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Full Length Research

CLUSTER ANALYSIS AND GENOTYPE × ENVIRONMENT (G × E) ASSESSMENT FOR ROOT YIELD IN 35 ORANGE-FLESHED SWEETPOTATO GENOTYPES

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ABSTRACT: Orange-fleshed sweetpotato (OFSP) is a biofortified food of *Beta* carotene that fights vitamin A deficiency and promotes nutritional security. The success to select and identify the superior genotype is limited by Genotype and Environment (G×E) interactions. The study was conducted to estimate the magnitude of G×E and to select stable and high yielding OFSP in three locations, and to identify the most discriminating test environments. Similarly, to characterized them according to similarities in traits. These genotypes were subjected to heatmap cluster analysis. The 35 OFSP genotypes were evaluated across 3 environments using a RCBD with three replications. The data were subjected to ANOVA using R package. The AMMI model analysis indicated that genotype (G) and environment(E) had significant effects on root yield and the contribution to the total sum of squares difference was 64.89% and 6.35%, respectively. The remaining 3.87 % of the variation resulted from GxE effects. G24, G35 and G34 exhibited high mean root yield across environments with high degree of stability. These hybrids have the potential for production across the test locations as well as others within the same agro-ecological zones. However, G3, G12 and G30 were not only low yielding but also among the least stable genotypes. The best genotype with respect to location include G15 and G14 which were best for Umudike (E1), while G34 and G4 were the best genotype for Igbariam (E1) area. G24 performed well in FUTO (E3). Among the locations, E1 was the most productive site in distinguishing genotypes and the most representative environment. The Cluster heatmap analysis grouped the 35 genotypes into 4 clusters with distinct features. Cluster I was recommended for high root girth, high root yield performance and high beta carotene content, while clusters II and IV were recommended for high dry matter and high starch. Cluster III was characterized with short vine length.

Keywords: *G x E interaction, additive main effect and multiplicative interaction (AMMI), stability, heatmap cluster analysis, OFSP*.

INTRODUCTION

The orange-fleshed sweetpotato (*Ipomoea batatas*) (OFSP) is grown in more than 100 countries (Woolfe, 1992). Among the tuber crops grown in the world, sweetpotato ranks fourth after cassava, yam and cocoyam (Ray and Ravi, 2005). It is grown as a starchy food crop throughout the tropical, sub-tropical and frost-free temperate climate zones in the world (ICAR, 2007, Nedunchezhiyan *et al*., 2012). The crop is very important in promoting nutritional security particularly in agriculturally backward areas (Srinivas, 2009) with poor soils. It can be

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reconstituted into fufu or blended with other carbohydrate flour sources such as wheat and cassava for baking bread, biscuits and other confectioneries (Nwankwo *et al*., 2012). The OFSPs are naturally biofortified food of *Beta* carotene and is important in combating vitamin deficiency in children. Recently, several promising genotypes of African origin were introduced and evaluated at different locations (Harriman, *et al.,* 2017b). These resulted in the recommendation of several OFSP genotypes for the sweetpotato growing regions in Nigeria (Harriman *et al.,* 2017a). However, the changing environmental conditions affect the performance of OFSP genotypes which requires a breeding programme that needs to take into account the consequences of environment and genotype interaction in the selection and release of improved genotypes. Crop breeders have been striving to develop genotypes with superior root yield and quality over a wide range of different environmental conditions with limited resources. This is because temperature and rainfall extremes may differ substantially between locations (Mekasha *et al.,* 2014). Genotype by environment (G x E) interactions, however, frequently interfere with the selection of widely adapted genotypes (Ceccarelli, 1989) as it complicates selection of broad adaptation in most breeding programmes. The phenotype of an organism is determined by the combined effect of the environment and the genotype which interact with one another. When environmental differences are large like in Nigeria, it may be expected that the interaction of G x E will also be higher. Hence, one genotype may have the highest yield in some environments while a second genotype may excel in others. Hence, it is important to know the magnitude of the interactions in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation (Gauch and Zobel, 1997). Evaluation of different genotypes in a multi-environment is not only important to determine high-yielding genotypes but also to identify sites that best represent the target environment (Yan *et al.*, 2001). Similarly, the successfully developed high-yielding potential new cultivar should have a stable performance and broad adaptation over a wide range of environments. A genotype is considered stable if it has adaptability for a trait of economic importance across diverse environments. To reduce the effect of G x E interaction, crop improvement programmes usually run performance trials across a wide range of environments to ensure that the selected genotypes have a high and stable performance across several environments. The GGE biplot in this regard provides a good tool for estimation of better performance and root yield stability across the innovative environments. Similarly, the changing environmental conditions and the expansion of OFSP to new agro-ecologies in Nigeria necessitate a continuous study of G x E interaction for crop improvement programme. Similarly, genetic diversity is the base for crop improvement (Iqbal *et al*., 2014). For high production in OFSP, the precise selection of elite genotypes is very important for any area (AshoftehBeiragi *et al.*, 2010). Multivariate analysis based on cluster analysis is mostly used to evaluate the magnitude of genetic diversity among the germplasm (Brown-Guedira, 2000). Hierarchical cluster analysis has been suggested for classifying entries of germplasm collections based on degree of similarity and dissimilarity (Van Hintum, 1995). Hence, the objective of this study were to (1) evaluate the G × E interaction using AMMI and GGE-biplot analysis for root yield of OFSP genotypes, (2) identify stable genotype in the South eastern region of Nigeria, and (3) select the best genotypes by using cluster analysis that can be exploited in future OFSP breeding programme.

MATERIALS AND METHODS

Description of the experiment and experimental design

The 35 genotypes of OFSP genotypes obtained from the (NRCRI) Umudike were grown in a plot size of 1 × 3m (3m^2) with a spacing of one seedling per stand, with inter and intra row spacing of 1.0 and 0.3m respectively giving a plant density of 33,333 plants per hectare. The experiment was arranged in a Randomized Complete Block Design in 2023 cropping season. The experiment was established in three different agro-ecological zones in Eastern Nigeria with three replicates. The plants were planted using vines that are free from virus infestation. The crop was fertilized with NPK fertilizer 15:15:15 one month after planting at the rate of 300kg/ha. Weeds were controlled manually. Weeding was done two times from the planting. Data were collected from 15 randomly selected plants from each plot in each replication in the field and analyses were done.

