

## Environmental impact and genetic expressions of new drought-tolerant maize genotypes in derived savannah agro-ecology

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### Abstract

Reduced water resources in sub-Saharan Africa will not only pose threat to the livelihood of poor resource farmers, but also food security in the region. Drought tolerant (DT) maize varieties hold promise to reducing poor resourced farmers' vulnerability and improve food security in sub-Saharan Africa. Ten maize genotypes obtained from the International Institute of Tropical Agriculture (IITA), were evaluated in 2015 and 2016 using a randomized complete block design experiment with three replications to estimate their genetic variability and predict their genetic advances in the derived savannah agro-ecology. Growth, phenological and yield data were collected from 10 middle row plants. Genetic advance, genotypic, phenotypic and environmental coefficients of variations and their variances were estimated. Principal component and hierarchical cluster analyses were also performed. The dendrogram showed that at 80% dissimilarity point, the genotypes were grouped into clusters A, B and C in both years. The first two principal components explained 91.8% and 93.3% of the total variation in 2015 and 2016, respectively. Number of grains cob<sup>-1</sup>, plant height and number of days to physiological maturity were consistent in explaining the variations observed in the maize population. Heritability estimates in broad sense ranged from 1.35% for number of leaves to 87.43% for grain yield per hectare. The genetic parameters studied showed significant variations among the growth, phenological and yield data collected that warrants selection and maize improvement program using the DT maize inbred lines in derived savannah agro-ecology.

**Keywords:** climate change; genetic improvement; heritability; sub-Saharan Africa; water stress; *Zea mays* L.

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### Introduction

Maize (*Zea mays* L.) is the third most utilized cereal crop after wheat and rice in Nigeria (OECD/FAO, 2016) and globally based on harvested area (Ramirez-Cabral *et al.*, 2017). In sub-Saharan Africa (SSA), maize

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Received: 28 Mar 2020. Received in revised form: 29 Dec 2020. Accepted: 12 Jan 2021. Published online: 19 Jan 2021.

From Volume 13, Issue 1, 2021, Notulae Scientia Biologicae journal will use article numbers in place of the traditional method of continuous pagination through the volume.

is the single most important staple crop for about 950 million people (OECD/FAO, 2016). Its consumption is projected to increase by 50% in the developing world by 2050 (Rosegrant and Msangi, 2011), while its yield is expected to decrease due to negative impact of climate change (Ramirez-Cabral *et al.*, 2017). The reduction in maize yield will be exacerbated by loss of land used in maize cultivation to other crops (NEPAD, 2014).

Strong growth in SSA agricultural output has accrued predominantly from area expansion as opposed to increase in yield per unit area (NEPAD, 2014) with rain-fed agriculture accounting for more than 95% of the farmed lands (IWMI, 2019). These farmlands are cultivated by poor resource farmers, who lack capacity to adapt to climate change. Hence, the present change in climate evident in reduced water resources in SSA will not only pose threat to the livelihood of these farmers, but also food security in the region. The African continent is facing one of its driest periods in the past three decades (Brandt *et al.*, 2018). Drought has been considered the most important climate factor affecting crop production. It causes decline in yield which affects farmer seed saving, resulting in reduced seed availability and affordability (Kansiime and Mastenbroek 2016).

In response to the water scarcity challenge, the 'Drought Tolerant Maize for Africa' (DTMA) project was launched by CIMMYT, IITA (CIMMYT, 2015; Fisher *et al.*, 2015), with Drought Tolerant (DT) maize varieties released in SSA. DT maize varieties hold promise to reduce poor resourced farmers' vulnerability and improve food security in SSA. However, farmer uptake of DT maize varies from 9% in Zimbabwe to 61% in Malawi, with the major barriers to adoption been unavailability of improved seed, inadequate information, lack of resources, high seed price and perceived attributes of different varieties (Fisher *et al.*, 2015). In Nigeria, DT maize is not common among farmers particularly in the derived savannah agro-ecology probably due to exclusion of the zone during the evaluation of the varieties (CIMMYT, 2015). Participatory breeding is a veritable option used in closing variety adoption gap and may ensure affordability and accessibility of seeds with increased knowledge of the new varieties. In addition to drought tolerance, the DT varieties have other attractive traits, such as resistance to major diseases, high protein content as well as beta-carotene in some, low soil nitrogen tolerant, and Striga resistant (CIMMYT, 2015). Thus, they can serve as good gene donors in maize improvement programme.

