

## Assessment of Genetic Diversity of Maize (*Zea mays* L.) in Sudan Savannah

Shaibu, A.S.\*, Muhammad, I.H. and Adnan, A.A.

Department of Agronomy, Bayero University, Kano, Nigeria

\*Corresponding author: asshuaibu.agr@buk.edu.ng

---

### ABSTRACT

*The success of any breeding program depends on the ability to determine germplasm diversity and genetic relationships among breeding materials. Genetic diversity is an invaluable aid in crop improvement. The study was aimed at identifying genetic diversity among twenty-two genotypes of maize sourced from International Institute of Tropical Agriculture (IITA). The genotypes were evaluated for variability in growth, yield and yield components in 2016 cropping season in the Sudan Savannah using a randomized incomplete block design with 3 replications. Principal component Analysis (PCA), cluster analysis, discriminant analysis and genotype by trait (GT) Biplot were used to assess the genetic diversity between the genotypes. A highly significant difference ( $P < 0.01$ ) was observed between the genotypes in all the traits studied except for days to emergence. The principal component revealed that the first six factors account for 93% variability. Factor 1 gave maximum variability and factor 2 and factor 3 can be utilized for hybridization program. The principal component biplot reveals the relationship among traits and the distance of each variable in determining variability among hybrids. The cluster diagram reveals four distinct groups. Group I consisted of 6 genotypes, group II, 6 genotypes, group III, 7 genotypes and group IV consisted of 3 genotypes. Both principal component and cluster analyses revealed the genetic diversity among the genotypes and identified genotypes that can be selected for hybridization and improvement of maize.*

**Key words:** Cluster analysis, genetic diversity, genotype by Trait, Principal component analysis

---

### INTRODUCTION

The importance of plant genetic resources and the need for screening adaptive traits cannot be overlooked. Their vital significance for their maintenance of genetic improvement and biodiversity has been recognized worldwide (Lester *et al.*, 1986). Adaptive characterization and evaluation is priority task for successful breeding program. Crop improvement techniques remain a major concern to plant breeders (Akbar and Kamran 2006; Aremu *et al.*, 2007a). Several factors that affect crop improvement for specific or general environment performance, such factors include climate, weather, soil, edaphic and biological, and more importantly crop genotype (Aremu *et al.*, 2007b).

Genotypes of crop are composed of different forms of crop that include; inbred or pure line hybrids, landraces, wild races, germplasm, accession, cultivars or varieties. These genotypes of crop have wide and diverse origin and genetic background known as genetic diversity. Genetic diversity studies are therefore a step wise process through which existing variations in the nature of individual or group of individual crop genotypes are identified using specific statistical method or combination of methods (Weir, 1996; Warburton and Crossa, 2000; Aremu 2005;

Christine *et al.*, 2009; Shaibu *et al.*, 2014). It is expected that the identified variations would form a pattern of genetic relationship useable in grouping genotypes. Multivariate statistical methods especially cluster analysis is a tool to classify varieties with similar conditions with respect to set of variables has gained increasing interest in recent years. The approach use to group varieties was cluster analysis which is well-known method within the multivariate statistical approach (Hair *et al.*, 1995).

Understanding the diverseness and relatedness among maize species in Sudan Savanna using multivariate techniques is needed. Thus, to achieve this, the phenotypic evaluation of genotypes for morphological classification remains the only tool for discovering genetic variability within a population, where higher precision diversity analysis techniques are not within the reach of the scientist. The aim of this study was to therefore understand the relatedness and diversity among maize genotypes in Sudan savanna and determine the genotype by trait association.

**MATERIALS AND METHODS**

The experiment was conducted at the Orchard of Agronomy Department, Faculty of Agriculture, Bayero University, Kano. The treatments consist of 22 maize genotypes which were laid out in a 11 × 2 Randomized Incompletely Block Design, with three replications. The land used for the experiment was ploughed and harrowed to a fine tilt. The farm area was marked out into 22 plots per replication and 2 seeds per hill were sown and later thinned to 1 stand at two weeks after sowing. The seeds were sown at 75cm by 25cm inter and intra row spacing. Weeding was carried out manually using hoe which was followed by hand weeding to remove the weeds that will establish after hoeing at 4 and 6 weeks after sowing and a week before harvesting to avoid competition for water, nutrients, space and light. Data was recorded on days to tasseling and silking, anthesis silking interval, plant and ear height as well as grain yield.