Description of the experimental sites

The geographical and climate conditions of three experimental sites are shown in Table 1.

Table 1: Basic information of the locations in the multi-environment trials in 2023

State	**Location**	Code	longitude	Latitude	Elevation(m)	Annual average rainfall (mm)	Soil type	Temperature (^{0}C)
Abia	Umudike	E1	07^0 33'E	05^0 29'N	122	2177	sandy loam ultisol	26
Anambra	Igbariam	E2	06^0 52'E	06^0 15'N	81	2100	Clay loam	30
Imo	FUTO (Owerri West)	E3	7^0 021 & 7^0 20^1 E	5^0 271 & 5^0 291 N	55.6	2500	sandy loam	29

Stability Analysis

The root yield data was subjected to combined analysis of variance across environment. Since, genotype x environment interaction was significant (Table 2) the data was subjected for biplot analysis. To explain the G×E interaction, the multivariate stability analysis was performed graphically based on GGE biplot and AMMI using R studio developed by the R Core Team. The GUI package of R studio was used for GGE biplots while the Agricolae package was used for AMMI (CRAN. 2016).), involving two concepts, the biplot concepts (Gabriel, 1971) and the GGE concept (Yan *et al*., 2000). The software was used to generate graphs showing (i) "which-won-where" pattern, (ii) ranking of genotypes on the basis of yield and stability, (iii) environment vectors, and (iv) comparison of environment to ideal environment (Yan and Kang, 2003). This GGE biplot is constructed by the first two principal components (PC1 and PC2) derived from subjecting environment centered yield data, i.e., the yield variation due to GGE, to singular value decomposition (Yan *et al.* 2000, Bernal and Villardon, 2012).

TABLE 2. Mean square estimate from ANOVA for root yield of OFSP obtained from multi-location trials conducted during 2023 in Nigeria.

Source	Df	Sum square	Mean Square	Total variation explained (%)	G x E Explained (%)	Pr(>f)
ENV	2	2448	1223.81	6.35		0.0389*
REP(ENV)	6	1254	208.95	3.25		0.00000512***
GEN	34	25021	735.9	64.89		4.03 x 10^{-51}***
GEN:ENV	68	1494	21.97	3.87		0.979
PC1	35	1334	38.1		3.46	0.295
PC2	33	160	4.85		0.41	0.0100**
Residuals	204	6851	33.58		-	-
Total	382	38561	100.94		-	-

df, degree of freedom; IPCA, interaction principal component axis. *, **, *** = Significant at 5, 1, and 0.1 % level of probability, respectively.

Results and Discussion

Results

Climatic Data

Among the environments, annual average rainfall varied from 2100mm at E2 (Igbariam) to 2500 mm at E3 (FUTO), the elevation ranged from 55.6m at E3 (FUTO) to 122 m at E1 (Umudike). In this study, the selected pilot environmental conditions represent different ecological types (Table1).

Yield Performance

The root yield performance data of these genotypes across the three environments is presented in Table 3. Genotype G24 (K 003) was the best performing genotype with the highest root yield, followed by G35 (Umuspo/3), G34 (Umuspo/1), G11 (A 097a) and G4 (A 01). G32 (Sumaia) was the lowest one among all the tested genotypes (Table 3).

Variance components

Genotype (G) and environment (E) affected both root yield. A combined ANOVA of genetic and environmental factors revealed significant effects of G ($P < 0.001$) and E ($P < 0.001$). The significant difference of variance analysis between environments indicated that the performance of environment was different at each location (Table 2).

Level of genotype x environment interactions

The AMMI analysis of variance for root yield of the 35 OFSP genotypes evaluated in 3 environments showed that G x E had no significant effect on yield values. The environment explained 6.35% of the total sum of squares implying that the environments were slightly diverse to differentiate between genotypes. The remaining 64.89 and 3.87 % of the variation resulted from genotype and G x E effects, respectively. The partitioning of the G x E interaction revealed that IPCA1 captured 3.46 % and IPCA2 0.41% of variation in root yield. The mean squares of the two components (IPCA1 and IPCA2) were significantly different and explained a total of 89.3% of the variance of the G x E interaction in root yield (Table 2 and Figure 1 and 2). Biplot graphs of the AMMI1 (IPCA1 vs. additive effects from genotypes and environment) and AMMI2 models (IPCA2 vs. IPCA1) are in Figures 1 and 2, respectively. The G35, G34, G24, G4 and G11 genotypes produced the highest root yields of OFSP. While genotypes; G3, G32, G12 and G5 were the lowest yielding.

However, the E3 (Owerri) and E2 (Igbariam) environments produced the smallest root yields of OFSP. While E1 (Umudike) environment produced the highest root yield. Environments and genotypes showed variation for the traits in terms of main effects and their interaction.

For example, genotype G32, G27, G6, G9, and G22 located very close to the origin in the biplot and showed low IPCA1 and IPCA2 values suggesting little interaction with the environment and a good performance for root yield compared to other genotypes. In contrast, G15, G24, G35, G34, G4, G11, G32, G14 and G12 were the most unstable genotypes because they were more distant to the origin of the biplot. Similarly, genotypes G24 and G15 were unstable, but presented high root yields. Genotypes G29, G31, and G21 presented intermediate stability. However, genotypes G11 and G34 presented not only high average root yield, but also low IPCA value, indicating adaptability (Fig 1).