Understanding the genetic variability in maize is necessary for a successful adoption and crop improvement programme. Estimating variability in yield and yield traits is vital in determining the environmental influence (Ullah *et al.*, 2012; Ene *et al.*, 2016). Concentrating solely on yield increase can be misinforming as several genetic and non-genetic factors as well as biotic and abiotic agents, interplay to determine crop yield. Selecting yield related traits with low environmental influence increases the chances of selecting genotypes with high yield potentials (Uba *et al.*, 2018).

We hypothesize that the genetic potentials of different DT maize varieties will vary under the derived savannah agro-ecological condition. Hence, the objective of this study was to study the genetic variability and estimate environmental influence on ten maize genotypes which included: eight DT, one commercial hybrid and a landrace in the derived savannah agro-ecology.

## Materials and Methods

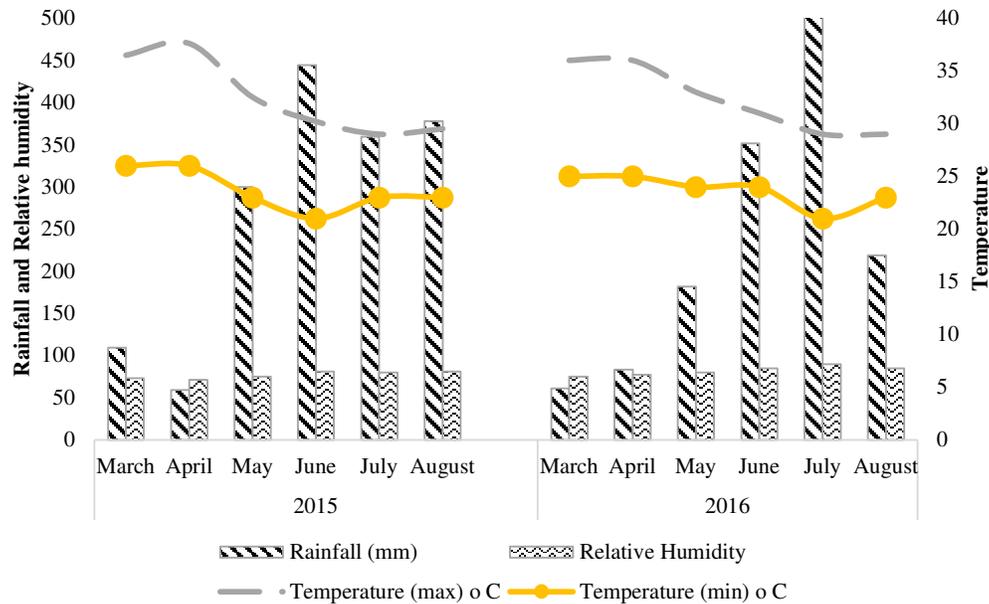
### *Description of experimental site*

The field trials were conducted in the Department of Crop Science and Technology, Research Farm, Faculty of Agriculture, Federal University of Technology, Owerri, Nigeria in 2015 and 2016 rain-fed cropping seasons (April to July). The Research Farm (07°02'E, 05°27'N; 91 m asl) is characterized by mean annual rainfall of  $\approx$  2300 mm - 2700mm, mean annual temperature of  $\approx$  18°C to 33 °C and relative humidity of  $\approx$ 72 to 86%. Owerri lies within the derived savannah agro-ecology of Nigeria.

Soil samples from the experimental site were analysed and classified as ultisol according to the soil taxonomy of the USDA (Soil Survey Staff, 2003). The textural class is loamy sand (sand 84.1%, silt 5.1% and clay 10.8%) that contains low organic carbon ( $\approx$ 1.6%), and low contents of nitrogen (0.1%), phosphorous

(17.8mgkg<sup>-1</sup>), basic cations (potassium 0.02, magnesium 1.2, calcium 1.6) in Cmolkg<sup>-1</sup> with pH of 5 and 3.8 in H<sub>2</sub>O and NaCl, respectively.

The monthly rainfall distribution, temperature and relative humidity during the field trial periods are displayed in Figure 1. The information was provided by the meteorological unit of the University.



**Figure 1.** Mean monthly rainfall, temperature, and relative humidity during the experiment interval  
**Source:** Meteorological Station, Department of Crop Science and Technology, Federal University of Technology, Owerri

*Biological material*

Ten maize genotypes consisting of eight drought tolerant obtained from the International Institute of Tropical Agriculture (IITA) ‘2008DTMA-YSTR’, ‘EVDT-Y2000 STRCO’, ‘TZE COMP.3C2DT’, ‘IWDC2 SYN- F2’, ‘IWDC3 SYN/DTSYN-1-W’, ‘DT-SR-WCQ’, ‘DT-SYN-7-WF2’ and ‘DT-SYN-11-YF2’; a commercial hybrid ‘Oba Super2’ obtained from the seed market and a landrace ‘Oka Awaka’ sourced from a local farmer were evaluated. The genotypes differ in their maturity periods and colour of the grains.