Data collected was subjected to Analysis of variance using mixed procedure statement of SAS (2015). The data was further subjected to principal component and Wards Hierarchical Cluster Analyses using various procedures of the JMP program (SAS, 2009). Genotype by trait (GT) biplot was constructed to visualize the relationship between the genotypes and traits measured. The GT biplot was constructed using R-Programme (R Core Team, 2013).

**RESULTS**

The mean performance for some agronomic traits of maize is presented in (Table 1). A significant difference was observed between the varieties for all the measured traits. The genotypes EVDTY2000STR, IWDC2 and M0926-8 have the highest grain yield of 5531, 5323 and 5228 kgha<sup>-1</sup>, respectively whereas 2009TZEEWDTSTR, OBA SUPER1 and TZEEWPOPSTRC5 x TZEE16 have grain yield of 3162, 3196 and 3214 kgha<sup>-1</sup> respectively.

**Table 1:** Mean performance of some agronomic traits of different maturity groups of maize

Genotypes	DTT	DTS	ASI	DTM	PH	EH	GYD	CYD	SW
2009TZEEWDTSTR	50	53.3	3.3	80.3	158.47	57.87	3162.27	4335	23.67
2011TZEWDTSTRSYN	52	55.7	3.7	85	160.47	61.13	4397.4	5555.33	22.33
2013DTEYSTR	56	59.7	3.7	88.5	149.6	56.47	3651.47	4543	25.33
2013TZEEWPOPDTSTR	52.7	55.3	2.7	79.3	158.1	56.6	4614.07	6313.67	24
99TZEEYPOPSTRQPMCO	51.7	54	2.3	81	164.63	68.13	4265.93	5417	24
DTSTRW	55.3	60	4.7	87	167.2	72.27	4540.83	5897.67	19.33
DTSTRY	55	58.7	3.7	89.3	164.97	71.13	5142.23	5762.67	22.33
EVDTW99STR	53	56.3	3.3	85.3	152.93	64.93	3493.9	5371.67	23
EVDTY2000STR	53.7	57.3	3.7	78.7	150.5	66.87	5531.93	8630.33	24.33
IWDC2	52	57	5	82.7	170	65.87	5323.17	5979	27.33
M0926-8	54.7	57.3	2.7	87.7	190.5	87.13	5228.33	6639.67	26.67
M1026-10	56.3	60.3	4	89.7	188.47	89.83	4328.57	5247	22.67
M1227-12	54	58.7	4.7	87.5	176.97	83.27	3663.4	4496.33	26
OBASUPER1	56.7	61	4.7	88.5	173.1	74.6	3196.07	3732	25
TZBSR	55.7	58.7	3	88.3	178.7	69.53	3905.77	4610	23
TZECOMP3DTC3	50	53.3	3.3	81.3	153.83	60.93	4179.1	6261	23.67
TZEEI29 x TZEEI21	51.3	54.7	3.3	78	164.83	70.87	3803.83	5345.67	26.67
TZEEWPOPSTRC5 x TZEE16	54	57.7	3.7	87	158.67	62.8	3214.57	3808.33	25
TZE24 x TZE25	51	54.7	3.7	79.3	164.17	63.47	3400.23	4403	24.67
TZEYPOPDTSTRC4 x TZEEI13	50.3	54	3.7	78.3	156.63	62.4	3870.63	5233.33	24.67
TZLCOMP1SYN	50	54	4	81	172.13	78.6	3694.3	4948.67	24.67
TZLCOMP4DTC2	54.7	57.3	2.7	87	182	90.2	4133.3	5076	26.67
SE	1.439	1.5538	0.5365	1.9646	7.4864	6.168	94.664	394.53	1.206
P level	0.0073	0.0075	0.0586	<.0001	0.0063	0.002	<.0001	<.0001	0.0024

DTE = Days to Emergence, DTT = Days to Tasselling, DTS = Days to Silking, ASI = Anthesis Silking Interval, DTM = Days to Maturity, PH = Plant Height, EH = Ear Height, GYD = Grain Yield, CYD = Cobs Yield, SW = Seed Weight

The principal component analysis is presented in (Table 2). The first six factors have eigen value greater than one and accounted for about 93% of the variability. Base on this, the first six factors were explained further. The first and third factors were loaded with phenological traits (Table 3) like days to tasselling, days to silking, days to maturity, plant height and ear height.