Mean performance and stability of genotype for yield

GGE biplot method can be used to identify superior OFSP genotypes for target sites. The biplot (Figure 3) represents a polygon, where some of the genotypes are positioned on the vertexes, while the rest are inside the polygon. As the genotypes positioned on the vertexes have the longest distance from the biplot origin, they are supposed to be the most responsive. Responsive genotypes are either best or the poorest at one or every environment. Considering this, the G15 and G14 had the highest root yield when planted in Umudike(E1). The three environments were positioned in different sector on the graph, which indicates that those environments differ significantly between themselves. Genotypes G15 and G14 were the highest yielding in Umudike (E1), G34, G35 and G4 in Igbariam (E2) and G24 in Owerri (E3)(Fig 3).

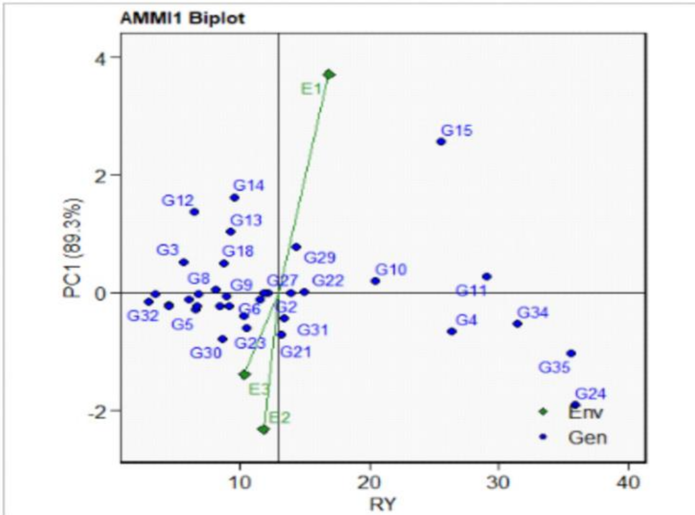

Fig. 1. AMMI 1 biplot for root yield of OFSP genotypes showing means of genotypes (numbers) and environments (E1 to E3) plotted against their IPCA1 scores. RY = root yield.

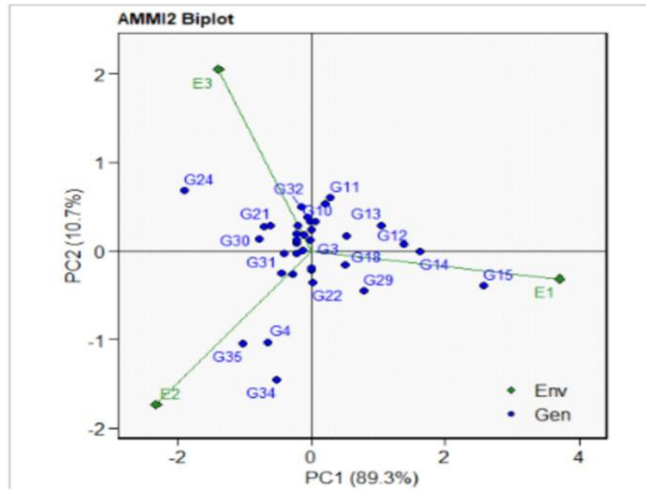

Fig. 2 . AMMI2 biplot showing the two main axes of interaction (IPCA2 vs. IPCA1) in in 35 genotypes of OFSP from three environments in South eastern Nigeria.

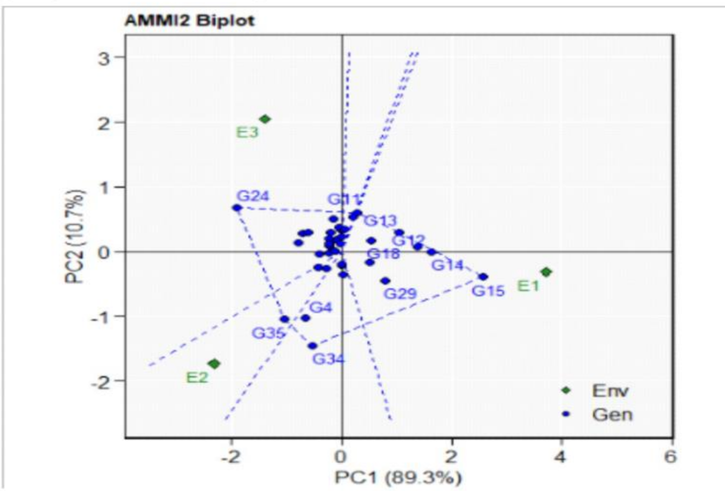

Fig. 3. The which-won-where view of the GGE biplot to show which genotypes performed best in which environments.

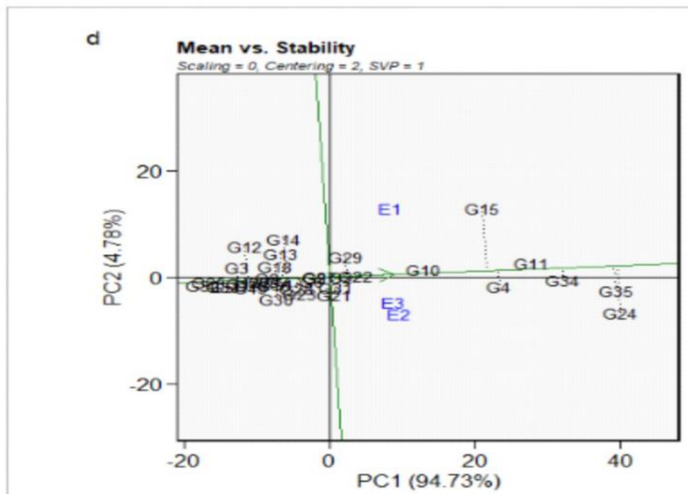

Fig. 4. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the means performance and stability of 35 OFSP genotypes.

