Genetic Resources [30]. Data for yield traits which include pod number, pod length, seeds per pod, hundred seed weight, and seed yield per plant were collected.

Analysis of data

The AMMI and GGE were analyzed using PB Tools software version 2014. This was carried out for G × E interactions and stability of evaluated yield traits of the genotypes. The model used for the analysis is given below:

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + \varepsilon_{ij}$$

Where:

Y_{ij} = the observed mean of the i^{th} genotype, (Gi) in the i^{th} environment, (Ej),

μ = the overall mean;

G_i = effect of the i^{th} genotype;

E_j = effect of the j^{th} environment;

GE_{ij}= the interaction effects of the i^{th} genotype, and the j^{th} environment; and

ε_{ij} = the error term.

Table 1: Pigeonpea accessions used in the study

S/N	Pigeonpea Accession	Genotype Code
1	ISC-1	G1
2	ISC -10	G2
3	ISC -100	G3
4	ISC -104	G4
5	ISC -109	G5
6	ISC -11	G6
7	ISC -111	G7
36	ISC -174	G36
37	ISC -175	G37
38	ISC -176	G38
39	ISC -178	G39
40	ISC -179	G40
41	ISC -180	G41
42	ISC -181	G42
72	ISC -38	G72
73	ISC -39	G73
74	ISC -4	G74
75	ISC -40	G75
76	ISC -41	G76
77	ISC -42	G77
78	ISC -46	G78

8	ISC -115	G8
9	ISC -118	G9
10	ISC -120	G10
11	ISC -122	G11
12	ISC -123	G12
13	ISC -124	G13
14	ISC -129	G14
15	ISC -13	G15
16	ISC -134	G16
17	ISC -135	G17
18	ISC -137	G18
19	ISC -14	G19
20	ISC -140	G20
21	ISC -141	G21
22	ISC -147	G22
23	ISC -150	G23
24	ISC -153	G24
25	ISC -155	G25
26	ISC -157	G26
27	ISC -158	G27
28	ISC -16	G28
29	ISC -166	G29
30	ISC -167	G30
31	ISC -168	G31
32	ISC -169	G32
33	ISC -170	G33
34	ISC -171	G34
35	ISC -172	G35
36	ISC -174	G36
43	ISC -182	G43
44	ISC -184	G44
45	ISC -185	G45
46	ISC -186	G46
47	ISC -187	G47
48	ISC -189	G48
49	ISC -197	G49
50	ISC -198	G50
51	ISC -2	G51
52	ISC -20	G52
53	ISC -200	G53
54	ISC -201	G54
55	ISC -202	G55
56	ISC -203	G56
57	ISC -204	G57
58	ISC -22	G58
59	ISC -23	G59
60	ISC -24	G60
61	ISC -25	G61
62	ISC -27	G62
63	ISC -28	G63
64	ISC -29	G64
65	ISC -3	G65
66	ISC -30	G66
67	ISC -31	G67
68	ISC -32	G68
69	ISC -35	G69
70	ISC -36	G70
71	ISC -37	G71
79	ISC -48	G79
80	ISC -5	G80
81	ISC -51	G81
82	ISC -58	G82
83	ISC -59	G83
84	ISC -6	G84
85	ISC -61	G85
86	ISC -62	G86
87	ISC -63	G87
88	ISC -65	G88
89	ISC -66	G89
90	ISC -74	G90
91	ISC -75	G91
92	ISC -76	G92
93	ISC -77	G93
94	ISC -78	G94
95	ISC -82	G95
96	ISC -83	G96
97	ISC -84	G97
98	ISC -86	G98
99	ISC -88	G99
100	ISC -89	G100
101	ISC -9	G101
102	ISC -90	G102
103	ISC -91	G103
104	ISC -92	G104
105	ISC -93	G105
106	ISC -95	G106
107	White	G107

Results

Characteristics of Locations used in the study and Analysis of Variance

Information on the three locations used in the study is presented in Table 2. Ejule (Kogi State) has the highest altitude, followed by Ekpoma (Edo State), while Akoka (Lagos State) has the lowest altitude. The three environments have similar soil texture, but with different mean rainfall. More rainfall was recorded in Lagos, followed by Edo State, while Kogi had the least rainfall in the planting season. Minimum temperatures for the three locations are not so different, but the maximum temperature showed that Kogi had the highest maximum temperature, followed by Edo, and then Lagos. Results for yield and yield components show highly significant differences ($p < 0.01$) within the genotypes, and the test locations, but not significant for genotype by environment interactions for all the yield components except 100 seed weight, where G × E showed highly significant differences (0.01) (Table 3).

Table 2: Environmental characteristics of the study locations

Site	Latitude	Longitude	Altitude (m)	Soil Texture	Mean Rainfall (mm)	Min Temp (°C)	Max Temp (°C)
Edo	6° 79′ N	6° 10′ E	256.6	Loam	1288.22	23.85	34.44
Kogi	7° 34′ N	7° 11′ E	369.6	Loam	1127.09	24.47	36.54
Lagos	6° 52′ N	3° 39′ E	7.3	Loam	2113.00	23.50	30.71

Additive Main Effects and Multiplicative Interaction (AMMI 1) Analysis for PC1 and Significant Influence of Traits

The AMMI analysis of variance of 107 pigeonpea genotypes evaluated for yield and yield components across three locations revealed that genotypes accounted for more than 84% of the total variation in all the traits considered, while the environment and genotype by environment each accounted for less than 9% of the total variation (Table 3). The mean squares of the Principal Component Analysis 1 (PCA1) and Principal Component Analysis 2 (PCA2) were significant (0.01), and explained more than 70% and about 27.6% of the total variation, respectively in all the traits (Table 3). PCA3 showed no variation (0%) in the study. Therefore, the PCA1 and PCA2 gave a cumulative contribution of 100.

Table 3: Mean Square from Combined ANOVA for Yield and Yield-contributing Traits of 107 Pigeonpea genotypes tested across three Locations.

