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GENETIC DIVERSITY OF EXTRA-EARLY YELLOW MAIZE HYBRIDS UNDER *STRIGA* ENVIRONMENTS

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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. This study was carried out to determine the genetic diversity among 70 extra-early yellow maize hybrids under *Striga* environments. Cluster and principal component (PC) analyses were used to determine the genetic diversity of the hybrids. Data on morphological and agronomical data were collected. The experiment was set up in two locations (Abuja and Mokwa) in a randomized incomplete block design experiment with two replications. A significant difference was observed among the hybrids in all the traits studied and a significant genotype × environment interaction was observed for all traits except for plant height, anthesis silking interval and *Striga* count at 8 and 10 WAP. The principal component reveals that the first three components account for 86% variability. PC1 gave maximum variability (43%) and was loaded with PC1 and the first four PCs can be utilized in hybridization programs. The principal component biplot reveals the relationship among traits and the distance of each variable in determining variability among hybrids. The cluster diagram reveals five distinct groups. Group IV consisted of Striga tolerant hybrids and group I consisted of susceptible hybrids. Both principal component and cluster analysis revealed the genetic diversity among the hybrids and identified genotypes that were Striga tolerant and could be selected as choice of parental materials to develop Striga resistant materials.

Keywords: Cluster analysis; Extra-early maize; Genetic diversity; Principal component; Striga

INTRODUCTION

Maize is an important staple crop but its production is faced with many constraints such as biotic and abiotic stresses. Surveys in the northern Guinea and Sudan savannas of Nigeria showed that *Striga* has remained a serious problem, attacking millet, sorghum, maize, and upland rice (Showemimo *et al*., 2002). In northern Nigeria, over 85% of fields planted to maize and sorghum were found to be infested (Dugje *et al*., 2006). Grain yield losses ranged from 10 to 100% for maize (Shaibu *et al*., 2021). Gressel *et al.* (2004) reported about 64% of land devoted to cereal production in West Africa severely infested with *Striga*. Genetic diversity is an invaluable aid in crop improvement and the choice of parents is of paramount importance in any breeding program. Assessment of a large number of inbreds for genetic diversity under *Striga* environments is of utmost importance. Genetic diversity study is a step-wise process through which existing variations like individual or group of individual of crop genotypes are identified using specific statistical method or combination of methods (Weir, 1996; Warburton and Crossa, 2000; Aremu, 2005; Kubik *et al*., 2009). It exposes the genetic variability in diverse populations and justifies for introgression and ideotype breeding programs to enhance crop performance. Mostafa *et al.* (2011) postulated that genetic diversity studies provide the understanding of genetic relationships among populations and hence direct assigning lines to specific heterogeneous groups useable in the identification of parents and hence choice selection for hybridization. Understanding the inter- and intra-specie genetic relationships as provided by diversity studies has proven to increase hybrid vigour and reduce or avoid re-selection within existing germplasm. Cluster and principal component analysis have been used in assessing the genetic diversity of maize. Cluster Analysis presents patterns of relationships between genotypes and hierarchical mutually exclusive grouping such that similar descriptions are mathematically gathered into the same cluster (Hair *et al*., 1995; Aremu, 2005). Cluster analysis is used to assign observations to groups (clusters) so that observations within each group are similar to one another for variables or attributes of interest, and the groups themselves stand apart from one

another. The principal component analysis is a multivariate technique that analyses data tables in which observations are described by several inter-correlated quantitative dependent variables (Aremu, 2012). Cluster and principal component analysis can be jointly used to explain the variations in breeding materials in genetic diversity studies. This study was conducted to identify the extent of genetic diversity among maize hybrids under *Striga* environments and determine the relative importance of principal component and cluster analysis in assessing the genetic diversity of maize.

Materials and Methods

Seventy hybrids were evaluated under *Striga* environments in 2013/2014 at Abuja and Mokwa. The experiment was laid out in a randomized incomplete block design with two replications. Three seeds were sown per hole and later thinned to two at 2 weeks after sowing. Each plot was a single row plot measuring 4m in length and 0.4 m and 0.75 m intra and inter-row spacing was used respectively. Fields were infested with about 5000 germinable *Striga* seeds as previously reported by Shaibu et al. (2021) and as described by Kim (1991). Fertilizer application was delayed until about 21 to 25 days after planting, 30-60 kg ha^{-1} N, 30 kg ha^{-1} P, and 30 kg ha^{-1} K were applied as NPK 15–15–15. Weeds other than *Striga* were controlled by hand weeding. Data were recorded on morphological and agronomical traits. Data were analyzed using the GLM procedure of SAS and principal component and cluster analysis were done using the PRINCOMP and CLUSTER procedure of SAS respectively (SAS, 2001).