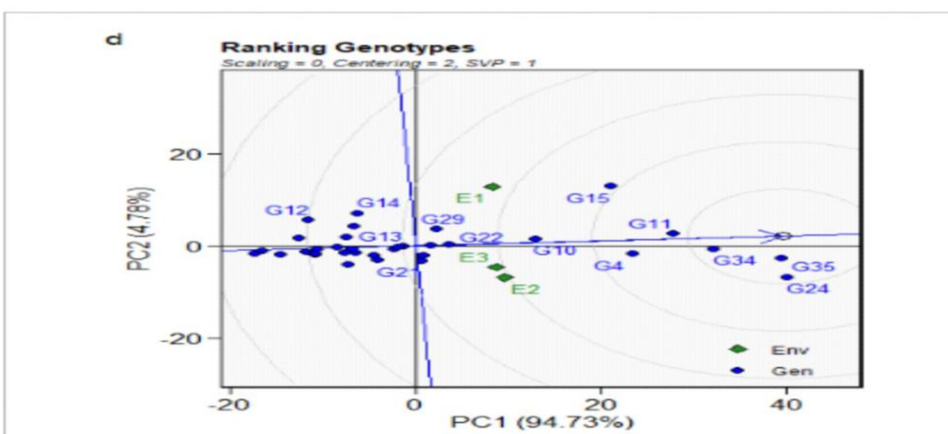

Fig. 5. The GGE biplot 'genotypes ranking' pattern for genotype comparison with ideal genotype showing G + G×E interaction effect of 35 genotypes of OFSP (The average-environment coordination (AEC) view)

Table 3. Mean root yield (t/ha) of 35 OFSP genotypes (G1 to G35) tested at three locations in South eastern Nigeria (E1 to E3) in 2023

GENOTYPE	GENOTYPE CODE	E1	E2	E3	MEAN	RANK
A 002	G1	12.13	8.37	6.99	**9.16**	20
A 005	G2	17.85	13.13	10.82	**13.93**	10
A 010a	G3	11.44	3.02	2.66	**5.71**	31
A 013	G4	28.05	28.47	22.46	**26.33**	5
A 017	G5	7.52	3.68	2.43	**4.54**	32
A 024	G6	14.98	10.68	9.1	**11.59**	15
A 031	G7	12.49	7.27	7.17	**8.98**	21
A 066	G8	12.09	6.27	6.1	**8.15**	25
A 079 b	G9	15.63	10.31	9.71	**11.88**	14
A 089	G10	24.87	17.89	18.61	**20.46**	7
A 097 a	G11	33.78	26.22	27.27	**29.09**	4
A 099	G12	15.42	2	2.08	**6.50**	29
A 106	G13	16.89	5.2	5.77	**9.29**	19
A 130	G14	19.42	4.61	4.62	**9.55**	18
Delvia	G15	39.01	19.06	18.45	**25.51**	6
E 027	G16	11.5	7.9	6.1	**8.50**	24
Erica	G17	9.45	4.84	3.95	**6.08**	30
Esther	G18	14.48	6.65	5.02	**8.72**	22
EX-Oyunga	G19	9.47	6.56	3.79	**6.61**	28
Gloria	G20	10.57	5.51	4.46	**6.85**	26
Ininda	G21	14.34	13.2	12.11	**13.22**	12
Irene	G22	19.03	14.4	11.58	**15.00**	8
Jane	G23	12.02	10.25	9.29	**10.52**	16
K 003	G24	32.48	37.97	37.3	**35.92**	1
Lourdes	G25	7.1	1.72	1.48	**3.43**	34
Malawi I	G26	9.63	5.69	4.73	**6.68**	27
Malawi II	G27	16.13	11.39	9.16	**12.23**	13
Malinda	G28	12.7	10.14	8.15	**10.33**	17
Namanga	G29	21.22	12.14	9.66	**14.34**	9
NRSP/12/060	G30	9.51	9.06	7.33	**8.63**	23
Solo - Abuja	G31	15.66	13.65	10.8	**13.37**	11
Sumaia	G32	6.11	1.25	1.51	**2.96**	35
Tio - Joe	G33	7.52	3.33	2.75	**4.53**	33
Umuspo/1	G34	33.8	34	26.51	**31.44**	3
Umuspo/3	G35	35.88	38.55	32.14	**35.52**	2
MEAN		**16.86**	**11.84**	**10.34**		

A line is then drawn through this average environment and the biplot origin; this line is called the average environment axis and serves as the abscissa of the AEC (Fig 4). Unlike the AEC abscissa, this has one direction, with the arrow pointing to a greater genotype main effect. The stability of OFSP genotypes and average root yield in all environments should be assessed within a single mega environment. Figure 4 shows the stability and mean performance of the evaluation. The AEC abscissa is a single arrowed line that points to higher mean yield across environments. Thus, the maximum root yield was G24, followed by G35, G34, G11, G4, G15 and so on. The acute angle between G24 and G35 indicates that these two genotypes respond similarly in all environments,. Whereas, an obsute angle (e.g., G24 vs G14) indicates that the genotypes reacted inversely, with the G24 outperforming the G14 and vice versa. The genotypes G22, G10 and G4 were extremely stable, whereas G15 was extremely unstable (Fig 4).

Ranking Genotypes Relative to the Ideal Genotype

An ideal genotype should have both high mean performance and high stability across environments. Figure 5 defines an "ideal" genotype (the center of the concentric circles) to be a point on the AEA ("absolutely stable") in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of AEA ("highest mean performance").

Therefore, genotypes located closer to the 'ideal genotype' are more desirable than others. Thus, G35 was more desirable than G24 even though G24 had higher average yield. G12 was, of course, the poorest genotype because it was consistently the poorest.

Cluster analysis

Thirty five OFSP genotypes were grouped into 7 clusters based on various agro morphological traits (Table 4). Figure 6 illustrates the seven clusters formed by hierarchical clustering. Table 4 summarizes the number of genotypes in each cluster. The first cluster is a group consisting of five genotypes. Second cluster consisted of ten genotypes. While the third cluster and fifth clusters comprise of two genotypes each. Clusters four, six and seven are made up of 3, 4 and 9 genotypes, respectively. Genotypes in cluster one are characterized by low value of root girth, days to 50% flowering, root weight per plant, root yield and vine length (Table 5). Genotypes in second cluster are characterize by high value of dry matter, starch, root girth, Root yield and low value of vine length and beta carotene. Genotypes grouped into cluster three had very long vines and high beta carotene with very low root yield, root weight per plant and low root girth. The cluster four was characterized with plants with very low dry matter, low starch, very high days to 50% flowering and very high root yield with high beta carotene. The genotypes categorized into cluster five does not flower and have high dry matter, high starch with long vines. The genotypes grouped into the cluster seven were characterized by highest value of dry matter, starch, high number of branches with low beta carotene value (Table 5).