The maize genotypes are described in Table 1.

**Table 1.** Maize genotypes used within the experiment and their characteristics

S/N	Maize genotypes	Grain colour	Duration	Remark
1	‘2008DTMA-YSTR’	Yellow	90days	Early
2	‘EVDT-Y2000 STRCO’	Yellow	90days	Early
3	‘TZE COMP.3C2DT’	White	90days	Early
4	‘IWDC2 SYN- F2’	White	110days	Intermediate
5	‘IWDC3 SYN/ DTSYN-1-W’	White	110days	Intermediate
6	‘DT-SR-WCQ’	White	110-115days	Late
7	‘DT-SYN-7-WF2’	White	110-115days	Late
8	‘DT-SYN-11-YF2’	Yellow	110-115days	Late
9	‘Oba Super 2’	Yellow	110-115days	Late
10	‘Oka Awaka’	Yellow	-	Late

**Source:** International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria

*Experimental layout and cultural practices*

The experimental design used was randomized complete block design with three replications. Land area measuring 558 m<sup>2</sup> (12 m x 46.5 m) was mechanically ploughed, harrowed and ridged. The prepared land was divided into three blocks (3 m x 46.5 m each) representing the replications. Each replication contained ten plots representing each genotype. Each plot measured 3 m x 3.75 m with a plant spacing of 0.75 m x 0.25 m containing 60 plants per plot and ≈ 53,333 plants per hectare. A pathway of 1 m was maintained within and between blocks.

Poultry manure was applied to the plots at 8 t ha<sup>-1</sup> 2 weeks before planting and was supplemented with inorganic fertilizer NPK 20:10:10 at a rate of 600 kg ha<sup>-1</sup> (split application) by the 2<sup>nd</sup> and 5<sup>th</sup> weeks after emergence. The plots were manually kept weed free.

*Data collection*

Data were collected from the 10 middle row plants in each plot. At 8 weeks after planting (WAP), plant heights (cm) were measured with a meter rule from the soil level to the tip of the plant and number of leaves was counted. Phenological data were monitored for number of days to 50% tassel and silk appearances. Tassel-silk interval was calculated by subtracting the number of days to tasselling from the number of days to silking. Number of days to physiological maturity was monitored and grain filling period determined. After harvest, cobs from each plot were weighed to obtain grain yield. Ten cobs were randomly selected from each plot to determine the average number of grains cob<sup>-1</sup>. Then, 100 seeds from the selected cobs were weighed to determine 100-seed weight (gram). Another randomly selected ten cobs per plot, as well as entire leaves from ten plants per plot were oven dried at 70 °C to constant weight in order to obtain the average cob dry weight (gram) and leaf dry matter, respectively.

*Statistical analysis*

The data collected were subjected to analysis of variance (ANOVA) using GenStat Release 10.3 Discovery Edition (PC/Windows; VSN International, Hemel Hempstead, Hertfordshire, UK) to obtain the ANOVA Table and means needed for the genetic calculation. Principal component and hierarchical cluster analyses were also carried out with the GenStat software to show the discriminating traits and level of relatedness among the genetic materials.

*Genetic parameters*

The means from ANOVA were used to calculate genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), genotypic variance, phenotypic variance, environmental variances, coefficient of variation (CV) and genetic advance to show variability in maize genotypes. The phenotypic variation for each trait was separated into genetic and environmental (non-genetic) factors and estimated according to Burton (1952) and Sharma (1988), as follows:

$$\sigma_e^2 = MSe \quad \text{equation 1}$$

$$\sigma_g^2 = (MSg - MSe)/r \quad \text{equation 2}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 \quad \text{equation 3}$$

$$\sigma_e^2 \% = (\sigma_e^2 / \sigma_p^2) * 100 \quad \text{equation 4}$$

Where:  $\sigma_p^2$ ,  $\sigma_g^2$  and  $\sigma_e^2$  are phenotypic variance, genotypic variance and environmental variance, respectively, and  $MS_g$ ,  $MS_e$  and  $r$  are the mean squares of genotypes, mean squares of error and number of blocks, respectively.

$$\%CV = \frac{\sqrt{MS_g}}{\bar{X}} \times 100 \quad \text{equation 5}$$

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100 \quad \text{equation 6}$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100 \quad \text{equation 7}$$

$$ECV = \frac{\sqrt{\sigma_e^2}}{\bar{X}} \times 100 \quad \text{equation 8}$$

Where:  $\bar{x}$  is the grand mean for each trait measured.