Source of Variation	**df**	**PDN**		**PDL**		**SPP**		**HSW**		**YPP**	
		MS	**TVE**	**MS**	**TVE**	**MS**	**TVE**	**MS**	**TVE**	**MS**	**TVE**
Genotype (G)	106	31585.93**	89.35	2.73**	98.21	3.22**	97.38	22.63**	86.92	951.38**	84.06
Environment (E)	2	45745.32**	2.44	7.40**	0.68	0.60**	0.34	73.09**	5.29	4268.71**	7.12
G X E	212	1450.40ns	8.21	0.046ns	1.10	0.04ns	2.28	1.01**	7.78	49.92ns	8.82
Error	642	1455.75	0.00	0.16	0.00	0.09	0.00	0.81	0.00	50.45	0.00
PCA1	107	2326.36**	72.4	0.08ns	94.2	0.07ns	80.8	1.99**	99.07	97.57ns	78.4
PCA2	105	557.75ns	27.6	0.00ns	5.8	0.00ns	19.2	0.02ns	0.93	1.36ns	21.6

*,** Significant at $p \leq 0.05$ and $p \leq 0.01$, respectively; ns = non-significant; df: degree of freedom; MS: mean square; TVE: total variation explained; PDN: pod number; PDL: pod length; SPP: seeds per pod; HSW: hundred seed weight; YPP: yield per plant

Results shown in Figure 1 show the genotype by environment interactions based on the AMMI1 model for total pod number (Figure 1a), pod length (Figure 1b), seeds per pod (Figure 1c), hundred seed weight (Figure 1d), and yield per plant (Figure 1e). The results revealed thatgenotypeswith positive PCA1 scores such as G67, G16, G6, G59, G34, G19, G64 and G82 had positive interactions with Edo (E1) and Kogi (E2) for pod number (Figure 1a), while for hundred seed weight (Figure 1d), G101, G83, G67, G82, G2, G45 had positive interactions with Edo (E1) and Lagos (E3). Genotypeswith positive PC1 scores such as G36, G100, and G35 for pod length (Figure 1b), G50, G85, G55 and G88 for seeds per pod (Figure 1c), had positive interactions with Lagos, and G23, G84, G16, G71, G89, and G29 (Figure 1e) had positive interactions with E1 (Edo). Conversely, genotypes with negative PCA1 scores such as G86, G106, G1, G90, G103, G24, G104, and G3 (Figure 1a), had positive interactions with only Lagos (E3). Similarly,genotypes with negative PCA1 scores such as G92, G103, G1, G14, G36, G52, and G100 (Figure 1d) had positive interactions with only E2. While negative PCA1 scores in G1, G23, G37, G61, G90, G4 (Figure 1b), and G1, G23, G56, G61, G98, G65 (Figure 1c) had positive interactions with E1 and E2. E2 and E3 had positive interactions with G33, G1, G91, G25, and G10 (Figure 1d) which had negative PCA1 scores.

The stable genotypes (Figure 1) with PCA1 scores close to zero are G88, G97, G32, G57, G77 and G5 (Figure 1a), G10, G100, G106, G47, G51, G52, G82, and G88 (Figure 1b), G54, G51, G10, G100, G102, G103 and G106 (Figure 1c), G101, G78, and G80 (Figure 1d), G23, G16, G84, G71, G89 and G29 (Figure 1e). As for high yield, superior genotypes for the total number of pods per plant are G67, G86, G16, G88, G34, and G100, then, G1, G23, G37, G58, and G49 for pod length (Figure 1b), G23, G56, G61, G49, G54, and G1 for seeds per pod (Figure 1c), G92, G100, and G88 for hundred seed weight (Figure 1d), and G23, G16, G84, G33, and G71 for yield per plant (Figure 1e) across the three environments. GenotypesG88, G82, G102, G101, and G23 are the most stable (Figures 1a, 1b, 1c, 1d, and 1e respectively), then G86, G1, G23, G92, and G23 (Figures 1a, 1b, 1c, and 1d) respectively are the superiorgenotypes, while genotypes G33, G85, and G40 (Figures 1b, 1c, 1d respectively) and genotypesG1 (Figures 1a, and 1e) had low yield.

Environment 2 (E2) had a PCA1 score that was nearly zero for pod number and seed yield per plant (Figures 1a, and 1e), and so contributed most to the stability of the genotypes. While E3 had a high PCA1 score for pod length and seeds per pod, contributing the highest to the GEI component, then E1 and E2 had low PCA1 scores in these two respective traits. A high PCA1 score was recorded in both E1 and E2 for hundred seed weight and low PCA1 in E3. The lowest yield was recorded in E3 for all traits, while the highest yield was recorded in E2 for hundred seed weight and E1 for the other traits. Edo (E1) and Kogi (E2) were correlated with similar PCA1 scores for pod number, pod length, and seeds per pod (Figures 1a, 1b, and 1c), while Edo (E1) and Lagos (E3) were correlated with similar PCA1 scores for hundred seed weight (Figure 1d), thus found on the same side of the perpendicular and horizontal lines. For seed yield per plant, Kogi (E2) and Lagos (E3) are seen to be correlated (Figure 1e).