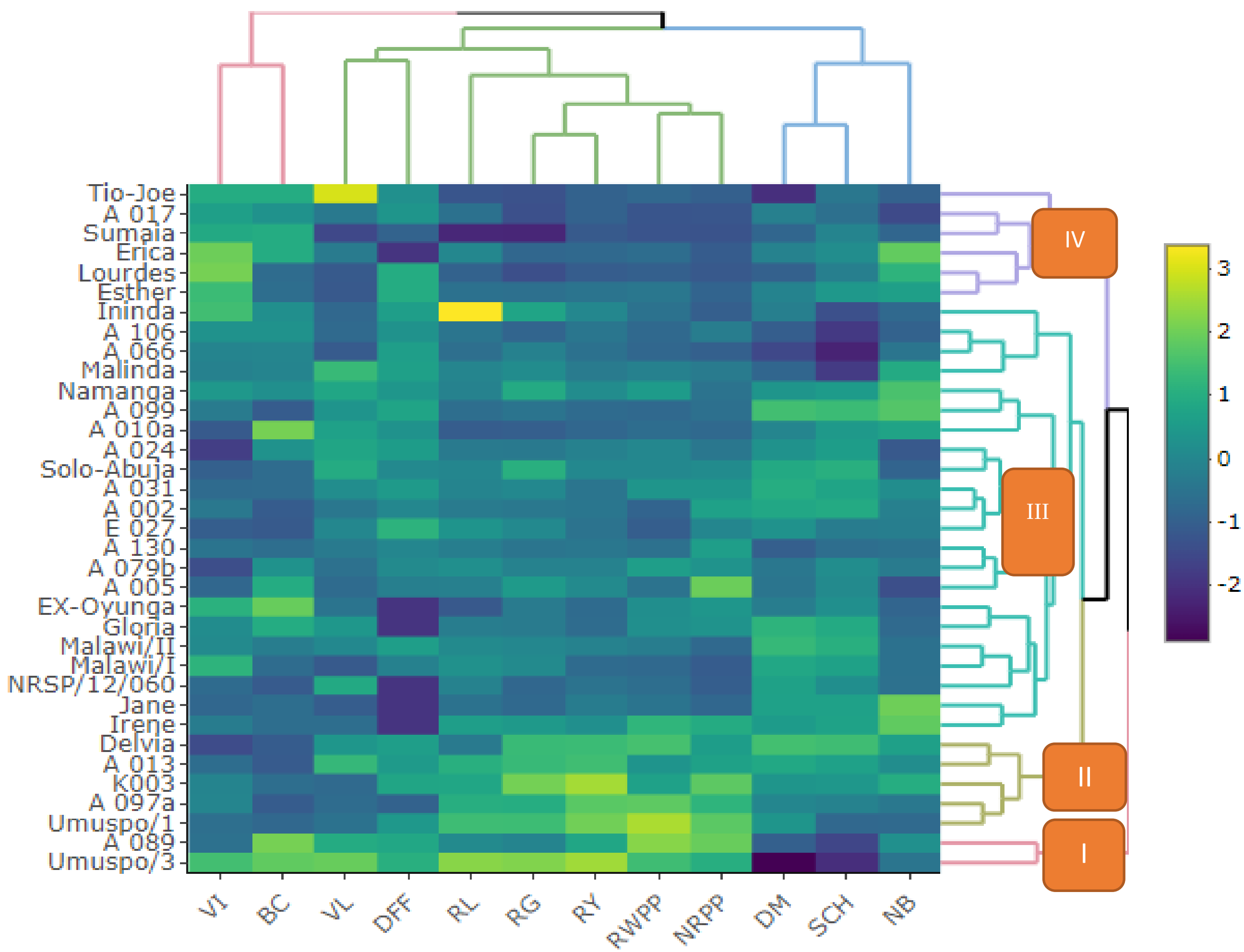

Table 3: Mean of 35 OFSP genotypes arranged in clusters with use of hierarchical clustering by Ward method evaluated in Nigeria

Cluster	Count	TRAITS											
		RY (t/ha)	DM (%)	SCH (%)	RL (cm)	RG (cm)	DFF	RWPP (kg)	NRPP	VL (cm)	VI (%)	NB	BC (Mg/100gFW)
I	2	20.04	22.46	24.33	12.84	17.10	52.64	2.21	4.35	230.94	15.16	2.65	9.05
II	5	12.34	50.94	37.73	10.26	15.77	54.04	1.77	4.07	115.09	10.11	3.56	1.00
III	22	12.43	40.61	31.05	10.74	13.80	34.27	1.63	4.26	66.46	12.76	3.22	3.71
IV	6	13.07	44.22	32.93	10.38	15.24	38.14	2.08	4.29	151.62	10.33	3.29	5.07

RY = Root yield, DM = Dry matter, SCH = Starch, Root girth = RL, Root length = RG, DFF = Days to 50% flowering, RWPP = Root weight per plant, NRPP = Number of roots per plant, VL = Vine length, VI = Virus incidence , NB = Number of branches, BC = Beta carotene,