**Table 2:** Cumulative variance explained by the factors

Factor	Variance	Percent	Cum Percent
Factor 1	2.7664	27.664	27.664
Factor 2	1.7472	17.472	45.136
Factor 3	1.6022	16.022	61.158
Factor 4	1.0646	10.646	71.804
Factor 5	1.0635	10.635	82.439
Factor 6	1.0097	10.097	92.536
Factor 7	0.5312	5.312	97.848
Factor 8	0.1196	1.196	99.044
Factor 9	0.0892	0.892	99.936
Factor 10	0.0064	0.064	100

The second factor was loaded with yields traits such as grain and cob yield. The cluster diagram reveals four

distinctive groups (Figure 1). Groups I and II consisted of six genotypes each, group III has seven genotypes and the last group IV with three genotypes. As group I consisted of six genotypes among which three are Extra Early, two are early maturing varieties and 1 late maturing variety. Also group II consisted of 6 genotypes which include 4 late maturing varieties, 1 Extra Early and 1 Early maturing varieties. Group III that has highest number of genotypes consisted of 4 late maturing varieties, 2 Early maturing varieties and 1 extra early maturing variety. Group IV with lowest number of genotypes consisted of 2 early and 1 late maturing varieties (Table 4).

The GT Biplot (Figure 2) shows that, different genotypes are sensitive to different agronomic traits. The Genotypes, WDC2, 2011TZEWDTSTRSYN, VDTW99STR, DTSTRY and DTSTRW are higher yielding with respect to cobs yield (CYD) and grain yield (GYD). Traits like days to maturity, days to silking and anthesis silking interval, Genotypes TZBSR, M0926-8, and M1026-10 respond greatly to that. For Genotypes TZLCOMP4DTC2, M1227-12, and OBASUPER1 show response to DTE, PH and EH traits and TZECOMP3DTC3, TZEYPOPDTSTRC4 x TZEI13, 2009TZEWDTSTR, TZE24 x TZE25, TZEI29 x TZEI21, and TZLCOMP1SYN genotypes were below average in their performance.

**Table 3:** Factor loadings of the first six factors

	Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	Factor 6
DTT	0.949955	-0.006194	0.267737	-0.068163	0.043922	-0.076625
DTS	0.935567	0.047807	0.247152	-0.049483	0.192906	-0.077242
ASI	0.152173	0.055026	0.199857	-0.062324	0.951385	0.157073
DTM	0.661486	0.049114	0.330879	0.017734	0.020881	-0.03848
PH	0.419455	-0.132443	0.748726	0.267795	0.224935	0.117683
EH	0.424345	-0.100769	0.841292	0.13444	0.191158	0.098544
PLT_No.	-0.111505	0.20683	0.104516	-0.013788	0.154711	0.953685
GYD	0.322093	0.887514	-0.063711	-0.107629	0.002952	0.137696
CYD	-0.222996	0.92798	-0.089735	-0.102347	0.06436	0.139364
SW	-0.077838	-0.141853	0.169083	0.970193	-0.059986	-0.015763

