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Genetic Variability Assessment and Agro-morphological Profiling of Elite Maize (*Zea mays* L.) Genotypes

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Maize (*Zea mays* L.) is important to nutrition and farmers' revenue in Nigeria. Forty-four genotypes of the crop were evaluated in Randomized Incomplete Blocks with three replications in 2021 to investigate the extent of genetic variability for grain yield and agro-morphological traits and to profile the genotypes for the traits. Data were collected on number of days to silking, plant and ear heights (cm), husk cover, plant and ear aspects, number of ears plant^{-1}, leaf angle (^{o}) and grain yield (kg/ha). Genetic components were estimated and principal component and cluster analyses were also performed. A genotype × yield-trait biplot was constructed to profile the genotypes. Phenotypic variance and coefficient of variance estimates were higher than genotypic values, underscoring the roles of genotype and environment in the observations. Heritability estimates were low and ranged from 0.03 to 18% for number of ears plant^{-1} and

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plant height, respectively, suggesting the possibility of low response to selection. The first three principal component axes controlled ≈ 60% of total variation and identified grain yield, ear and plant aspects, and husk cover as the main contributors. Cluster analysis produced four distinct clusters which suggested there was variability within the maize genotypes for selection. Genotype DK 920 Yellow was associated with number of ears per plant while LY1501-1, LY1914-14, LY1501-8, LY20001-5, and LY1901-23 were associated with the other measured traits. Genotypes could be selected across clusters to exploit heterosis for important traits. The trait profiles of genotypes that were not profiled could be determined in other studies.

Keywords: GYT biplot; improvement; maize; selection; trait profile; variability.

1. INTRODUCTION

Maize (*Zea mays* L.) is a grass, belonging to the Poacea family and evolved from a wild grass called *teosinte* in Mexico around 7000 years ago. It is the second most important food crop after cassava on the African continent (De Vries & Toenniessen, 2011) and the most important grain crop in West Africa in terms of quantities produced and consumed (Tweneboah, 2010). It serves as a multi-purpose crop for food, medicinal purpose, animal feed, biofuel, and raw material in the synthesis of a broad range of industrial products (Akande & Lamidi, 2016). Apart from its nutritional importance, maize provides a supplementary source of income to farmers, especially rural women. Between now and 2050, in the developing world maize demand will double (Anley et al., 2013).

The plant is cultivated in Africa mainly for its kernel which is rich in carbohydrate. According to FAO (FAO, 2020) the area in West Africa countries planted to maize increased from 3.2 million ha in 1961 to 8.9 million ha in 2015. Between 1987 and 2017, the area increased from 8 to 16 million Ha (FAO, 2020). The phenomenal expansion of the land area devoted to maize resulted in increased production from 2.4 million tonnes in 1961 to 10.6 million tonnes in 2005. However, although the average yield in the developed countries is up to 8.6 t/Ha, production in several areas of West Africa is still very low at an average of 1.3 ton/Ha (FAO, 2020). The characteristic low yield levels have been attributed to poor several factors including poor genetic resources.

Maize is one of the crops that have the highest level of morphological variability resulting in high yield variances among genotypes and from one agro-climatic zone to another. Grain yield in maize is determined by the growth and development of the maize plant, the amount of photosynthesis during the growing season, and how efficiently the photosynthate is partitioned into grain. Yield can also be considered to be the result of the interaction of genotype, management, and environmental factors (Fageria et al., 2016). The most important environmental factors are solar radiation, water and temperature. These factors cannot be controlled by the grower and vary with growing season. Management practices such as tillage, irrigation, nutrient supply, and pest management strive to maximize economic yield, but responses to these practices vary across environments.