Discussion

Breeding for stable yield would involve evaluation of crop varieties across diverse environments to identify superior genotypes with broad or specific adaptation due to GxE interaction. And it has been shown that varietal adaptation differs significantly across environments (Kaya and Taner 2002; Thillainathan and Fernandez 2001; Yan *et al.* 2007). The results of this research confirmed the presence of significant statistical difference among genotypes and environments, suggesting the need to assess the stability of genotypes across environments. This indicated the significant influence of environment on yield performance of OFSP genotypes in South-eastern Nigeria. In other word, the mean yield of genotypes differed from location to location. Moreover, the genotype effect scores were more scattered than the environmental effect scores, indicating that variability due to the genotypes is greater than variability caused by environmental effects (Figure 1). Similar results were recorded by other authors (Dagne, 2008). The highest root yield (39.01t/ha) was obtained from Delvia (G15) at Umudike and lower root yield was also obtained from this genotype (18.45t/ha) at FUTO. Taking the mean yield for the assessment of the environments, K003 (G24) gave the best yield (35.92t/ha), while Sumaia (G32) gave the lowest yield (2.96t/ha). This suggests that genotypes that produce high root yields in a distinct environments (locations) can be considered as adapted genotypes for that location. Ramagosa and Fox (1993) concluded that if a genotype maintains high yield over a wide range of environments, it is referred to as having general or wider adaptation. On the other hand, if this is true only for a limited range of environments, that genotype has specific or narrow adaptation. Genotypes at the vertices of polygon (biplots) are either best or poorest in one or more environments. For root yield, G15 and G14 were the best genotype in Umudike (E1), and G35 in Igbariam(E2). This finding is supported by Yan, (2001). Each test environment also played an important role in the selection of genotype; as the environments had different discriminative powers for the genotypes (Bose *et al*., 2014). Environment E3 had the strongest resolution and had a good discriminating power for the genotypes. Environment E1 had the weakest discrimination for the genotypes (Kang, 1998).

The greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments (Purchase, 1997). The more IPCA scores approximate to zero, the more stable the genotype to overall environments sampled (Adugna and Labuschagne, 2002). Umudike(E1) is the most favorable environment for all genotypes with nearly similar yield response. The rest of the environments (Igbariam(E2) and FUTO(E3)) were the least favorable environments for all genotypes with different yield response. Genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment. Here, G15 and G14 showed similar performance as they are close to each other (Figure 3), indicating similar response of the genotypes to the environment. Genotypes with a smaller vector angle in between and have similar projection, designate their proximity in the root yield performance. Those genotypes that are clustered closer to the centre tend to be stable, and those plotted far apart are unstable in performance. From fig 4, genotype G15, G24 and G14 were unstable as they are located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores.

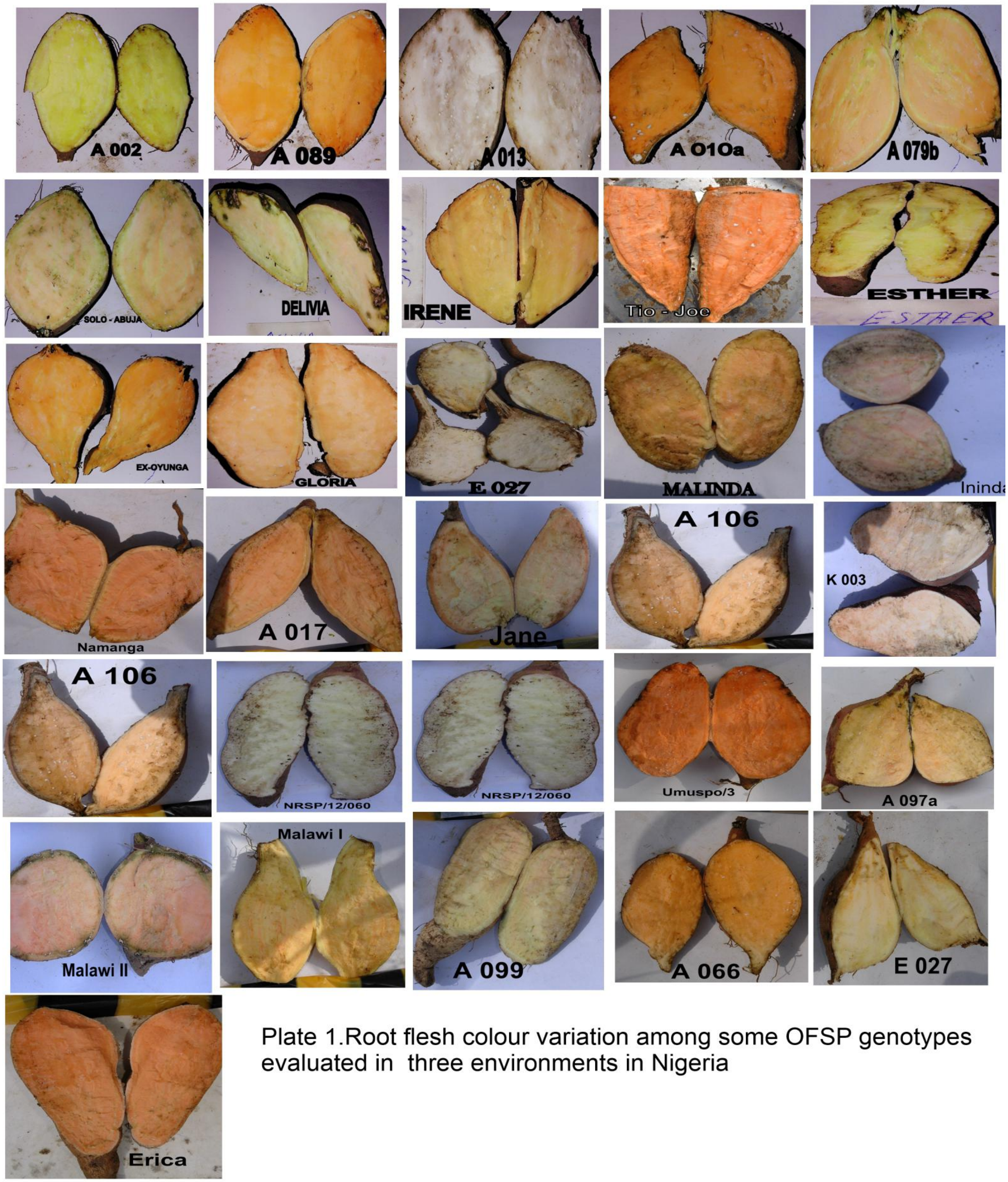

Plate 1.Root flesh colour variation among some OFSP genotypes evaluated in three environments in Nigeria

Genotypes G22, G10 and G4 were genotypes positioned closer to the origin of the biplot which indicates their stability in performance across environments.