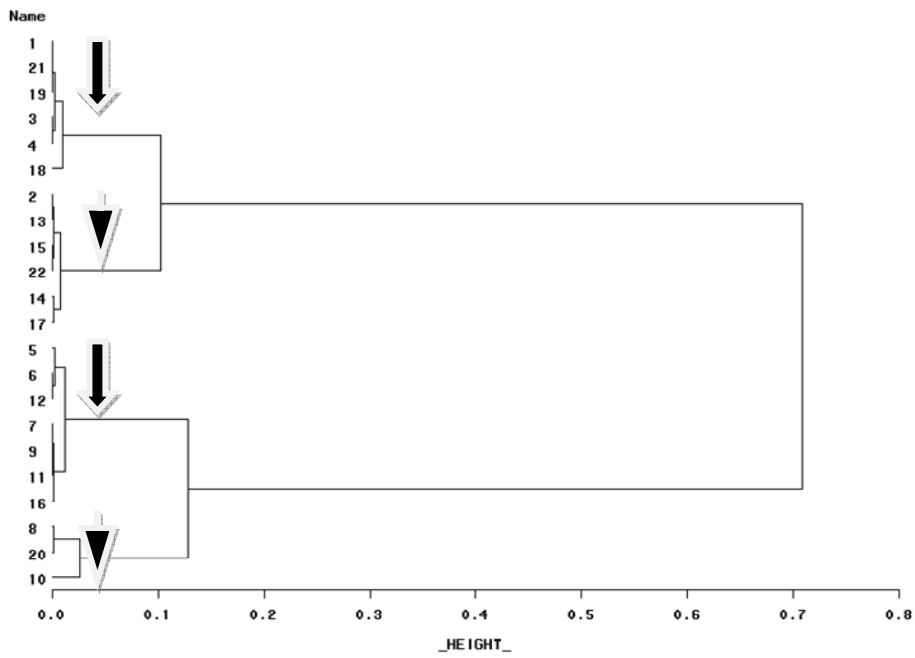


Figure 1: Cluster Diagram of the 22 maize genotypes

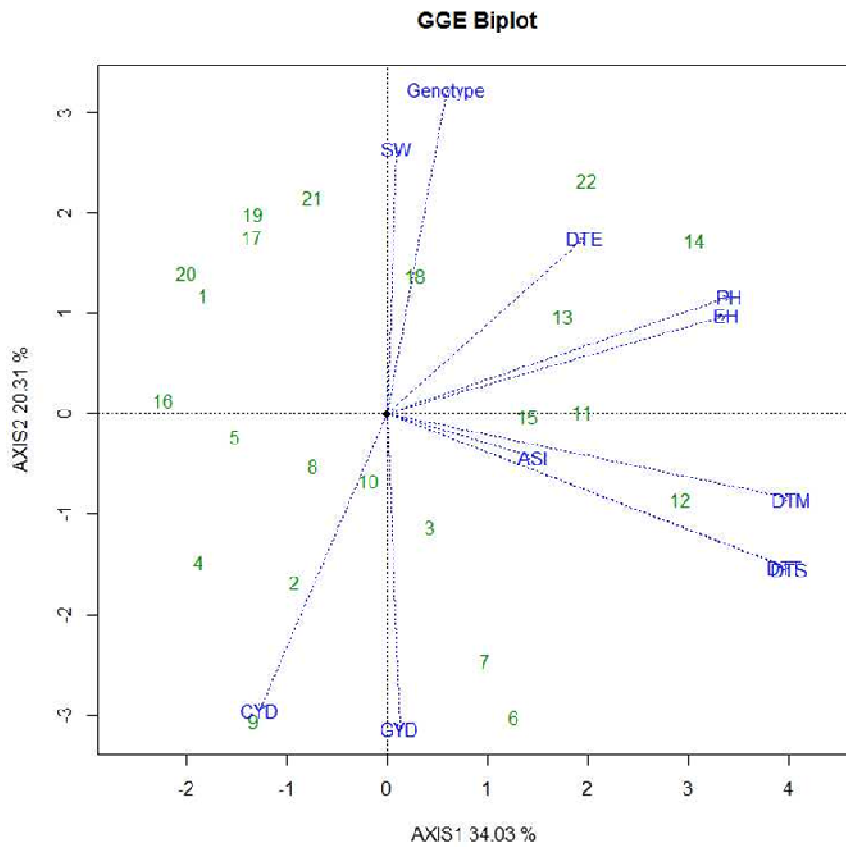


Figure 2: Genotype by trait biplot

**Table 4:** Summary of Groupings

Maturity group	Group I	Group II	Group III	Group IV
Extra Early	2009TZEEWDTSTR, 2013TZEEWPOPDTSTR, TZEEWPOPSTR5 x TZEE16	TZEE129 x TZEE121	99TZEEYPOPSTRQPMCO	
Early	TZE24 x TZE25, 2013DTEYSTR,	2011TZEWDTSTRSYN	TZECOMP3DTC3	EVDTW99STR, TZEYPOPDTSTR4 x TZEE113
Intermediate				IWDC2
Late	TZLCOMP1SYN	M1227-12, TZBSR, TZLCOMP4DTC2, OBA SUPER1	DTSTRW, M1026-10, DTSTRY, EVDTY2000STR, M0926-8	