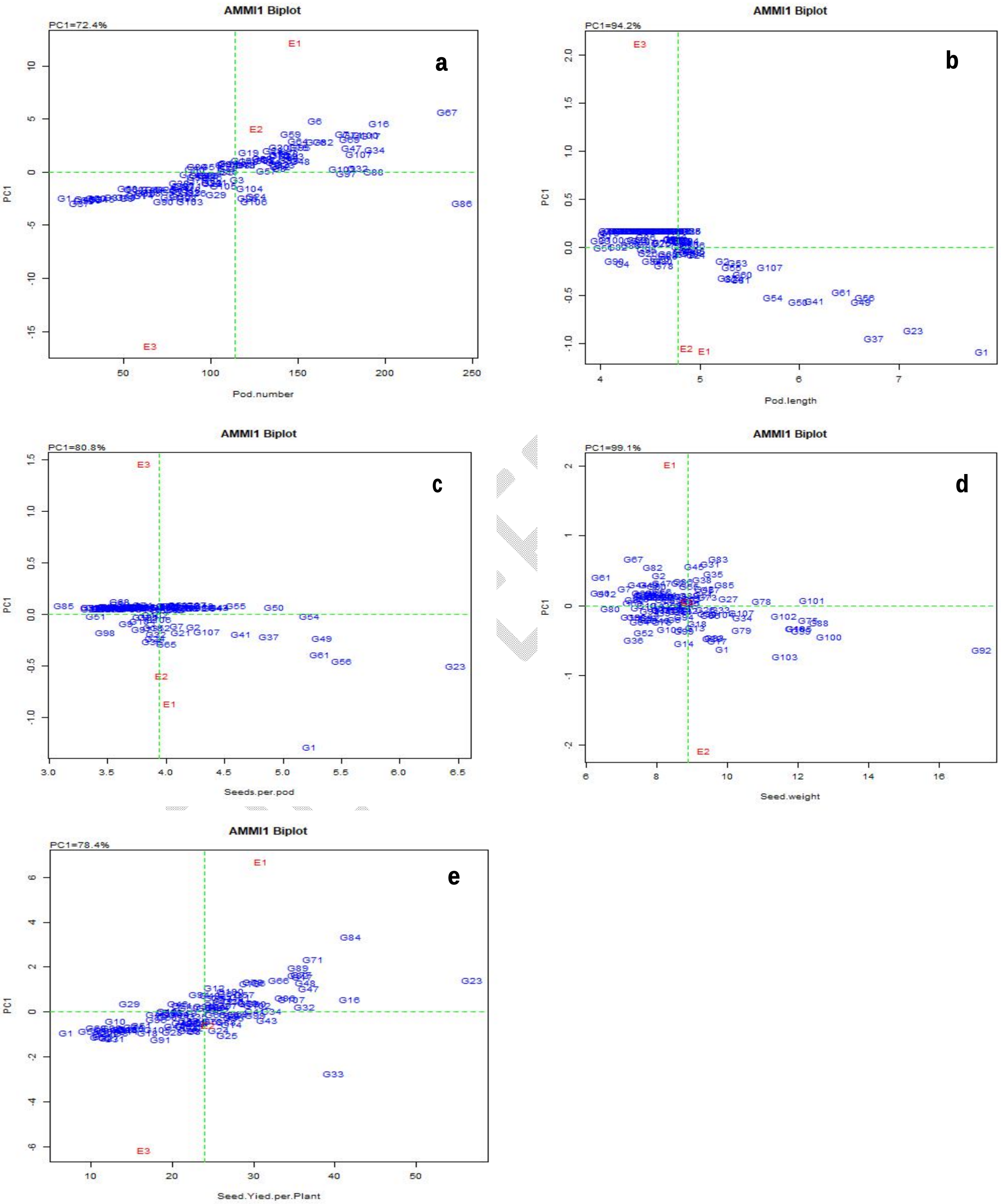


Figure 1: GEI biplot based on AMMI 1 model for the PCA1 scores of 107 pigeonpea genotypes evaluated in three environments in Nigeria for the number of pods (a), Pod length (b), Seeds per pod (c), 100 seed weight (d), and yield per plant (e).

AMMI 2 Analysis for PC1 and PC2 Scores-Based Graphical Representation

The AMMI biplot demonstrates the magnitude of the G x E interaction by joining environmental scores to the origin by side lines. Short vectors do not show strong interactive forces in terms of discriminating ability, whereas long vectors show a strong ability to discriminate between the genotypes. From Figure 2, E3 had the longest vector for pod number, pod length, and seeds per pod (Figures 2a, 2b, and 2c), while E1 has the longest vector for both hundred seed weight and yield per plant (Figures 2d, and 2e). E2 has the shortest vector for pod number, seeds per pod, and yield per plant (Figures 2a, 2c, and 2d), while E1 has the shortest vector for pod length and E3 for hundred seed weight. This means that E3 was a more differentiating environment, for pod number, pod length, and seeds per pod, and E1 for hundred seeds weight as well as yield per plant, while E2 is the least discriminating environment in three of these two traits.

The majority of the genotypes were near the origin and so are not sensitive to environmental interaction for all traits considered. Genotypes G6, G30, G7, and G71 are correlated with the vector for E1 and so are best adapted to the environment, while G95, G62, and G1 are correlated with the vector for E2, and G46, and G68 with E3 for pod number (Figure 2a). For pod length, genotypes G1, G41, G2, G53, and G24 are correlated with E1, G81, G43, G54 and G37 with E2, while genotypes G91 and G28 were shown to be correlated with E3 (Figure 2b). For seeds per pod, G56, and G61 are correlated with E1, then G97, G87, and G43 with E2, and G88 with E3 (Figure 2c), while in hundred seed weight, G83, G67 are correlated with E1, G14, and G16 with E2, and G35, G9 with E3 (Figure 2d). For yield per plant, genotypes G84, G23, and G89 are correlated with E1, G96, G91, and G81 with E2, and genotypes G33, and G55 are correlated with E3 (E).