Broad sense heritability ( $h^2_{bs}$ ) expressed as the percentage of the ratio of the genotypic variance ( $\sigma_g^2$ ) to the phenotypic variance ( $\sigma_p^2$ ) was estimated as described by Burton (1952).

Genetic advance (GA) was estimated by the methods of Fehr (1987) as:

$$GA = K (S_p) h^2_{bs} \quad \text{equation 9}$$

Where: K is a constant (2.06) at 5% selection pressure,  $S_p$  is the phenotypic standard deviation ( $\sqrt{\sigma_p^2}$ ),  $h^2_{bs}$  is the heritability ratio.

GA was also calculated as percentage of mean.

## Results and Discussion

### *Genetic variability*

Variation among a given plant population is highly indispensable in order to achieve success in any crop improvement programme. Table 2 showed the estimates of the variances and genetic parameters of the 10 maize genetic materials evaluated in 2015 and 2016 planting seasons for various quantitative traits. Variability of a trait is necessary for its inclusion in crop improvement programme (Chukwudi and Agbo, 2016; Ene *et al.*, 2016). Percentage coefficient of variation (CV%) provides comparative assessment of the amount of variability between crop traits (Ene *et al.*, 2016). In 2015, the highest coefficient of variation was recorded in leaf dry matter, followed by tasselling silking interval and grain yield hectare<sup>-1</sup>, while tasselling silking interval took the lead in the 2016 evaluation, followed by grain yield hectare<sup>-1</sup> and leaf dry matter. Grain filling period showed low coefficient of variation in both years of study and was followed by cob dry weight and 100-seed weight in 2015. The implication of these low coefficients of variation is the lesser ability of the affected traits to be advanced in selection due to low variation in the traits among the maize population.

The genotype evaluation in 2015 showed phenotypic variance in the range of 1.83 for grain yield to 5,393 for number of grains cob<sup>-1</sup>. The highest value obtained from number of grains per cob was followed by cob dry weight, leaf dry matter and plant height. Phenotypic variance is influenced by genotypic variance and environmental variance (Andrade, 2019). Among the four traits with high phenotypic variances, number of grains per cob and leaf dry matter had higher genotypic variance than environmental variance, while cob dry weight and plant height had higher environmental variance than genotypic variance. The contribution (%) of the environmental variance to the phenotypic variance was highest for the number of leaves (98.7%), followed by cob dry weight (85.5%), plant height (82.2%) and 100-seed weight (77.4%). Environmental variance contributions on the other traits were below 50%. In 2016 evaluation, the patterns of environmental and genotypic contributions to the phenotypic variance were similar to those observed in 2015 evaluation. The contribution of the environmental variance on number of leaves, cob dry weight, plant height and 100-seed weight were 99.5%, 96.2%, 88.6% and 67.1%, respectively, with the other traits having < 50% contribution from the environment. These high environmental contributions may account for the non-significant difference

observed in the mean square of the genotypes as the four traits with above 50% environmental contribution were not significant in both evaluations. Table 2 revealed that as environmental contribution to the phenotypic variance increased, the broad sense heritability decreased. In both evaluations, the traits with the highest environmental contribution had the least broad sense heritability *vis-a-vis* the traits with the lowest environmental contribution. Heritability in broad sense signifies the genetic variability among genitors, indicating their propensity to respond to selection pressure (Milatovic *et al.*, 2010; Rahman *et al.*, 2017). High heritability shows a minimal environmental effect on the observed variation (Bhiusal *et al.*, 2017).

High genetic advance was observed for number of grains per cob, leaf dry matter and number of days to physiological maturity, while number of leaves per plant and 100-seed weight showed low genetic advance in both evaluations. Moderate to high heritability and genetic advance estimates for a given trait signify additive genes as being responsible for its performance, hence, distinguishes the trait for direct selection (Ndukauba *et al.*, 2015; Bhiusal *et al.*, 2017). Medium to high heritability and genetic advance estimates recorded for number of grains per cob, leaf dry matter and number of days to physiological maturity in both evaluations give them an edge for selection in maize improvement programme in the derived savannah agro-ecology.