RESULTS AND DISCUSSION

The mean squares of the traits are presented in Table 1. Significance difference was observed among the hybrids in all the traits measured. The significant difference observed in some of the characters studied were indications that there is adequate genetic diversity among the hybrids. Selection can also be made from these hybrids to breed for better drought tolerance/resistance hybrids. Shaibu et al. (2021) also reported significant differences among extra-early maize hybrids under Striga environments. Also, a significant genotype by environment (G × E) interaction was observed for all traits except anthesis silking interval, plant height and *Striga* count at 8 and 10 WAP. The lack of significance G × E interaction for *Striga* count at 8 and 10 WAP indicates that the environment had a similar effect on *Striga* emergence. The principal component reveals that the first four components account for 86% variability and gave more than one eigenvalue out of the 13 components and were given due importance for further explanation (Table 2). This is similar to the findings of Maqbool *et al.* (2010). The variances also decrease from around 42% to 10% (Figure 1). From the scree plot, an elbow was observed at the 4th PC and after which it tends to straight (Figure 1). From the scree plot, it was clear that maximum variation was observed in PC1. The loadings of the principal components are shown in Table 3. The loadings of the characters in each PC were according to their percentage contribution and for good hybridization, hybrids should be selected from PC1 and PC2. The first component was loaded with *Striga* ratings at 8 and 10 WAP, ear aspect, days to silking, anthesis silking interval and stem lodging but had a negative effect for yield. The second component was loaded with days to silking, days to anthesis, plant height and ear height. The third component was loaded with *Striga* emergence count at 8 and 10 WAP, plant and ear height. While the 4th component was loaded with anthesis silking interval, plant height, ear height and stem lodging. The principal component biplot reveals the relationship among traits (Figure 2). The biplot shows that the variables are superimposed on the plots as vectors. The distance of each variable for PC1 and PC2 shows the contribution of the variable in the variation of hybrids. The PC biplot will assist a breeder in selecting hybrids with relation to a trait of interest. The biplot also revealed traits that are related. Breeding for a particular trait in a group will indirectly lead to breeding for other traits in the group. The cluster diagram reveals five distinct groups (Figure 3). Group I consisted of 9 hybrids, group II 14 hybrids, group III 7 hybrids, group IV 15 hybrids and group V consisted of 25 hybrids. Group IV hybrids consisted of *Striga* tolerant inbreds and group I hybrids consisted of *Striga* tolerant hybrids. The clustering of hybrids into four groups indicates that maximum genetic diversity is achieved in four groups. For hybridization program, the grouping will guide a breeder in making crosses between groups rather than within-group because more variability exists between groups than within groups.

CONCLUSION

Both principal component and cluster analysis revealed the genetic diversity among the hybrids and identified genotypes that can be selected for drought-prone environments. Also, the study revealed that principal component and cluster analysis are tools that can be used by researchers in agriculture in other to reduce redundancy in experiments.

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Table 1: Mean squares of 12 traits of extra-early yellow maize hybrids

Source	DF	Days to silking	Anthesis silking interval	Plant height (cm)	Ear height (cm)	*Striga* count at 8WAP	*Striga* count at 10WAP	*Striga* rating at 8WAP	*Striga* rating at 10WAP	Ear aspect	Stem lodging	Grain yield (kg/ha)
Block	6	3.419255	1.76	213.96	127.98	0.32**	0.24**	2.67**	0.99	0.69	2.47	1394011.4*
Rep	1	15.09*	0.057	2610.80**	1033.73**	0.58**	0.39**	3.21*	0.8	0.09	34.26**	16688.8
Env	1	627**	80.36**	26715.09**	6860.7**	3.66**	4.31**	0.13	2.23*	5.43**	966.06**	47728097.8**
Entry	69	11.03**	2.98**	395.12**	179.14**	0.10**	0.07**	3.86**	3.10**	1.63**	4.79**	2450035.6**
Entry*Env	69	4.95**	2.05	180.53	87.48	0.06	0.04	1.20*	0.77*	0.76**	3.61**	863322.9**
Block(Rep*Env)	18	5.14*	1.65	631.77**	244.66**	0.18**	0.14	2.54**	1.40**	1.42**	4.06**	1808840.4**
Rep(Env)	1	0.003	0.23	0.8	89.16	0.22*	0.40**	2.8	0.004	0.03	3	1458565
Error	114	2.85	1.75	155.62	91.57	0.05	0.04	0.74	0.48	0.39	1.7	495197.6

* and ** represents significance at 5 and 1% level of probability respectively.