Yield is composed of physical components that directly correlate to the amount of grain produced by a crop. Yield components are interrelated, have compensatory effects, and develop sequentially at different stages. First order yield components of maize consist of the number of ears m^{-2} (or ears $plant^{-1}$), kernels ear^{-1}, and kernel weight. First order yield components are sometimes referred to as primary components and have a direct effect on final yield as well as indirect effects through later developing yield components (Fageria et al., 2016). Yield components that can be considered second order or secondary are those that indirectly effect yield through their effect on first order components. These components consist of rows ear^{-1}, ear length, kernels $rows^{-1}$ and ear circumference. Previous studies (Mohammadi et al., 2013) of maize yield components have identified ears plant $^{-1}$ as a primary yield component of maize (Stanger & Lauer, 2006) rather than ears m^{-2}. When looking at yield on an area basis rather than a per plant basis, ears m^{-2} gives a more accurate measure of yield per unit area than ears $plant^{-1}$, which is of greatest importance to farmers. Path coefficient analysis has indicated that the number of ears $plant^{-2}$ had a larger effect on grain yield than any of the other yield components (Agrama, 1996) as also found for other crops such as wheat (*Triticum aestivum* L.) (Dhungana et al., 2007) and barley (*Hordeum vulgare* L.) (Dofing & Knight, 1992). (Abendroth et al., 2011) stated that higher yield per acre is generally produced with relatively high plant populations combined with an adequate number of kernels ear^{-1} rather than a low plant population with a large number kernels ear^{-1}. This leads one to believe that ears m^{-2} has a larger correlation with yield in maize than the other components.

Noticeable differences in agro-morphological traits are an effective plant breeding tool to discriminate genetic materials and as such can be used to deduce estimates of genetic diversity (Akin-Idowu et al., 2016) and to determine genotypic superiority. According to (Yan & Fregeau-Reid, 2018) and (Oyetunde et al., 2021), since the estimation of genetic superiority is often based on multiple traits rather than a single trait, estimation of genetic superiority is subject to interrelationships among a set of target traits. So-called superior genotypes will, thus, be those that have been found to be desirable for several traits of interest to the Breeder bearing in mind that yield is the ultimate. Consequently, an understanding of the pattern and extent of genetic variability as well as and the trait profiles of genotypes will aid the exploitation of existing genotypic diversity for improvement of the crop for desired traits.

Of late, a new approach to overcome the challenges faced in multiple trait-based evaluations of genotypes was proposed by (Yan & Fregeau-Reid, 2018). The procedure was built on the principles of the genotype + genotype × environment (GGE) biplot and it was described as the genotype × yield-trait (GYT) biplot. In this approach, the worth of a genotype is determined by its value for yield in combination with other traits (YT) rather than its levels for an individual trait. This study investigated the level and pattern of genetic variability among maize hybrids, and also profiled the maize genotypes for yield and agro-morphological traits with a view to identifying useful resources for improvement.

2. MATERIALS AND METHODS

2.1 Experimental Location

The experiment was carried out at the Teaching and Research Farms of Lagos State Polytechnic, Ikorodu, Lagos State Nigeria. The area located at latitude 5^{o}10'N and longitude 3^{o}16'E of the Greenwich meridian. It has an elevation of 50 m above sea level and a mean temperature of 25^{o}C to 29^{o}C with an annual rainfall ranging between 1670 mm and 2200 mm and relative humidity between 65% and 68%.

2.2 Genetic Materials

A number of 43 maize genotypes were obtained from Institute of Agricultural Research and Training, Moor Plantation, Ibadan, Nigeria. The genotypes were evaluated with a locally adapted cultivar as check. The names of the 44 genotypes used in the study are presented in Table 1.

2.3 Experimental Design, Field Establishment and Maintenance

Single-row plots 5 m were arranged in a serpentine style and laid out in Randomized Incomplete Block Design with three replications. Three seeds were planted per hill at inter- and intra-row spacing of 0.75 m and 0.5 m respectively. Seedlings were thinned to two plants per stand after establishment. Four border rows were planted on either side of each block, to take care of border effects. In the first instance, weeds were controlled using a combination of atrazine and glyphosate as pre- and post- emergence herbicides at recommended rates immediately after planting. Subsequently, weeding was done manually when necessary subject to field condition.

2.4 Data Collected

Plant observation began at flowering. Data were collected on numbers of days to 50% silking, plant and ear heights, plant and ear aspects, husk cover, leaf angle, and grain yield. Leaf angle was determined by means of a protractor while other measurements were taken according to the procedure described by (Oyetunde et al., 2020).