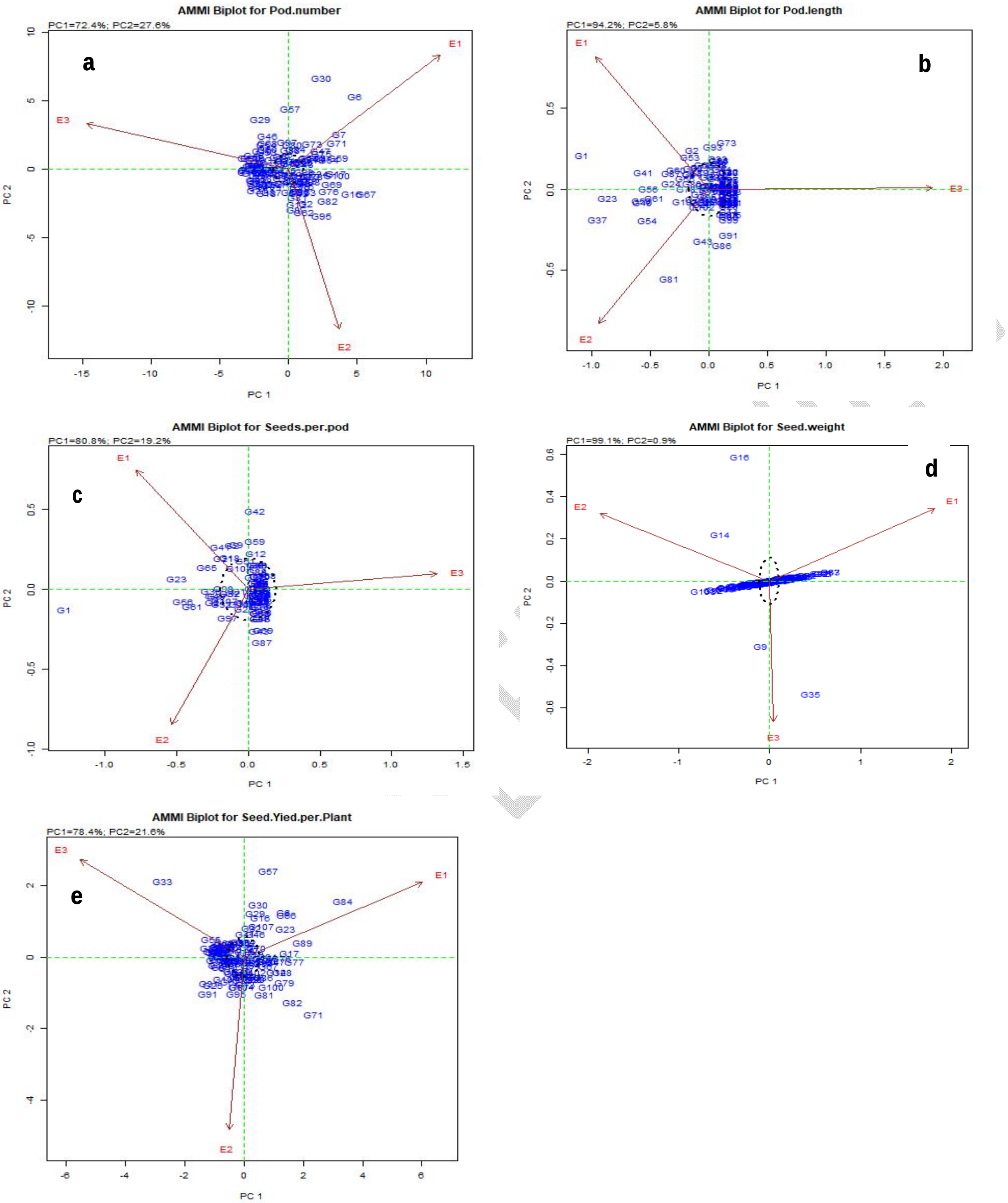


Figure 2: GEI biplot based on AMMI 1 model for the PCA1 scores and PCA2 scores of 107 pigeonpea genotypes evaluated in three environments in Nigeria for the number of pods (a), Pod length (b), Seeds per pod (c), 100 seed weight (d), and yield per plant (e).

Comparisons of Genotypes across the Environments Using GGE Analysis

What-Won-Where Polygon View across the Environments

The GGE what-won-where biplot of the 107 pigeonpea genotypes tested in the three environments showed the extent of genotype and environment interaction (Figure 3). The biplot was divided into 4 sectors for pod number, seeds per pod, seed weight, and seed yield per plant (Figures 3a, 3c, 3d, and 3e respectively), and 3 sectors for pod length (Figure 3b), with genotypes present in all sectors of the polygon. Genotypes G67, G6, G30, G1, G3, and G86 located at the vertices of the polygon were considered superior genotypes for pod number (Figure 3a), genotypes G1, G56, G26, G28, G33, and G3were superior for pod length (Figure 3b), genotypes G23, G54, G50, G85, G98, and G1 at the apex for seeds per pod (Figure 3c), genotypes G92, G83, G67, G61, G40, G80, G36, and G103 for seed weight (Figure 3d), genotypes G33, G23, G84, G29, and G1 for yield per plant (Figure 3e).

All three environments were located in one of the sectors for pod length, seeds per pod, and hundred seed weight (Figures 3b, 3c, and 3d), indicating the presence of a single mega-environment except for pod number where E2 and E3 were located in one sector and E1 in another sector, indicating two mega-environments (Figure 3a). Similarly, two mega-environments were delineated for yield per plant, where E1 and E2 were located in one sector and E3 in another sector. Genotype G67 was at the apex of the sector with E1, and G86 was at the apex of the sector containing E2 and E3 for pod number (Figure 3a). G1, G23, and G92 at the apices of the sectors with all three environments in the polygons for pod length, seeds per pod, and hundred seed weight respectively (Figures 3b, 3c, and 3d), while for yield per plant, G23 was located at the apex of the sector with E1 and E2, and G33 at the apex of the sector with E3 (Figure 3e), indicating that these genotypes were the best performers in the three environments.