**Table 2.** Mean square and genetic parameters for 12 quantitative traits in maize genotypes

Traits	Mean	V <sub>p</sub>	V <sub>g</sub>	V <sub>e</sub>	PCV	GCV	ECV	%CV	H <sup>2</sup> <sub>bs</sub> (%)	GA	MSG
<b>2015</b>											
PH	90.43	725.83	129.33	596.50	29.79	12.58	27.01	34.70	17.82	9.89	984.50 <sup>ns</sup>
NOL	9.01	3.71	0.05	3.66	21.38	2.48	21.23	21.64	1.35	0.05	3.80 <sup>ns</sup>
LDM	52.35	746.77	508.87	237.90	52.20	43.09	29.46	80.24	68.14	38.36	1764.50 <sup>**</sup>
D50T	65.73	59.13	46.76	12.37	11.70	10.40	5.35	18.80	79.08	12.53	152.65 <sup>**</sup>
D50S	70.17	93.56	76.67	16.89	13.78	12.48	5.86	22.39	81.95	16.33	246.91 <sup>**</sup>
TSI	4.43	5.15	3.43	1.72	51.23	41.81	29.60	78.21	66.60	3.11	12.00 <sup>**</sup>
GFP	40.17	13.71	7.12	6.59	9.22	6.64	6.39	13.16	51.93	3.96	27.94 <sup>**</sup>
PMT	110.53	144.35	114.31	30.04	10.87	9.67	4.96	17.47	79.19	19.60	372.98 <sup>**</sup>
NGC	277.52	5393	2757	2636	26.46	18.92	18.50	37.63	51.12	77.33	10907.00 <sup>**</sup>
100SW	21.85	13.34	3.02	10.32	16.72	7.95	14.70	20.14	22.64	1.70	19.37 <sup>ns</sup>
CDW	167.4	2328	338	1990	28.82	10.98	26.65	32.74	14.52	14.43	3004.00 <sup>ns</sup>
GY	2.92	1.83	1.60	0.23	46.33	43.32	16.42	76.79	87.43	2.44	5.03 <sup>**</sup>
<b>2016</b>											
PH	86.18	714.60	81.70	632.90	31.02	10.49	29.19	34.38	11.43	6.29	878.00 <sup>ns</sup>
NoL	8.63	3.80	0.02	3.78	22.59	1.64	22.53	22.65	0.53	0.02	3.42 <sup>ns</sup>
LDM	55.93	457.50	308	149.50	38.24	31.38	21.86	58.58	67.32	29.66	1073.50 <sup>**</sup>
D50T	65.97	79.73	75.97	3.76	13.54	13.21	2.94	23.07	95.28	17.53	231.66 <sup>**</sup>
D50S	70.17	120.74	112.71	8.03	15.66	15.13	4.04	26.51	93.35	21.13	346.17 <sup>**</sup>
TSI	4.20	5.05	3.93	1.12	53.51	47.20	25.20	85.53	77.82	3.60	12.90 <sup>**</sup>
GFP	40.37	15.51	9.11	6.40	9.76	7.48	6.27	14.39	58.74	4.77	33.74 <sup>**</sup>
PMT	110.67	177.02	154.86	22.16	12.02	11.24	4.25	19.94	87.48	23.98	486.74 <sup>**</sup>
NGC	278.38	6927.67	5404.67	1523	29.90	26.41	14.02	47.84	78.02	133.77	17737.00 <sup>**</sup>
100SW	22.13	0.85	0.28	0.57	4.17	2.39	3.41	5.34	32.94	0.63	0.23 <sup>ns</sup>
CDW	212.57	24.61	0.93	23.68	2.33	0.45	2.29	2.42	3.78	0.39	26.46 <sup>ns</sup>
GY	2.87	1.28	0.79	0.49	39.42	30.97	24.39	58.99	61.72	1.44	2.87 <sup>**</sup>

PH = Plant height (cm) @ 8 week after planting, NOL = number of leaves @ 8 week after planting; D50T = Days to 50% tassels appearance, D50S = Days to 50% silk appearance, LDM = Leaf dry matter (g), TSI = Tassel-silk interval, GFP = Grain filling period, PMT = Day to physiological maturity, NGC = Number of grains per cob, 100SW = 100-Seed weight (g), CDW = Cob dry weight (g), GY = Grain yield per hectare (ton). V<sub>p</sub> = Phenotypic variance, V<sub>g</sub> = Genotypic variance, V<sub>e</sub> = Environmental variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, ECV = Environmental coefficient of variation, %CV = Percentage coefficient of variation, GA = Genetic advance, H<sup>2</sup><sub>bs</sub> = Broad-sense heritability, MSG = Mean square of genotypes, \*\*\* = very highly significant, \*\* = highly significant, \* = significant and ns = non-significant