2.5 Data Analysis

Data collected were subjected to analysis of variance (ANOVA) using PROC GLM of SAS version 9.4 (SAS Institute, 2012). When significant, means were separated using the Duncan’s Multiple Range Test at 5% probability. Genetic components were estimated using the method described by (Ogunniyan & Olakojo, 2015). A genotype by yield-trait (GYT) biplot was constructed to profile the maize genotypes for the measured traits according to the procedure proposed by (Yan & Fregeau-Reid, 2018) and modified by (Oyetunde et al., 2021) Briefly, genotype × yield-trait (GYT) combination estimates were obtained by either multiplying or dividing grain yield value by mean value of other traits depending on positive or negative correlation coefficient signs respectively of the traits with grain yield. The obtained GYT values were standardized in Microsoft Excel (Excel, 2010). To select accessions for the GYT biplots, a superiority index (SI) was computed for the accessions, based on the standardized GYT estimates. The SI value of an accession was computed as the arithmetic mean of its standardized estimates. Ten accessions comprising seven and three accessions with the highest and lowest SI values respectively were

Table 1. Genotype and sources

S/N	Genotype	Sources
1.	30Y87	IITA
2.	A1312-12	IITA
3.	A1706-2	IITA
4.	A1736-13	IITA
5.	A1736-6	IITA
6.	A1802-4	IITA
7.	A1804-14	IITA
8.	A1804-15	IITA
9.	A1804-67	IITA
10.	DK 920 Yellow	IITA
11.	Ife Hybrid-3	IITA
12.	Local check	IITA
13.	LY1001-23	IITA
14.	LY1409-61	IITA
15.	LY1501-1	IITA
16.	LY1501-5	IITA
17.	LY1501-6	IITA
18.	LY1501-7	IITA
19.	LY1501-8	IITA
20.	LY1501-9	IITA
21.	LY1901-12	IITA
22.	LY1901-14	IITA
23.	LY1901-16	IITA
24.	LY1901-18	IITA
25.	LY1901-19	IITA
26.	LY1901-20	IITA
27.	LY1901-21	IITA
28.	LY1901-23	IITA
29.	LY190124	IITA
30.	LY1913-16	IITA
31.	LY1914-14	IITA
32.	LY20001-1	IITA
33.	LY20001-10	IITA
34.	LY20001-11	IITA
35.	LY20001-12	IITA
36.	LY20001-13	IITA
37.	LY20001-2	IITA
38.	LY20001-3	IITA
39.	LY20001-4	IITA
40.	LY20001-5	IITA
41.	LY20001-6	IITA
42.	LY20001-7	IITA
43.	LY20001-8	IITA
44.	LY20001-9	IITA

IITA: International Institute of Tropical Agriculture selected for the GYT biplot. The select 10 genotypes were graphically displayed on the GYT biplot according to the procedure of (Oyetunde et al., 2021). The ANOVA was performed using the Statistical Analysis System Software, (SAS Institute, 2012) while the biplot was obtained using the GGEBiplotGUI software in R.

3. RESULTS AND DISCUSSION

3.1 Genetic Components of Measured Traits of Maize

A perusal of the genetic components of measured traits (Table 2) revealed consistently higher estimates of phenotypic variance and coefficients of variation than the genotypic counterparts. Phenotypic coefficient of variance ranged from 45.39% to 3.66% observed for grain yield and number of days to silking respectively while the highest and lowest genotypic estimates were 12.28% and 0.71% for the same respective traits. These observations underscore the roles of genotype and environment in expression of the measured traits as reported by (Ogunniyan & Olakojo, 2015). Generally, broad-sense heritability estimates were low to moderate, ranging from the highest 18% for plant height to 0.3% for number of ears per plant while genetic advance as percentage of mean ranged from 0.29 to 5.62 for number of days to silking and ear aspect respectively. The low heritability estimates further shows the significant influence of the environment in the inheritance of the measured traits. Consequently, offspring of the genotypes will likely perform differently in comparable environment. (Ogunniyan & Olakojo, 2015) recommended that heritability should be considered together with genetic advance to predict the effect of selecting superior crop genotypes. Thus, plant height and ear aspect with moderate estimates of the two components could effectively predict response to selection among the evaluated genotypes.