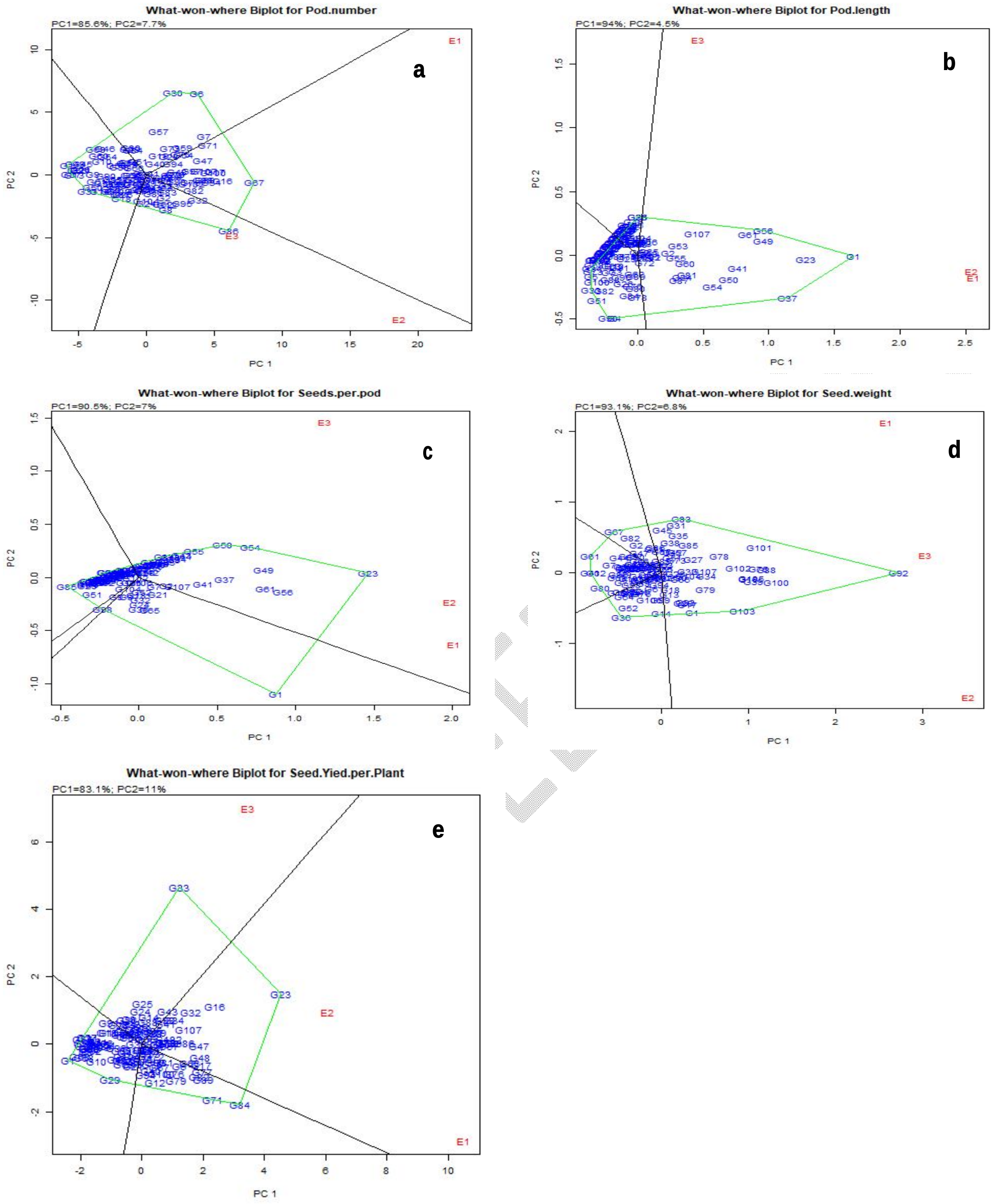


Figure 3: What-won-where GGE biplot view displaying the genotype main effect and GE interaction effect of 107 Pigeonpea genotypes in three environments for the number of pods (a), Pod length (b), Seeds per pod (c), 100 seed weight (d), and yield per plant (e).

GGE Biplot of Mean and Stability Analysis and Ideal Genotype Assessment

What-won-where polygon suggested winning pigeonpea genotypes in the environments. However, there is a need to assess the mean performance and stability of all the pigeonpea genotypes to aid the selection decision. The Average Environment Axis (AEA) makes it possible to visualize the performance and stability of GGE graphically. The blue dotted line is the AEA abscissa and the perpendicular line is the ordinate (Figure 4). The length of the abscissa to the right of the origin is above average yield, while the length to the left of the origin is below average yield. Length of ordinate on the other hand approximates the GEI. Shorter ordinate signifies lower variability, and higher stability and vice versa.

These results (Figure 4) revealed that G32, G95, G40, G76 (Figure 4a), G65, G107 (Figure 4b), G49, G24, G55, G41, G107, G37 (Figure 4c), G92, G100, G88, G101 (Figure 4d), G16, G54, G43, G14 (Figure 4e) are above average in yield, length, and weight as the case may be, with more stability, whereas G87, G98, G6, G57, G90, G7, G71 (Figure 4a), G1, G23, G37, G81, G49, G54 (Figure 4b), G1, G23, G56, G81 (Figure 4c), G103, G1, G83 (Figure 4d), and G23, G33, G84, G71 (Figure 4e) are above average yielding genotypes, but with comparatively lower stability. Genotypes G1, G54, G9, G68 (Figure 4a), G51 (Figure 4b), G85, and G51 (Figure 4c), and G29, G51, and G35 (Figure 4e) are stable but their yields are below average, with the majority of the genotypes appearing to be relatively stable and clustered around the AEA abscissa. Genotypes G31, G14, G18 (Figure 4a), G4, G78 (Figure 4b), G98 (Figure 4c), G67, G56 (Figure 4d), and G1, G91 (Figure 4e) are both below-average yielders and are less stable.

The ideal genotypes have the highest yield and absolute stability in the AEA arrowhead and the concentric circles along the arrowhead rank the inclusion of the genotypes. The closest genotype to the ideal line is G67, followed by G96, and G18 (Figure 4a), G1 is closest to the ideal line, followed by G23, and G37 (Figure 4b), G23, followed by G56, G49, G81, and G1 (Figure 4c), G92, followed by G100 and G88 (Figure 4d), G23, followed by G16 (Figure 4e). These ideal lines can serve as reference lines in the evaluation of these genotypes.