*Principal component analysis*

Principal component analysis is used in evaluating the patterns of variation in germplasm (Chukwudi and Agbo, 2016). The Principal component analysis results indicated that the first two axes explained 91.8% and 93.3% of the total variation in 2015 and 2016, respectively (Table 3). In 2015, the principal component axes 1 (PC1) explained 65.1% of the total variation, while PC2 accounted for 26.62% of the variation unaccounted for by PC1. Number of grains cob<sup>-1</sup>, cob dry weight and plant height influenced the first principal component axis, while cob dry weight, leaf dry matter and number of days to physiological maturity affected the second principal component axis. In 2016, number of grains cob<sup>-1</sup>, plant height and number of days to physiological maturity influenced the first principal component axis which accounted for 85.2% of the total variation. In the hereby study, number of grains cob<sup>-1</sup> was implicated as the most discriminating trait, portraying greater variation among maize lines in both years. It was followed by plant height and number of days to physiological maturity in both years. Cob dry weight was inconsistent in influencing the variation in the maize population in both years. Number of grains cob<sup>-1</sup>, plant height and number of days to physiological maturity were consistent in explaining the variations observed in the maize population. These traits had been flagged by Azad *et al.* (2012) and Hartings *et al.* (2008) as being important in explaining variations in maize germplasm. Therefore, they should be considered in maize improvement program in derived savannah agroecology. Principal component analysis has been successfully used for explaining observed variations in germplasms of *Vigna unguiculata* (Ansah *et al.*, 2016), *Telfairia occidentalis* (Chukwudi and Agbo, 2016), *Cucumis sativus* L. (Ene *et al.*, 2016), pointed gourd (Verma *et al.*, 2017).

**Table 3.** Percentage variation and latent loading of the principal component axes of maize genotypes

Traits	2015		2016	
	PC1	PC2	PC1	PC2
Plant height (cm)	0.20636	-0.01028	0.11456	-0.85002
No of leaves	0.01385	-0.00114	0.00721	-0.05208
Leaf dry matter (g)	0.02242	0.49433	-0.02352	0.44150
Days to 50% tassel appearance	-0.05761	0.09034	-0.07971	0.12646
Days to 50% silk appearance	-0.07482	0.11436	-0.10248	0.13726
Tassel-silk interval	-0.01721	0.02403	-0.02277	0.01080
Grain filling period	-0.00586	0.03548	-0.01646	0.01114
Days to physiological maturity	-0.08071	0.14834	-0.11964	0.14442
No of grains cob <sup>-1</sup>	0.92084	-0.24727	0.97683	0.15346
100-Seed weight (g)	0.02741	0.02769	-0.00095	-0.00345
Cob dry weight (g)	0.30349	0.80531	-0.00037	0.01631
Grain yield ha <sup>-1</sup> (tons)	0.01219	-0.00477	0.01068	0.00837
<b>Percentage variation</b>	65.13	26.62	85.17	8.10
<b>Cumulative variation</b>	65.13	91.75	85.17	93.27

Plant height and no. of leaves were recorded at 8 weeks after planting, PC1 and PC2 = First and second principal component axes

*Cluster analysis*

The dendrogram showed that at 80% dissimilarity point, the maize varieties studied were grouped into three clusters (A, B and C) in both years. In 2015, cluster A consists of an outlier 'Oka Awaka', while cluster B is made up of five varieties namely 'DT-SR-WCQ', 'TZE COMP.3C2DT', 'DT-SYN-7-WF2', 'DT-SYN-11-YF2' and 'Oba Super 2' (Figure 2). The remaining four varieties ('2008DTM A-YSTR', 'IW DC3 SYN/DTSYN-1-W', 'IWDC2SYN-F2' and 'EVDY-Y2000STRCO') fell into cluster C. There was similarity in the clustering for both years except for 'DT-SYN-11-YF2' inbred line, that moved from cluster B in 2015 to cluster C in 2016 (Figures 2 and 3).

The cluster means are presented in Table 4. In 2015, 'Oka Awaka' gave the highest number of days to 50% tassel and silk appearance, tassel-silk interval, grain filling interval, physiological maturity and cob dry weight compared to clusters B and C. Its 100-seed weight was above the population mean, while its plant height, number of leaves, grains  $\text{cob}^{-1}$  and yield per hectare were the lowest and below the population mean. Cluster B gave the highest mean for number of leaves, grains  $\text{cob}^{-1}$ , 100-seed weight and grain yield per hectare. Its plant height was above the population mean, while the floral attributes were below the population mean and was least in number of days to 50% tassel appearance, silk appearance and tassel-silk interval. The highest plant height mean was obtained in cluster C with number of leaves that was above the population mean. The floral attributes of cluster C are similar to cluster B as they were below the population mean. However, cluster C gave the lowest means for 100-seed weight and cob dry weight. In 2016, the cluster means followed the same trend as in 2015 except that 'Oka Awaka' produced the highest 100-seed weight. Also, the number of grains  $\text{cob}^{-1}$  in cluster C was above the population mean.