3.2 Principal Component Analysis of Measured Traits

Principal component analysis of the measured traits revealed that the first three principal components (PCs) together accounted for 56.56% of the observed variation within the maize genotypes and were considered important in determining the important traits to variation based on their Eigen factor strengths of 2.21, 1.48 and 1.40 for PCs 1, 2, and 3, respectively which explained 24.56, 16.43 and 15.57%, in that order, of the total variation (Table 3). In one or more of PCs 1-3, all the measured traits had loading ≥ 0.3. Plant aspect, grain yield, ear aspect, and husk cover characterized PC 1, with loadings of 0.51, -0.50, 0.49, and 0.30 respectively while PC 2 was dominated by number of days to silking, plant height, and leaf angle with loadings of -0.55, -0.48 and -0.43 respectively with number of ears per plant and grain yield having a loading 0.30. PC 3 was characterized by stem girth ear height, plant height, husk cover and leaf angle and had loading of 0.62, 0.44, 0.40, and 0.39 respectively in the axis. The Eigen vector of a principal component axis represents the strength of judgement of that axis. The significant loadings of husk cover, plant and ear aspects, and grain yield in PC 1 are an indication that the traits were the chief contributors to variation among the maize genotypes. These traits are, therefore, key to maintaining variability among the genotypes and should be considered for selection foe maize improvement. (Kumar et al., 2017) employed principal component analysis to identify important traits to variation among 32 maize genotypes.

3.3 Summary of the Grouping from Ward's Minimum Variance Cluster Analysis

The dendrogram from Ward's minimum variance cluster analysis (Fig. 1) grouped all the maize genotypes into four distinct clusters at a genetic dissimilarity of 0.5. Cluster 1 was composed of 12 genotypes which included the local check. Other genotypes in cluster 1 were 30Y87, A1804-14, A1736-13, A1802-4, A2904-15, LY1901-20, LY20001-20, LY20001-10, LY1501-7, LY20001-4, and LY20001-8. Cluster 2 contained 10 genotypes: LY1409-61, LY20001-2, LY1501-6, LY1901-14, LY1501-1, LY1913-16, LY20001-5, LY1501-8, LY1914-14, and LY1901-21. The genotypes making up cluster 3 were A1312-12, A1736-6, LY1901-16, LY1001-23, LY1901-19, LY20001-12, LY1901-18, LY1901-24, LY20001-7, LY1501-5, LY20001-9, LY1501-9, LY20001-3, LY20001-6, A1804-67, LY1901-23, DK 920 Yellow, and Ife hybrid 3 while genotypes A1706-2, LY20001-13, LY1901-12, and LY20001-11 formed cluster 4. The fact that the maize genotypes were classified into distinct clusters reiterated the existence of sufficient genetic variability for possible selection. Selection can thus be made across clusters to develop maize hybrids with broader genetic base.

Table 2. Genetic components of measured traits of maize evaluated for the experiment

Genetic Components	Days to Silking	Plant Height	Ear Height	Husk Cover	Plant Aspect	Ear Aspect	Ears Per Plant	Grain Yield
Environmental variance	5.17	92.54	99.88	0.71	0.45	0.47	1.36	1614531.28
Genotypic variance	NE	20.02	2.17	0.02	0.04	0.06	NE	NE
Phenotypic variance	4.98	112.56	102.05	0.73	0.48	0.53	1.35	1500459
Environmental coefficient of variance	3.73	6.18	15.24	29.89	21.62	24.12	NE	47.02
Genotypic coefficient of variance	0.71	2.87	2.25	5.23	6.09	8.34	NE	12.28
Phenotypic coefficient of variance	3.66	6.81	15.41	30.35	22.47	25.53	NE	45.39
Heritability (Broad sense)	-0.04	0.18	0.02	0.03	0.07	0.11	-0.003	-0.07
Genetic advance	-0.18	3.89	0.44	0.05	0.11	0.16	-0.008	-184.87
Genetic advance as percentage mean	-0.29	2.49	0.68	1.86	3.41	5.62	NE	-6.84