Although, G15 and G24 were very unstable, they were very high yielding. These results are consistent with those of Badu-Apraku *et al*. (2012) and Makumbi *et al*. (2015), who identified high-yielding but unstable varieties in different, contrasting environments. The results of this research confirmed that the main problem in selecting superior varieties in Nigeria is associated with the unpredictable environmental conditions. However, the findings of these trials are in accordance with other workers (Mosisa and Habtamu, 2008; Solomon *et al*., 2008) who reported that rainfall and other environmental factors are important in selecting crop genotypes.

The estimation of genetic diversity and relationships among germplasm accessions facilitates the selection of parents with diverse genetic background which is very essential for breeding program (Murphy *et al* 1986, Souza and Sorrels 1991). In this study considerable morphological variation was found mainly due to genetic factors and also subjected to environmental factors (Table 1). The dendrogram constructed classified the 35 genotypes into seven groups based on agronomic and other yield characteristics combined together. The selection from the cluster II and cluster IV is worthwhile as it has genotypes performing better in terms of yield and yield attributing characters. This is similar to the findings by Ali *et al*. (2008) and Singh and Dwivedi (2002) who reported that cluster analysis can be helpful for finding high yielding genotypes. The selection of genotypes from clusters V and VII means the selection of genotypes having higher value of dry matter which leads to selection of high flour yielding genotypes considering the relationship according to the finding of Wali *et al.* (2006). Clusters I and III also include genotypes with low root yield with high dry matter. Thus, the genotypes from Clusters II and IV can be used for breeding program with hybridization for a high dry matter and high yield. Rahim *et al.*(2010) showed that the genotypes with maximum dissimilarity result in high yield and so the cross between the most dissimilar genotypes shown from the cluster analysis can be done in breeding program to achieve higher heterosis.

Conclusion

The major proportion of the total variation in root yield was explained by genotype followed by environment. The study has clearly proved that the AMMI model can summarize patterns and relationships of genotypes and environments successfully. The information from the AMMI model could be important to release genotypes to target environments based on their responsiveness. G24, G35 and G34 exhibited high mean root yield across environments and average responsiveness with high degree of stability indicating general adaptability and thus can be recommended for the south eastern region of Nigeria. The best genotype with respect to location G15 and G14 were best for Umudike (E1) while G34 and G4 were the best genotype for Igbariam (E1) area. G24 performed well at FUTO (E3). Therefore, it is reasonable to recommend these varieties according to their specific adaptation. It can be observed from the present study that high level of genetic diversity was present in agro-morphological traits of OFSP. The 35 OFSP genotypes, with the help of cluster analysis, were successfully characterized and accurately grouped into 7 clusters with distinct promising features. Clusters II and IV were recommended for high root yield performance, while clusters II, V, VI and VII were recommended for flour production (high dry matter). Clusters I, III, IV and VI were characterized with high beta carotene content.

Conflicts of interest

Authors do not have any conflicts of interest.

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REFERENCES

Adugna, W. and Labuschagne, M.T. (2002). Genotype-environment interactions and phenotypic stability analyses of linseed in Ethiopia. Plant Breeding Manual. 121:66-71.

Ali, Y., Atta, B. M., Akhter, J., Monneveux, P. and Lateef, Z. (2008). Genetic variability, association and diversity studies in wheat (Triticumaestivum L.) germplasm. *Pak J Bot.* 40: 2087-2097.

AshoftehBeiragi, M., SiahSar, B.A., KhavariKhrasani, S., Golbashy, M., Mahdi Nejad, N., Ali Zade, A. (2010): Effects of genotype by environment interactions on morphological traits, yield and yield components of new grain corn (Zea mays L.) varieties. Journal of Agroecology 2(1):136-145.

Badu-Apraku, B., Oyekunle, M., Obeng-Antwi, K., Osuman, A.S., Ado, S.G., Coulibay, N., Yallou, C.G., Abdulai, M., Boakyewaa, G.A. and Didjeira, A. (2012). Performance of extra-early maize cultivars based on GGE biplot and AMMI analysis. *The Journal of Agricultural Science* **150**, 473–483.

Bernal, E. F. and Villardon, P. G. (2012). Package 'GGEBiplotGUI' http://cran.r project.org ages/ GGE Biplot GUI/GGEBiplotGUI.pdf

Bose, L.K., Jambhulkar, N.N., Pande, K. and Singh, O.N. (2014). Use of AMMI and other stability statistics in the simultaneous selection of rice genotypes for yield and stability under direct-seeded conditions. *J. Agric. Res*., 74: 3–9.

Brown-Guedira, G.L. (2000): Evaluation of genetic diversity of soybean introductions and North American ancestors using RAPD and SSR markers. *Crop Science* 40:815-823.

Ceccarelli, S., (1989). Wide adaptation: How wide? *Euphytica* 40: 197-205.

CRAN, (2016).comprehensive R archive network. Comprehensive R Archive Network for the R programming language. cited 2016 December. http://cran.r-roject.org/web/packages/available_ packages_byname.html#available-packages-A. Accessed on 20 Feb 2021.

Dagne, W. (2008). Genotypic variability and combining ability of quality protein maize inbred lines under stress and optimal conditions. Philosophiae Doctor Department of Plant Sciences. University of the Free State, South Africa.

Gabriel, K. R. (1971).Te biplot graphic display of matrices with application to principal component analysis. Biometrika 58, 453–467.

Gauch, H.G. and Zobel, R.W., (1997). Identifying mega-environments and targeting genotypes. *Crop Science* 37: 311-326.

Harriman, J. C., Okocha, P. I., Nwofia, G. E. and Afuape, S.O (2017a): Comparative yield performance of 47 different orange fleshed sweetpotato (OFSP) genotypes for root yield, dry matter and β-carotene. *Genetics Society of Nigerian*. www.geneticssocietyng.org

Harriman, J. C., Okocha, P. I., Nwofia, G. E. and Afuape, S.O (2017b): Association Between Root Yield And Other Traits In Orange Fleshed Sweetpotato. *Nigerian Journal of Genetics*. 31(1). 2017. pp. 115 -123 ISSN: 0189-9686.