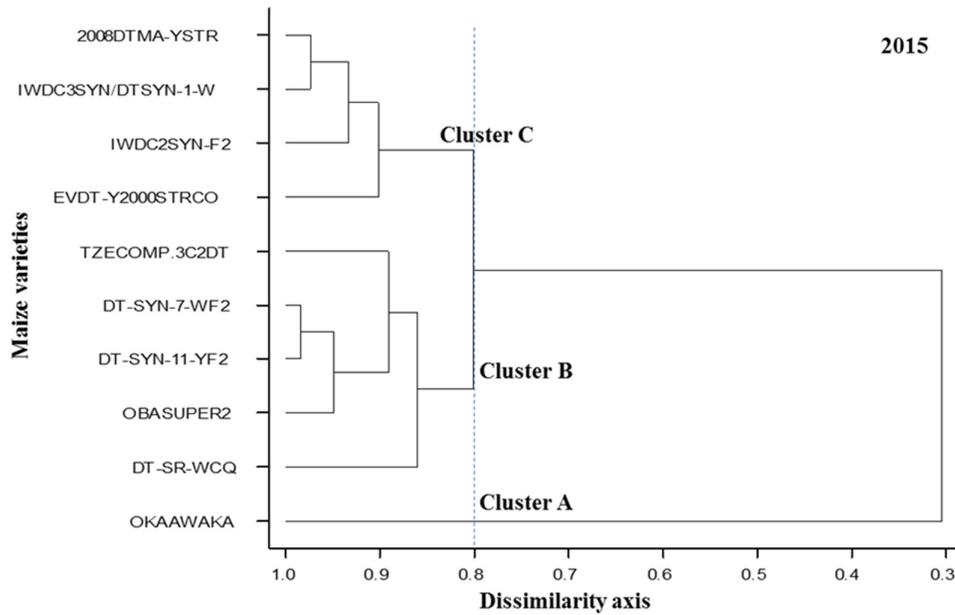
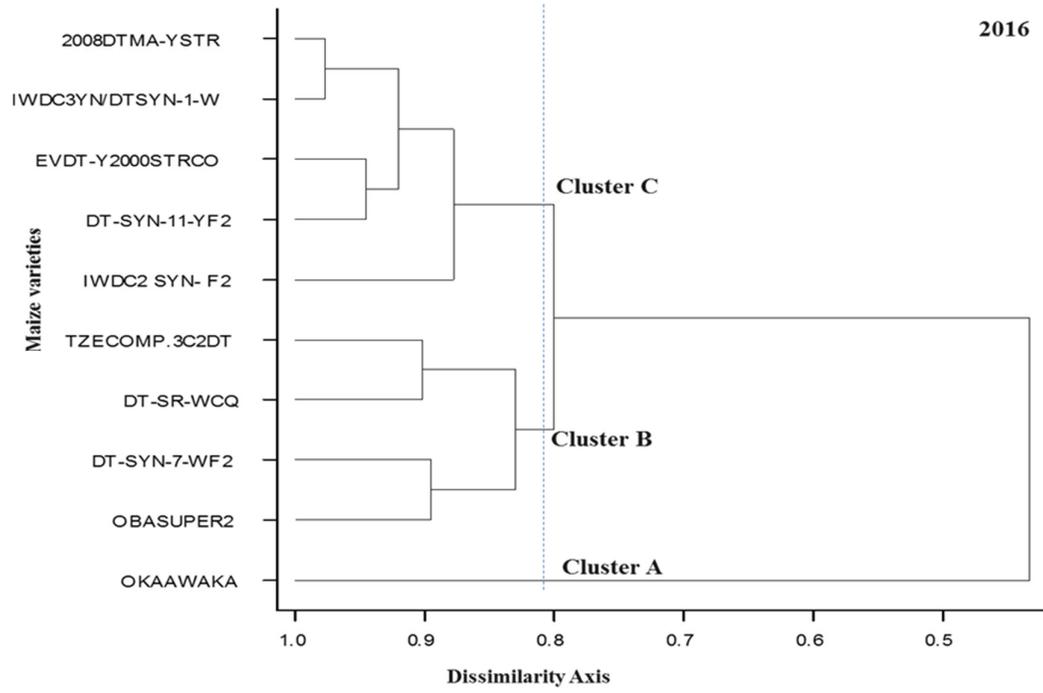