Table 3. Summary of principal component analysis of measured traits of maize genotypes

Measured trait	Principal component axis 1	Principal component axis 2	Principal component axis 3
Days to silking	-0.05	-0.55	-0.19
Plant height	-0.19	-0.48	0.44
Ear height	-0.26	0.05	0.62
Husk cover	0.30	-0.15	0.40
Plant aspect	0.51	0.04	0.12
Ear aspect	0.49	0.27	0.05
Ears per plant	-0.23	0.30	-0.25
Leaf angle	0.01	0.43	0.39
Grain yield	-0.50	0.30	0.06
Eigen value	2.21	1.48	1.40
Percentage variation	24.56	16.43	15.57
Cumulative percentage variation	24.56	40.99	56.56

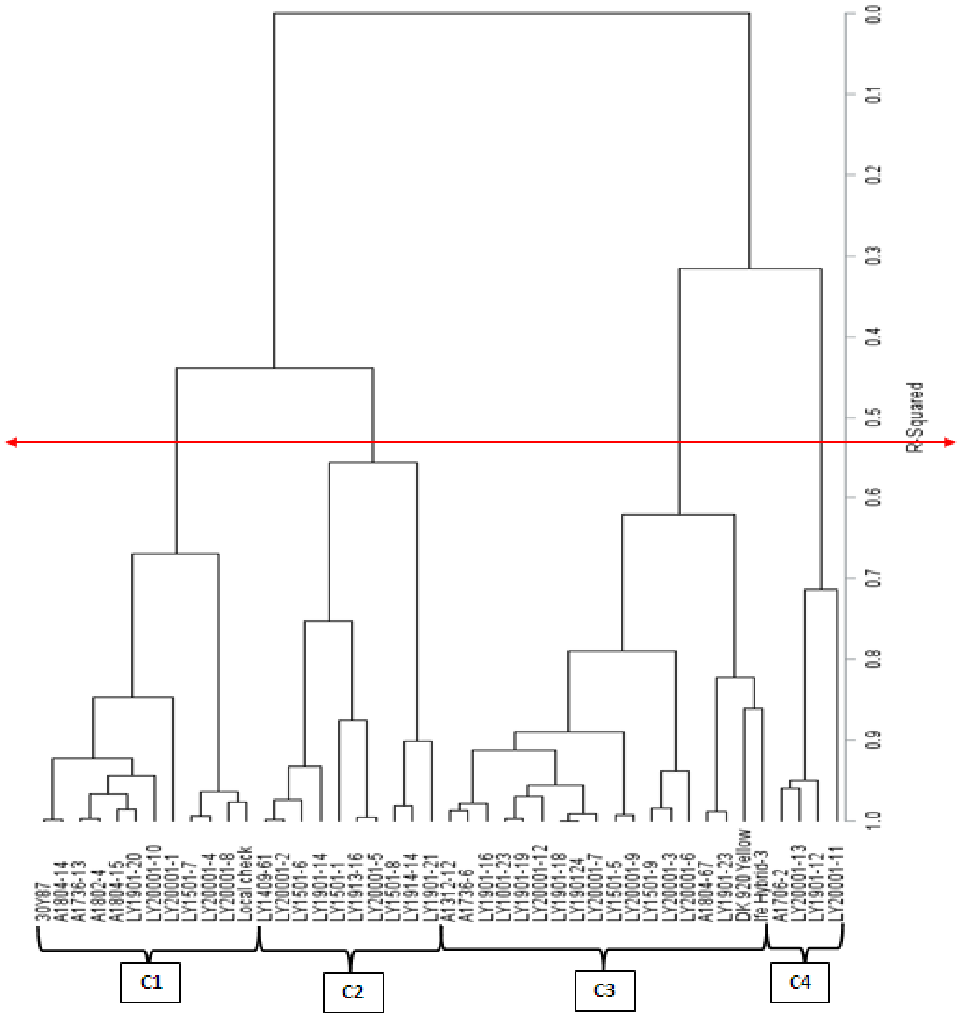
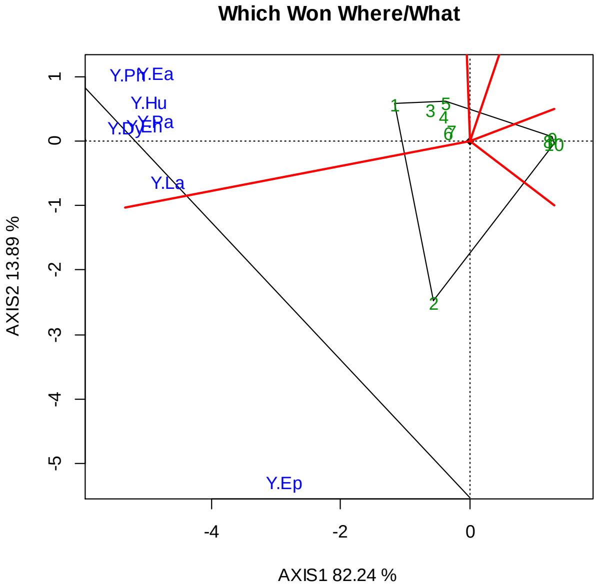