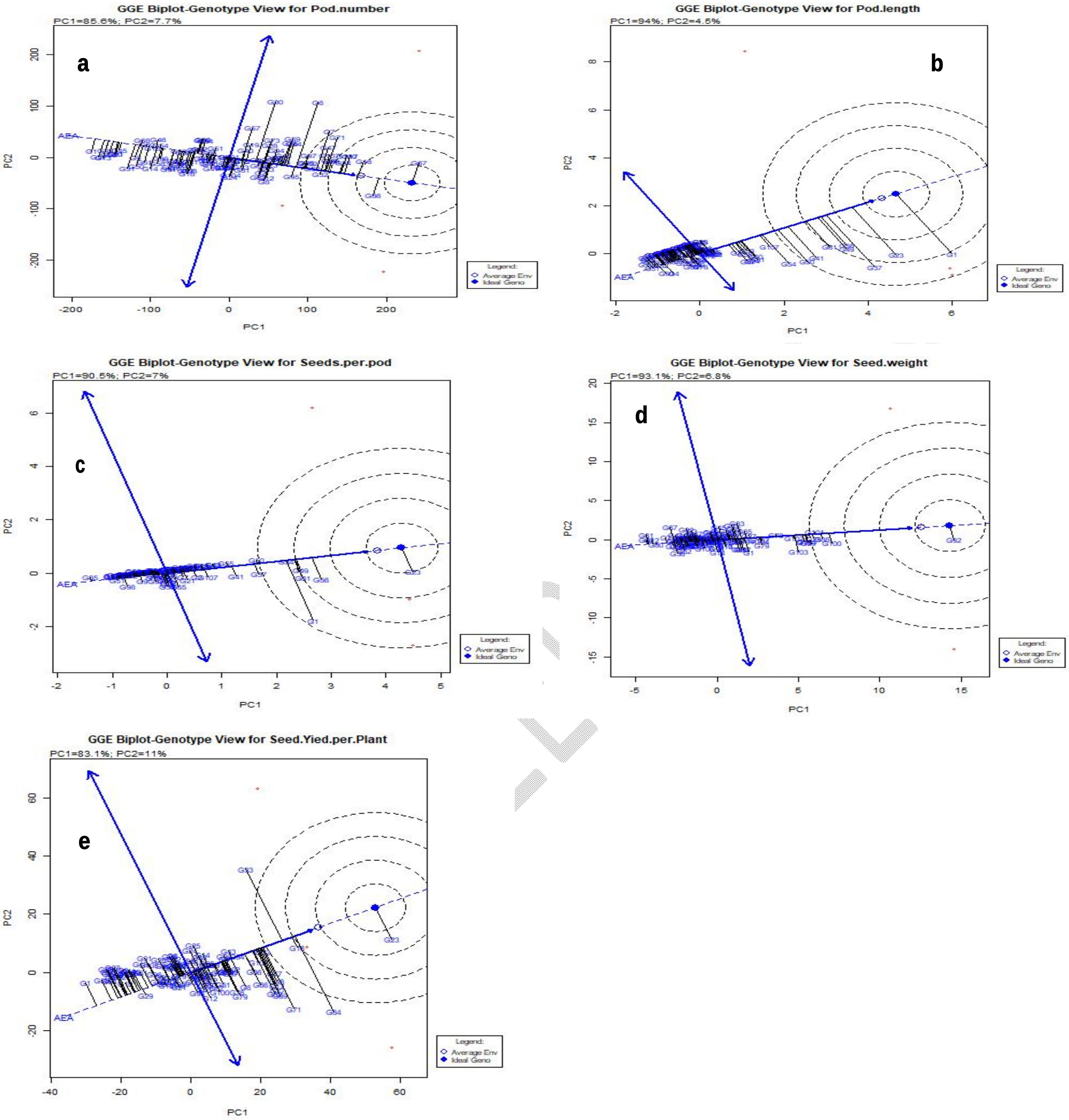
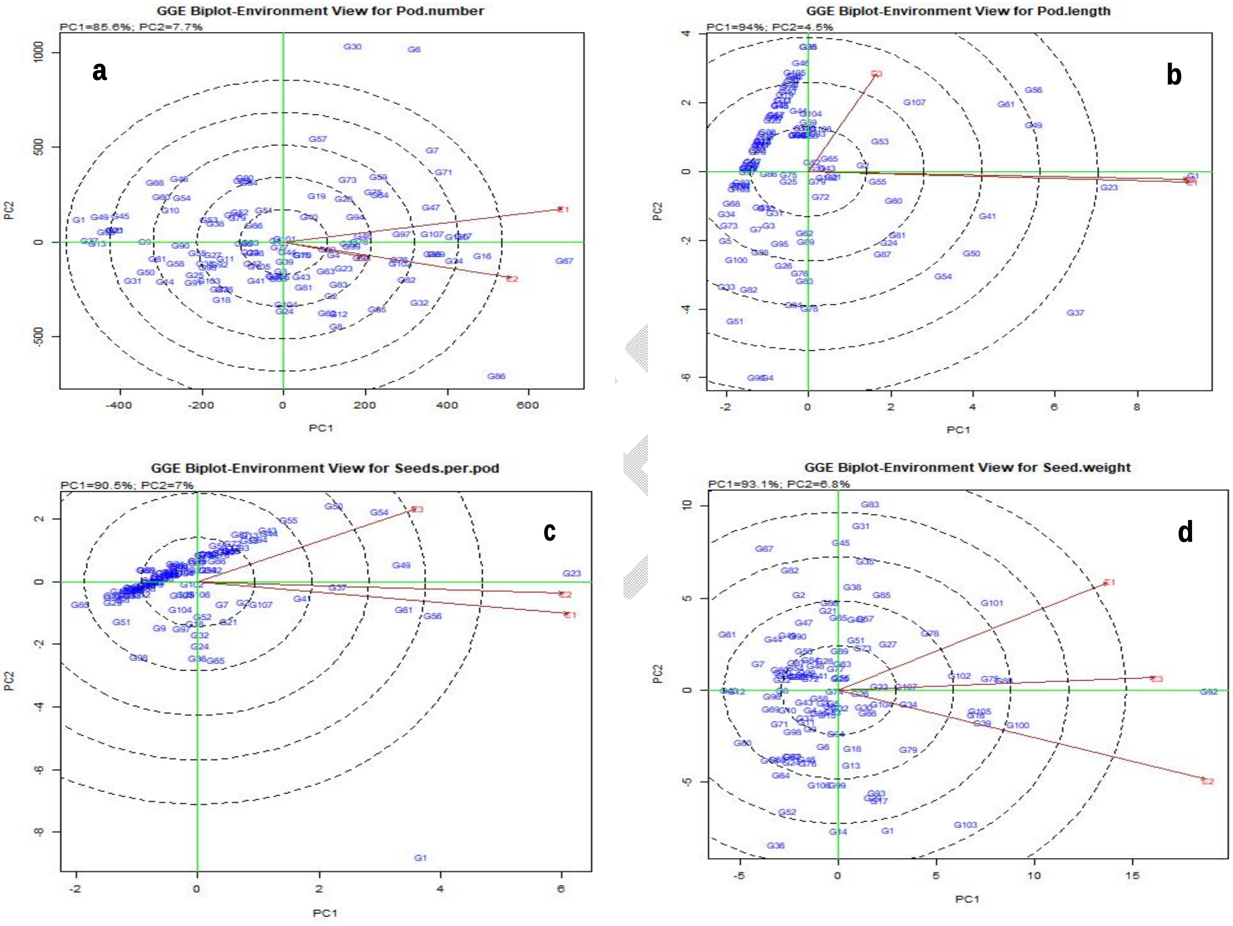


Figure 4: Average Environment Axis (AEA) view to rank genotypes concerning Ideal Genotypes for the number of pods (a), Pod length (b), Seeds per pod (c), 100 seed weight (d), and yield per plant (d).

Relationship among Test Environments

In this study, the three environments were distributed into two groups for all the traits (Figure 5). For pod length (Figure 5b), seeds per pod (Figure 5c), and yield per plant (Figure 5e), E1 and E2 are the two environments that are closely related, while E2 and E3 are closely related for pod number (Figure 5a). For hundred seed weight (Figure 5d), E1 and E3 are two environments that are closely related, while E2 is in a different group. In biplots for all the traits, all three environments are located within an angle of less than 90°, indicating that the three environments share similarities, but E1 and E2 share more.



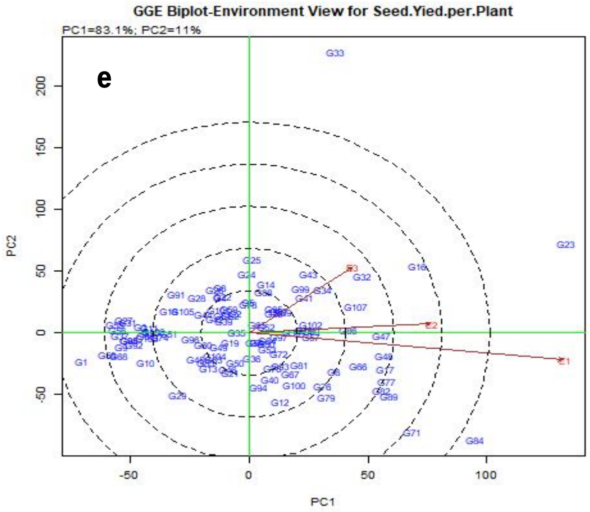


Figure 5: Environment view of the GGE biplot view displaying the genotype main effect and GE interaction effect of 107 Pigeonpea genotypes in three environments for number pods (a), Pod length (b), Seeds per pod (c), 100 seed weight (d), and yield per plant (e).