Figure 2. Dendrogram of the 10 genotypes of maize following Ward's method



**Figure 3.** Dendrogram of the 10 genotypes of maize following Ward's method

**Table 4.** Cluster means of 12 traits used in the classification of maize genotypes

Traits	Cluster A	Cluster B	Cluster C	Population mean
<b>2015</b>				
Plant height (cm)	58.4	93.9	94.1	82.1
No of leaves	6.9	9.5	9.0	8.5
Leaf dry matter (g)	115.6	52.6	36.2	68.2
Days to 50% tassel appearance	83.7	63.7	63.8	70.4
Days to 50% silk appearance	93.3	67.2	68.1	76.2
Tassel-silk interval	9.7	3.5	4.3	5.8
Grain filling period	45.3	40.9	38.0	41.4
Days to physiological maturity	138.7	108.2	106.4	117.8
No of grains cob-1	184.1	326.2	240.1	250.1
100-Seed weight (g)	22.1	23.6	19.6	21.8
Cob dry weight (g)	233.3	177.7	138.1	183.0
Grain yield ha-1 (tons)	1.5	3.9	2.0	2.5
<b>2016</b>				
Plant height (cm)	57.0	88.8	89.9	78.6
No of leaves	6.8	8.7	9.0	8.1
Leaf Dry Matter (g)	100.2	59.8	44.0	68.0
Days to 50% tassel appearance	88.7	63.3	63.5	71.8
Days to 50% silk appearance	98.0	66.3	67.7	77.3
Tassel-silk interval	9.3	3.0	4.1	5.5
Grain filling period	45.0	40.5	39.3	41.6
Days to physiological maturity	143.0	106.8	107.3	119.0
No of grains cob <sup>-1</sup>	128.8	341.0	258.2	242.7
100-Seed weight (g)	22.8	22.3	22.2	22.4
Cob dry weight (g)	213.5	212.3	212.6	212.8
Grain yield ha <sup>-1</sup> (tons)	1.7	3.7	2.5	2.6

Plant height and no. of leaves were recorded at 8 weeks after planting

The cluster means revealed that the varieties were grouped based on their growth, floral and yield performances. 'Oka Awaka' was poor in the measured growth and floral traits. It had prolonged vegetative phase compared to clusters B and C. The growth and floral traits of clusters B and C were similar, but the yield traits differentiated the two clusters. Cluster B showed superior yield performance over cluster C. The grouping of the varieties aligned to their initial growth duration (Table 1). 'Oka Awaka' previously unclassified based on growth duration took 139 days to reach physiological maturity. The varieties in cluster B are late maturing varieties except 'TZE COMP.3C2DT' that was classified as early maturing. Cluster C contained the early and intermediate maturing varieties. The grain colour was randomly distributed among the clusters. The superior yield performance of varieties in cluster B over 'Oka Awaka' and cluster C implied that they can be used for maize improvement program or direct introduction in the derived savannah agro-ecology. Cluster analysis has proved to be an effective method in grouping accessions (Shukla *et al.*, 2010; Chukwudi and Agbo, 2016) which is important in maintaining their biodiversity and utilization in crop improvement program (Chukwudi and Agbo, 2016). Cluster analysis had been used in maize improvement studies in different parts of the world (Bhussal *et al.*, 2017; Hartings *et al.*, 2008; Liu *et al.*, 2006; Rahman *et al.*, 2017; Subramanian and Subbaraman, 2010).

## Conclusions

The maize genotypes evaluated in the current study expressed their genetic diversity within the growth, floral and yield traits investigated. Environmental contribution to the phenotypic variance was the highest for the number of leaves, followed by cob dry weight, plant height and 100-seed weight in both years. Moderate to high heritability and genetic advance estimates were observed for the number of days to physiological maturity, leaf dry matter and number of grains per cob in both years. However, the principal component analysis indicated that the number of grains per cob, plant height and number of days to physiological maturity were consistent in explaining the variations observed in the maize population. Growth, floral and yield traits were used in grouping the varieties into three clusters. Cluster B gave the highest mean for number of leaves, number of grains per cob, 100-seed weight and grain yield per hectare, with plant height that was above the population mean, while its floral attributes were below the population mean. 'Oba Super 2', a commercial hybrid and three DT genotypes namely 'DT-SR-WCQ', 'TZE COMP.3C2DT' and 'DT-SYN-7-WF2' were consistently grouped into cluster B in both years. These three DT maize genotypes should be used in maize breeding programs or directly introduced to farmers in the derived savannah agro-ecology.

## Authors' Contributions

PI: Conceptualization, investigation and methodology; COE: Writing - original draft; AE: Data curation; UPC: Writing - review and editing; UNI: Supervision; Visualization.

All authors read and approved the final manuscript.

## Acknowledgements

The authors are grateful to IITA, Ibadan, Nigeria for providing them with the eight-drought tolerant maize shortly after their release in 2015.

## Conflict of Interests

The authors declare that there are no conflicts of interest related to this article.

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