Fig. 1. Dendrogram of relatedness among maize genotypes (X-axis) based on genetic similarity (Y-axis) from Ward's minimum variance cluster analysis. The red double-arrowed line delineates the accessions into clusters at approximately 50% level of similarity; C1, C2, C3, and C4 are clusters 1, 2, 3, and 4, respectively



Genotype/Trait	ID on Biplot
LY1501-1	1
DK 920 Yellow	2
LY20001-1	3
LY1914-14	4
LY1501-8	5
LY20001-5	6
LY1901-23	7
A1706-2	8
LY1901-12	9
LY20001-11	10
Days to silking	Y.Dy
Plant height	Y.Pl
Ear height	Y.Eh
Plant aspect	Y.Pa
Ears per plant	Y.Ep
Ear aspect	Y.Ea
Husk cover	Y.Hu
Leaf angle	Y.La

Fig. 2. GYT biplot for agro-morphological profiling of maize (*Zea mays* L.) genotypes evaluated in Ikorodu

3.4 Agro-morphological Profiling of Maize Genotypes using the GYT Biplot

Fig. 2 is a biplot visual display of the association of the evaluated maize genotypes with measured yield-trait combinations (described in accompanying legend). The polygon view delineated the genotypes into three distinct sectors with LY20001-11, DK 920 Yellow, and LY1501-1 as the vertex genotypes in sectors 1, 2, and 3 respectively in a clockwise orientation. Other genotypes in sector 1 are A1706 and LY1901-12 while LY1914-14, LY1501-8, LY20001-5, and LY1901-23 are in sector 3. Genotype DK 920 Yellow is the sole genotype in sector 2. It was observed that all the seven highest ranked genotypes (based on the superiority indices selection) were associated with one or more of the traits measured in the study while the lowest ranked genotypes were not associated with any of the traits. For instance, genotypes in sector three were associated with days to silking, plant and ear heights, plant and ear aspects, husk cover, and leaf angle while the sector 2 genotype was associated with number of ears per plant. The GYT biplot is useful for profiling of crop genotypes (Oyetunde et al., 2021) though the association of closely-related YT combinations with studied genotypes (Yan & Fregeau-Reid, 2018). The association of DK 620 Yellow with number of ears per plant is an indication of superior trait profile of the genotype for the trait. In the same vein, LY1501-1, LY20001-1, LY1914-14, LY1501-8, LY20001-5, and LY1901-23 have superior profile for the associated traits with LY1501-1 being the most superior. These genotypes would be resourceful for improvement of the respective traits.