ICAR,(Indian Council of Agricultural Research) (2007). Handbook of Agriculture.Directorate of Information and Publication, India Council of Agricultural Research, *New Delhil pp*. 512-516.

Iqbal, J., Z.K. Shinwari, M.A. Rabbani and S.A. Khan. (2014). Genetic variability assessment of maize (Zea mays L.) germplasm based on total seed storage proteins banding pattern using SDS-PAGE. Eur. Academic. Research., 2(2): 2144- 2160.

Kang, M.S. (1998). Using genotype by environment interaction for crop cultivar development. *Advances in Agronomy* 62: 199-246.

Kaya, Y. and Taner, S. (2002). Additive main effects and multiplicative interactions analysis of yield performances in bread wheat genotypes across environments. Turkey J. Agric For 26: 275-279.

Makumbi, D., Kanampiu, K., Mugo, S. and Karaya, H. (2015). Agronomic performance and genotype_environment interaction of herbicide resistant maize varieties in eastern Africa. *Crop Science* **55**, 540–555.

Mekasha A, Tesfaye K, and Duncan AJ (2014). Trends in daily observed temperature and precipitation extremes over three Ethiopian eco-environments. International Journal of Climatology. 34(6):1990–1999.

Mosisa, W. and Habtamu, Z. (2008). Genotype x Environment interaction and yield stability of sweetpotato. *East African Journal of Sciences* 2: 7-12.

Murphy, J.P., Cox, T.S. and Rodgers, D.M. (1986). Cluster analysis of red winter wheat cultivars based upon coefficients of parentage. Crop Science, 26:672-676.

Nedunchezhiyan, M, Byji, G. and Jata, S. K. (2012). Sweet Potato Agronomy; *Journal of Agricultural University Puerto Rico*, 60(2): 163-171.

Nwankwo, I.I.M, Bassey, E.E, Afuape, S.O., Njoku, J., Korieocha D.S., Nwaigwe, G. and Echendu, T.N.C. (2012). Morpho-Agronomic characterization and evaluation of in-country sweet potato accessions in southeastern Nigeria. *Journal of Agricultural Science*, 4(11): 281-288.

Purchase, J.L. (1997). Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat.Ph.D. Thesis, Department of Agronomy, Faculty of Agriculture of the University of the Free State, Bloemfontein, South Africa. 2(10): 21-34.

Rahim, M. A., Mia, A. A., Mahmud, F., Zeba, N. and Afrin, K. (2010). Genetic variability, character association and genetic divergence in Mungbean (*Vignaradiata* L. Wilczek). *Plant Omic.* 3: 1-6.

Ramagosa, I. and Fox, P.N. (1993). Genotype x Environment interaction and adaptation. In: Hayward M.D., Bosemark N.O. and Ramagosa I. (eds.). Plant breeding: Principles and prospects. Chapman and Hall, London. pp. 373-390.

Ray, R.C and Ravi, V. (2005).Post harvest spoilage of sweet potato and its control measures. *Critical Review of Food Science and Nutrition*, 35: 623-644. . (2001).

RStudio. (2014). RStudio: Integrated development environment for R (Computer sofware v0.98.1074). RStudio. http://www.rstudio.org/. Accessed on 16 Jan 2021.

Singh, S. P. and Diwivedi, V. K. (2005). Genetic divergence in wheat (*Triticumaestivum* L.). *Agricultural Science Digest.* 25(3): 201-203.

Solomon, A., Mandefro, N., and Habtamu, Z.(2008). Genotype-Environment Interaction and Stability Analysis for Grain Yield of Maize (*Zea mays* L.) in Ethiopia. *Asian Journal of Plant Sciences* 2: 163-169.

Souza, E. and Sorrells, M.E. (1991). Relationships among 70 North American oat germplasm: I. Cluster Analysis using quantitative characters. Crop Science, 31:599-605.

Srinivas, T. (2009).Economics of sweet potato production and marketing, In: Loebenstein, G and Thottapilly, G (eds.). *The sweet potato, Spring Science Business Media, BV* 2009, 436-447.

Thillainathan, M. and Fernandez, G.C.J. (2001). SAS application of Tai's stability analysis and AMMI model genotype x environmental interaction (GEI) effects. Journal of Heredity 92(4): 367-371.

Van Hintum, T.J.L. (1995): Hierarchical approaches to the analysis of genetic diversity in crop plants. In: Hodgkin, T., Brown, A.H.D., Van Hintum T.J.L., Morales, E.A.V. (Eds.) Core collection of plant genetic resources. John Wiley and Sons, pp. 23-34.

Wali, M. C., Salimath, P. M., Prashanth, M., and Harlapur, S. I. (2006). Studies on character association as influenced by yield, starch and oil in maize (*Zea mays* L.). *Karnataka Journal of Agricultural Science.* 19(4): 932-935.

.

Woolfe, J.A. (1992). Sweet Potato: An untapped food resources. International Potato Centre (CIP), Peru/Cambridge University Press, Cambridge, pp. 16-19.

Yan, W. and Kang, M. S. (2003). GGE biplot analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, FL. Agronomy Journal., 54: 11–23.

Yan, W., (2001). GGE Biplot- A windows application for graphical analysis of multi environ ment trial data and other types of two-way data. Agronomy Journal., 93: 1111–1118

Yan, W., Cornelius, P. L., Crossa, J. and Hunt, L. A. (2001). Two types of GGE biplots for analyzing multi-environment trial data. Crop Science Manual, 41, 656–663. doi:10.2135/cropsci 2001.413656.

Yan, W., Hunt, L. A., Sheng, W. Q. and Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Science, 40: 597–605.

Yan, W., Kang, M.S., Ma, B.L., Woods, S. and Cornelius P.L. (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Science, 47: 643-653.

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