Discriminativeness and Representativeness Pattern of the GGE Biplot

A total of 93.3%, 98.5, 97.5%, 99.9%, and 94.1% (Figures 6a, 6b, 6c, 6d and 6e respectively) of the variance was explained by the first two principal components (PCs), with PC1 explaining 85.6% and PC2 7.7% for pod number (Figure 6a), PC1 explaining 94% and PC2 4.5% for pod length (Figure 6b), PC1 explaining 90.5% and PC2 7% seeds per pod (Figure 6c), PC1 explaining 93.1% and PC2 6.8% seed weight (Figure 6d), and PC1 explaining 83.1% and 11% for PC2 seed yield per plant(Figure 6e). The ideal environment is the environment presented with a blue dot (Figure 6), while the open red circle represents the average environment. The dotted line is the AEA, and environments with long vectors and small angle with AEA is more informative and representative, while an environment with a short vector gives less information. In this study, E1 has the longest vector in all traits except in hundred seeds weight (Figure 6d), while E3 has the shortest vector for all traits in the study. The ideal environment lies in between E1 and E2 for pod number (Figure 6a), and in between E2 and E3 for the other traits (Figure 6b, 6c, 6d, and 6e), with the average environment located close to E2 for all traits (Figure 6a, 6b, 6c, and 6e) except for hundred seed weight where the average environment is located near E3 (Figure 6d).

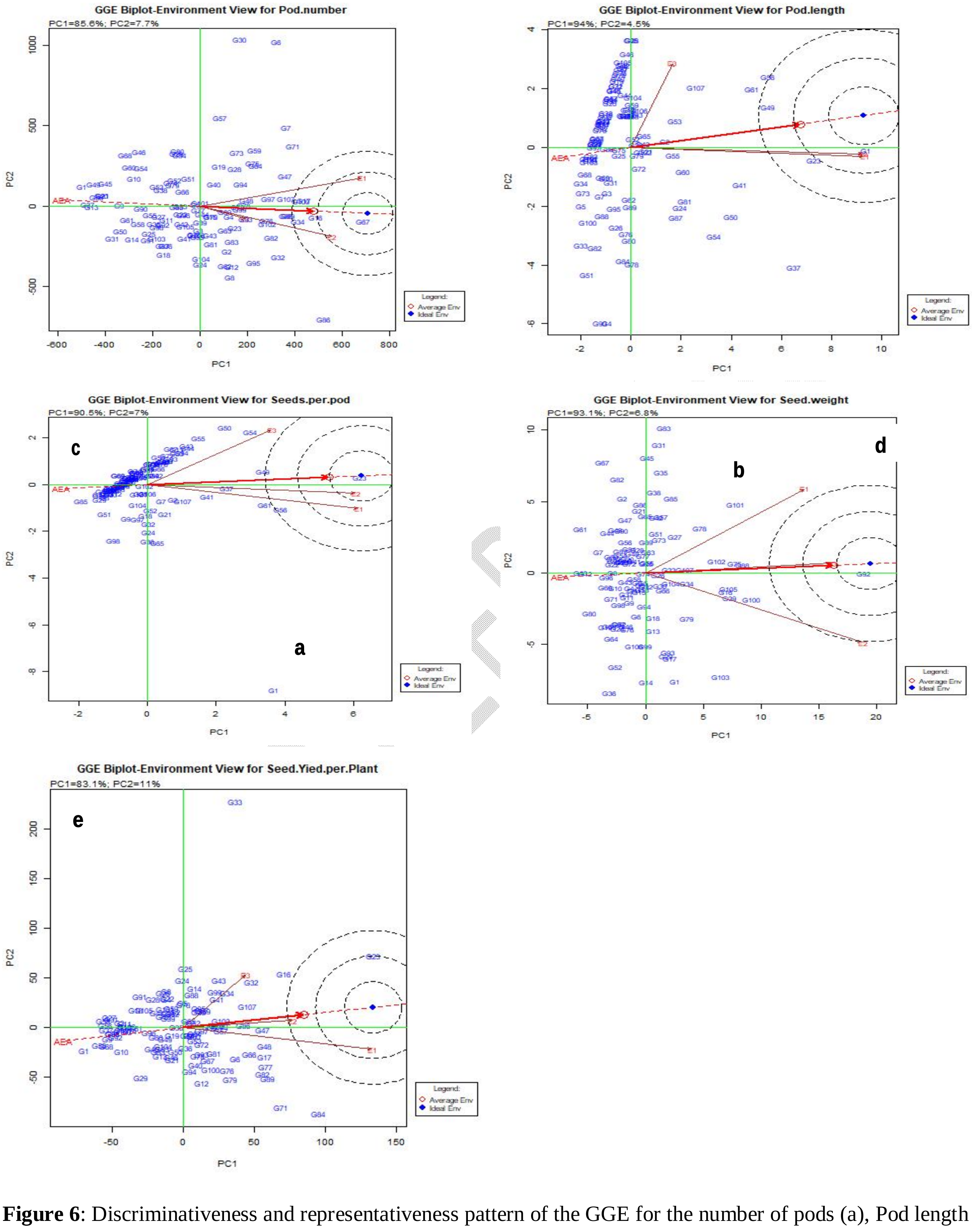


Figure 6: Discriminativeness and representativeness pattern of the GGE for the number of pods (a), Pod length (b), Seeds per pod (c), 100 seed weight (d), and yield per plant (e).

Discussion

The mean squares for the PCA explained by the first two principal components account for 100% of the G x E interaction. Since several authors including Biswas [31]and Rao [32] have confirmed that two PCAs are sufficient for evaluating GEI, these two PCAs were used in analyzing the AMMI biplot. Gebremedhin [33] used significant PCA1 to appropriately explain the GEI, and their adaptation in barley. This revealed that the differences in the yield and yield components across the three locations were mostly due to the genotypes of the pigeonpea and to some extent the genotype by environment. The environment had the least influence on variation except in yield per plant where the environment had a higher influence than the genotype by environment. The minimal influence of the environment on the performances of the pigeonpea genotypes in this study may be because the climatic and edaphic factors of the environments are similar, and so exerted similar selection pressures on the plants. Performances of the genotypes were significant as a result of genotypic variance, and so selection based on the overall mean is dependable since GEI was minimal. These findings agree with that of Singh [28] who reported significant variation in pigeonpea yield and the total number of pods on account of genotype.