## DISCUSSION

The significant differences observed in the traits were indications that there is adequate genetic diversity among the genotypes. Selection can also be made from these genotypes to breed for improved maize varieties. Principal component (PC) revealed that a greater variability was accounted for about 93% for the first 6 factors. The loading of the traits in each factor was according to their percentage contribution and for good hybridization, genotypes should be selected from factor 1, 2, and 3 for phenological and yield traits as factor 2 was loaded with yield related traits. Maximum variability was achieved in the 1<sup>st</sup> PC as also reported by Shaibu *et al.* (2014). The PC distinguished growth related traits from yield related traits. Cluster analysis grouped the genotypes according to their maturity and yielding abilities. Therefore, genotypes with similar traits belong to the same group and as such group I genotypes are mostly Extra Early maturing, group II and III are mostly Late maturing and group IV Early maturing varieties. The clustering of genotypes into four groups indicates that maximum genetic diversity is achieved in four groups. This is similar to the findings of (Aremu *et al.*, 2005; Christine *et al.*, 2009; and Shaibu *et al.*, 2014). For hybridization program the grouping will aid or guide the breeders in making crosses between groups rather than within group, this is because more variability exists between groups than within group (Shaibu, 2015).

## CONCLUSION

Principal component, cluster analyses and genotypes by trait biplot revealed the genetic diversity and relationship among the genotypes. Thus, these tools can be used to assess genetic diversity in maize varieties in Sudan savannah agro-ecological zone. Researchers in Agriculture could also use the two analyses to reduce redundancy in experiments.

## REFERENCES

- Akbar, A.A. and Kamran, M. (2006). Relationship among yield components and selection criteria for yield improvement of Safflower...*Journal of Applied Sciences*, 6:2853-2855.
- Aremu, C.O. (2005). Diversity selection and genotypes Environment interaction in cowpea unpublished Ph.D. Thesis. University of Agriculture, Abeokuta, Nigeria. P. 210
- Aremu, C.O. (2012). Exploring Statistical Tools in Measuring Genetic Diversity for Crop Improvement, Genetic Diversity in Plants, Prof. Mahmut Caliskan (Ed.), In Tech, Available from: <http://www.intechopen.com/books/genetic-diversity-in-plants/exploring-statistical-tools-in-measuring-geneticdiversity-for-crop-improvement>
- Aremu, C.O., Adebayo, M.A., Ariyo O.J, and Adewale B.D. (2007a). Classification of genetic diversity and choice of parents for hybridization in cowpea vignaungiculata (L) walp for humid savanna ecology. *African Journal of Biotechnology*, 6 (20): 2333-2339.
- Aremu, C.O., Adebayo, M.A., Oyegunle, M. and Ariyo, J.O. (2007b). The relative discriminatory abilities measuring Genotype by environment interaction in soybean (*Glycine max.*) *Agricultural journal*, 2 (2): 210-215.
- Christine, J., H., William, A., and Stacy, A. (2009). Genetic diversity of creeping bentgrass cultivars using SSR markers. *International Turf Grass Society Research Journal*, 11:533-547.
- Hair. F., R. L. Tatham, R. E. Anderson and W. Black. (1995). Multivariate data analysis 5<sup>th</sup> Edition, Prentice Hall. New Jersey. U.S.A 768p.
- Lester, N., J. Hakiza, N. Stavropoulos and M. Taxeira (1986). Variation patterns in the African scarlet

- eggplant (*Solanumaethiopium* L.) In: Styles, B.T. (Ed): Intraspecific of wild and cultivated plant, 823 – 307. Oxford University Press, Oxford U.K. 360P.
- R Core Team (2013). R: A language and environment for statistical,computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>.
- SAS Institute, (2015). Statistical Analysis Software (SAS). Users' Guide. SAS Inst., Cary, NC. UK.
- SAS Institute, (2009). JMP 12.0.1. SAS Inst., Cary, NC. UK.
- Shaibu, A. S., Ahmed A., Adnan, A. A. and Ibrahim, M. (2014). Genetic diversity studies in cowpea (*Vigna unguiculata* (L.) walp) genotypes grown in Sudan savanna. Proceeding of First International Conference of Dryland Agriculture. pp 158-163.
- Shaibu, A.S. (2015). Combining Ability and Heterotic Pattern of Extra-Early Yellow Maize (*Zea mays* L.) Inbreds Under *Striga*-Infested and *Striga*-Free Environments unpublished M. Agric. Dissertation. Federal University of Agriculture, Abeokuta, Nigeria. P. 61
- Warburton, M. and Crossa, J. (2000). Data analysis in the CIMMYT. Applied Biotechnology Center for fingerprint and Genetic Diversity Studies. CIMMYT, Mexico.
- Weir, B.S. (1996). Intraspecific differentiation in D.M. Hillis *et al.* (ed). Molecular systematic 2<sup>nd</sup> edition Sunderland M.A. P.385-403.

\*\*\*\*\*