Table 2: Eigen-values for first 3 PCs

	Eigenvalue	Difference	Proportion (%)	Cumulative (%)
1	5.54	3.25	42.62	42.62
2	2.29	0.26	17.62	60.24
3	2.03	0.77	15.63	75.87
4	1.26	0.50	9.67	85.55

Table 3: Principal component (PCs) for 12 characters in 70 hybrids of extra-early yellow maize

	Prin1	Prin2	Prin3	Prin4
Days to silking	0.22	0.48	0.02	-0.28
Days to pollen	0.08	0.52	-0.05	-0.50
Anthesis silking interval	0.26	-0.05	0.13	0.41
Plant height (cm)	-0.15	0.46	0.20	0.40
Ear height (cm)	-0.16	0.49	0.20	0.36
Striga rating at 8WAP	0.39	0.02	0.01	-0.03
Striga rating at 10WAP	0.41	-0.02	-0.07	0.01
Ear aspect	0.39	-0.04	-0.11	0.09
Yield (kg/ha)	-0.40	-0.07	0.13	-0.03
Number of ears per plant	-0.37	-0.07	-0.02	-0.14

Stem lodging	0.21	-0.02	0.16	0.31
Striga count at 8WAP	0.09	-0.13	0.65	-0.19
Striga count at 10WAP	0.09	-0.13	0.65	-0.21