This study revealed that E2 contributed most to the stability of the number of pods and seed yield, while E3 contributed most to the stability of the hundred seed weight. These environments provided suitable conditions for the genotypes to reach optimum yield potential compared to other environments for the three traits. Genotypes such as G67, G1, G23, G92, and G23 may be suitable for planting in many environments because they are relatively stable, with an above-average yield as revealed in this study.

The GGE analysis for mean and stability analysis grouped the genotypes into those that are stable and high yielding, low stability and high yielding, those that have high stability, but low yielding, and those with low stability and low yield. The highly stable and high-yielding genotypes are G32, G65, G49, G92, and G16. Those that have low stability and are high yielding are G87, G1, G103, and G23. G1, G51, G85, and G29 have high stability and low yield (although G1 has the longest length of the pod as well as the highest number of seeds per pod, their yield is low in terms of pod number and yield per plant), while G31, G4, G98, G67, and G1 are both low yielders and less stable. According to Khan [34], genotypes with seemingly undesirable traits are good for breeding programs, as they have yield component compensation criteria. This means that these plants may be low-yielders and less stable, but they may have other beneficial qualities such as the ability to recover quickly from environmental stresses.

The biplot analysis is the most powerful interpretative tool for AMMI analysis [35]. The AMMI model revealed that E1 was the best environment with the highest yield, while the least yield was recorded in E3. Pigeonpea has been cultivated in both Edo and Kogi for years, but the rainfall and lower average temperatures may be some of the reasons why Edo performed comparatively better than Kogi. According to Patil [36], seed yield in pigeonpea decreases with an increase in temperature, and as such, pigeonpea planted in Kogi had different climatic conditions given Kogi's proximity to the encroaching desertification. Similarly, Edo's derived savanna is expected to have better soil since the area was formally a rainforest. Planting was carried out in June in Kogi, and July in Edo and Lagos, and around the time of flowering of medium-duration genotypes (in Kogi), there was a cessation of rainfall for about two weeks in both Edo and Kogi. The crops in both locations were water-stressed during this period. However, crops in Kogi had already started flowering during this stress. This may have affected yield since the crops were at a critical stage of their reproductive development. Sinha [37] cited Lopez to have reported that yields are affected during late flowering and early pod development stages.

The adoption of the polygon to analyze 'what-won-where' is important in GGE. This study placed the three study environments under one or two sector(s) out of the three or four sectors in the biplots. The genotypes at the vertices in the sectors are G1, G23, G92, G33, G67, and G86, so can be recommended for planting in the three locations. These genotypes were the closest to the ideal lines for high yield and stability. Yohane [26] reported that either of the two sites of two mega-environment can be substituted for future pigeonpea genotype trials. Since the study revealed two mega-environments for pod number and yield per plant and the other traits as a single mega-environment, breeding efficiency can be increased by selecting either Edo or Kogi for evaluation to increase the mega-environment. The relationship among test environment biplots grouped the locations into two. From this study, Edo and Kogi are more alike, and reducing costs will mean dropping either of these locations.

In terms of discrimination and relatedness in this study, E1 has the longest vector for all traits except hundred seed weight, whereas E2 has the longest vector and smaller angle with AEA, and so are the most discriminating environments and can be used to test genotypes for specific adaptability as well as suitable for general adaptation selection. E3 has the shortest vector for all traits considered. E2 is closest to the ideal environment for all traits, while both E2 and E3 appear as the closest to the ideal environment for cultivating pigeonpea in terms of seed weight, unfortunately, the study was carried out in a much more controlled environment in E3, and most likely the reason for its closeness to the ideal environment for the trait. Hence, a field experiment in E3 is needed to determine the certainty of the idealness of this environment for pigeonpea cultivation.

Vector for E3, being the shortest vector for all traits has the least discriminating ability, as it offered little information on the genotype variability. Although the difference in lengths of E1 and E2 are almost indistinguishable in most traits, this is not surprising as the two locations are the agroecological locations where the crop is cultivated. The cosine of the angle between the environments depicts the interrelationship between the environments. The angle between all three locations is less than 90°, showing a positive, but low correlation coefficient between all environments, however, E2 and E1 have a high correlation coefficient than E3 and E1 or E3 and E2.

Conclusions

This study evaluated the stability and adaptability of yield and yield components of pigeonpea genotypes using AMMI and GGE biplot analysis. Assessing the adaptability and stability of pigeon pea genotypes in different environmental conditions can be achieved through the use of the Multi-Environmental Trail (MET). In order to determine the suitability of a genotype for commercial cultivation, it is important to evaluate its susceptibility to genotype by environment interaction (GEI). This study revealed that genotypes G67, G86, G1, G23, G92, and G33 are ideal genotypes with high yields and relatively high stability. The three locations contributed to the morphological traits. Edo contributed the highest to the GEI and thus revealing its suitability for specific adaptation of pigeonpea genotypes, while Kogi contributed to the stability of the genotypes for pod number and seed yield per plant, and Lagos for seed weight. The environment had the least influence on variation. ISC 169, ISC-3, ISC197, ISC-76, and ISC 134 pigeonpea genotypes were highly stable and high yielding across all environments, and Kogi was revealed to be the closest to the ideal environment for pigeonpea production, while Edo is a highly suitable location for specific adaptation of pigeonpea genotypes.

This study grouped the pigeon pea accessions into four major stability and mean yield groups. The first group comprises those that are highly stable and have high yield potentials, and they include G32 (ISC-169), G65 (ISC-3), G49 (ISC-197), G92 (ISC-76), and G16 (ISC-134). The second group is comprised of those that have low stability, but high yield potential and they include G87, G1, G103, and G23. The third group comprises those with high stability but low yield, and they include G1, G51, G85, and G29. The last group comprises genotypes with low stability and low yield, and they include G31, G4, G98, G67, and G1. G88, G16, G23, G71, and G100 performed well across all environments and are relatively stable. Therefore, they are the ideal genotypes for the study and the reference crop for breeding programs across environments. Kogi is the ideal environment for testing genotypes, and since it is an agroecological zone for pigeonpea cultivation, it makes it easier. Lagos has a low altitude and the planting in Lagos was carried out in a screen house where climatic factors were controlled. There is, therefore, a need to replicate this experiment on the field in Lagos to ascertain whether or not Lagos supports the cultivation of pigeonpea.

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