4. CONCLUSIONS

The existing genetic variability among the evaluated maize genotypes would sufficiently allow improvement through selection. Selection would be most effective with focus on plant and ear aspects, and grain yield which characterized PC 1. Genotypes LY1501-1, LY20001-1, LY1914-14, LY1501-8, LY20001-5, and LY1901-23 profiled for yield-trait combinations including plant and ear heights should be resourceful genetic materials to improve the identified traits. Evaluation in more environments is needed to profile the other genotypes used in the study.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

Abendroth, L. J., Elmore, R. W., Boyer, M. J., & Marlay, S. K. (2011). *Corn growth and development* (PMR 1009). Iowa State University Extension.

Agrama, H. A. S. (1996). Sequential path analysis of grain yield and its components in maize. *Plant Breeding*, *115*, 343–346.

Akande, S. R., & Lamidi, G. O. (2016). Performance of quality protein maize varieties and disease reaction in the derived-savannah agro-ecology of South-West Nigeria. *African Journal of Biotechnology*, *5*(19), 1744–1748.

Akin-Idowu, P. E., Gbadegesin, A. M., Uterdzua, O., Ibitoye, D. O., & Odunola, O. A. (2016). Characterization of grain amaranth (*Amaranthus* spp.) germplasm in South West Nigeria using morphological, nutritional, and random amplified polymorphic DNA (RAPD) analysis. *Resources*, *5*(1), 615.

Anley, W., Zeleke, H., & Dessalegn, Y. (2013). Genotype by environment interaction of maize (*Zea mays* L.) across North Western Ethiopia. *Journal of Plant Breeding and Crop Science*, *5*, 171–181.

De Vries, J., & Toenniessen, G. (2011). *Securing the harvest: Biotechnology, breeding and seed system for Africa crops*. CAB International.

Dhungana, P., Eskridge, K. M., Baenziger, P. S., Campbell, B. T., Gill, K. S., & Dweikat, I. (2007). Analysis of genotype-by-environment interaction in wheat using structural equation model and chromosome substitution lines. *Crop Science*, *47*, 477–484.

Dofing, S. M., & Knight, C. W. (1992). Alternative model for path analysis of small-grain yield. *Crop Science*, *32*, 487–489.

Fageria, N. K., Baligar, V. C., & Clark, R. (2016). Physiology of growth and yield components. In *Physiology of crop production* (pp. 61–94). Food Products Press.

FAO. (2020). *Maize*. http://www.fao.org/inpho/maize (Accessed December 10, 2021)

Kumar, R., Chikkappa, G. K., Singh, S. B., Ganapati, M., Kaul, J., Das, A. K., Sravani, D., Olakh, D. S., & Bhatia, D. (2017). Multivariate analysis for yield and its component traits in experimental maize hybrids. *Journal of Agricultural Science*, *9*(3), 219–225.

Mohammadi, S. A., Prasanna, B. M., & Singh, N. N. (2013). Sequential path model for determining interrelationships among grain yield and related characters in maize. *Crop Science*, *43*, 1690–1697.

Ogunniyan, D. J., & Olakojo, S. A. (2015). Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Nigerian Journal of Genetics*, *28*(2), 24–28. https://doi.org/10.1016/j.nigjg.2015.06.005

Oyetunde, O. A., Badu-Apraku, B., Ariyo, O. J., & Alake, C. O. (2020). Efficiencies of heterotic grouping methods for classifying early-maturing maize inbred lines. *Agronomy*, *10*, 1198. https://doi.org/10.3390/agronomy10081198

Oyetunde, O. A., Olayiwola, M. O., & Osho, B. T. (2021). Genotypic diversity and trait profiles of some *Amaranthus* accessions. *Advances in Horticultural Science*, *35*(3), 277–284.

SAS Institute. (2012). *SAS system for Windows* (Release 9.4). SAS Institute Inc.

Stanger, T. F., & Lauer, J. G. (2006). Optimum plant population of Bt and non-Bt corn in Wisconsin. *Agronomy Journal*, *98*, 914–921.

Tweneboah, C. K. (2010). *Modern agriculture in food crops* (pp. 30–46). Co–Wood Publishers.

Yan, W., & Fregeau-Reid, J. (2018). Genotype by yield × trait (GYT) biplot: A novel approach for genotype selection based on multiple traits. *Scientific Reports*, *8*, 8242.

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