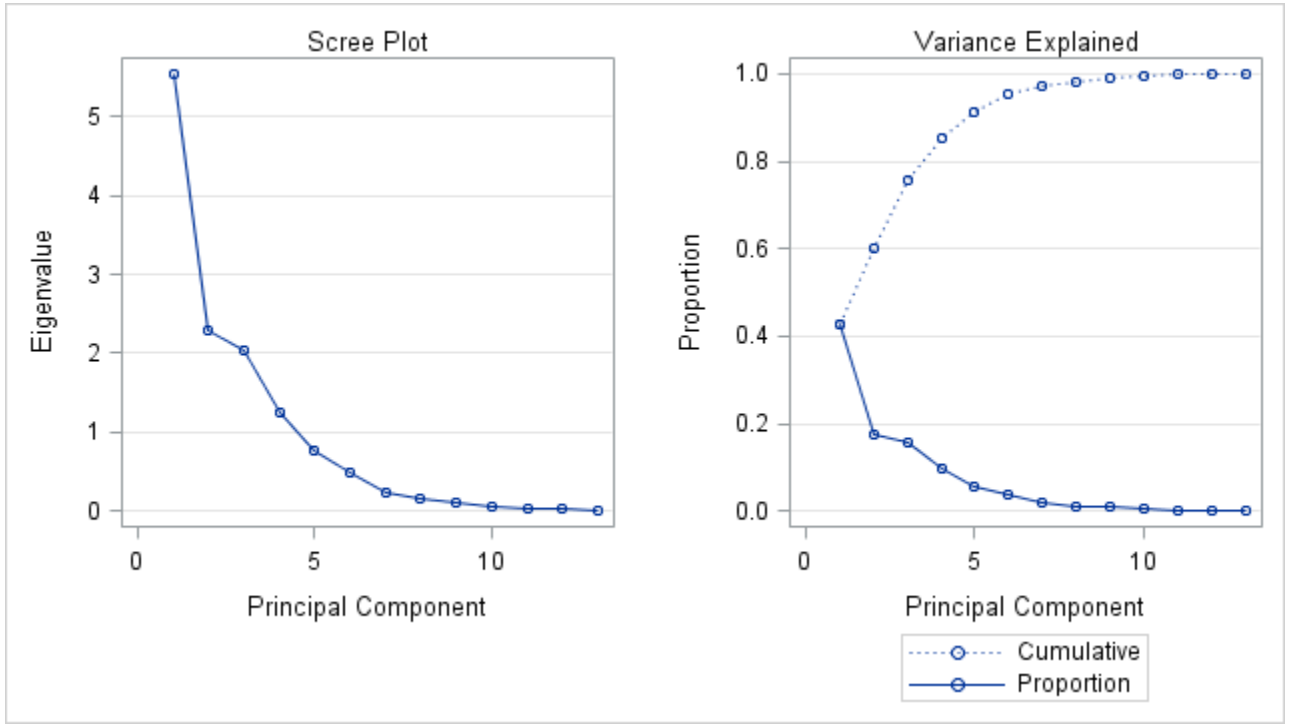

Figure 1: Scree plot and variance explained for the principal components

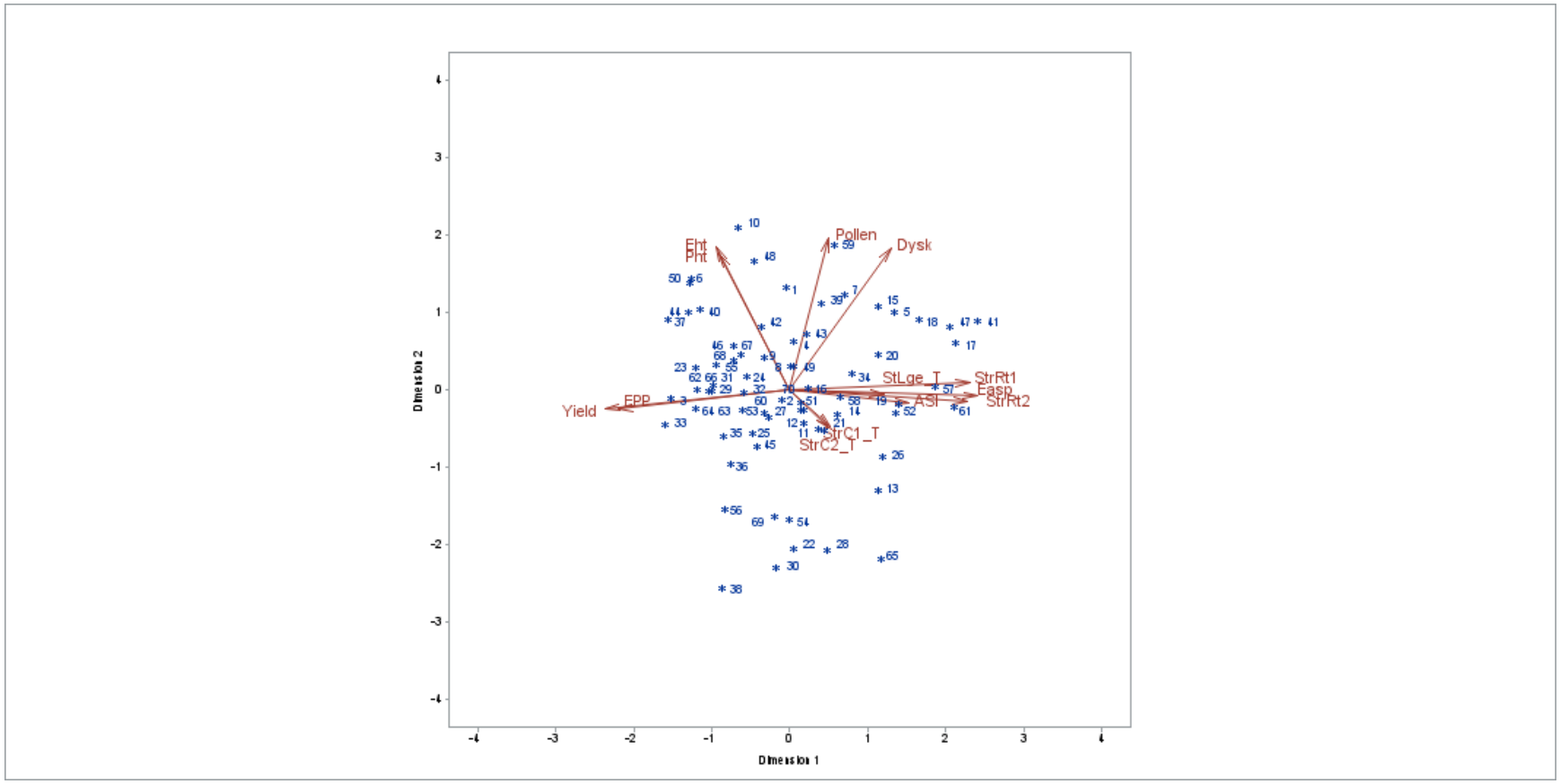

Figure 2: biplot of PC1 and PC2

Figure 3: Dendrogram of the extra-early yellow maize using ward minimum variance