



PRINCIPAL COMPONENT ANALYSIS OF MAIZE INBRED LINES FOR DROUGHT AND HEAT STRESS CONDITIONS IN SUDAN SAVANNA NIGERIA

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Abstract

This study used principal component analysis to assess the agronomic variability of 64 maize inbred lines under low moisture and heat stress conditions in Nigeria. The study was conducted at Teaching and Research Farm of Aliko Dangote University of Science and Technology, Wudil locations during the 2022 dry season. Principal component analysis showed the first four PCs having Eigen value >1 explaining principal components that accounted for 70.1% of the total variation among the inbred lines. The first three principal components PC1, PC2, and PC3 with values of 44.57%, 15.46% and 12.1% respectively contributed more. Days to 50% Silking, Anthesis Silking Interval, Tassel Blast, Barren Plant and Leaf Death Score. Whereas for PC2 Tassel Blast, Barren Plant and Leaf Death Score plant height, Ear Height and Grain Yield were the most important traits influencing the variability among the inbred lines.

Introduction

Maize (*Zea mays* L.) is one of the most important staple crops in Ethiopia, serving as a vital source of food security and livelihood for millions of people (Shiferaw *et al.*, 2011). However, the productivity of maize is significantly affected by various abiotic stresses, including low moisture conditions (Jemal and Berhanu, 2018). In Nigeria, where the majority of maize cultivation is rainfed, low moisture and high temperature stress poses a major challenge to maize production in several regions (Vido *et al.*, 2019).

Understanding the genetic diversity and population structure of maize inbred lines under low moisture and heat stress conditions is crucial for the development of improved varieties with enhanced drought

and heat tolerance. Principal Component Analysis (PCA) is a powerful tool that can aid in unraveling the genetic variation and relationships among different maize inbred lines.

PCA is a statistical technique that reduces the dimensionality of a dataset while preserving most of its variation. The most important factors or principal components that account for the majority of the genetic variance can be found by using PCA in the genetic data of maize inbred lines (Yang *et al.*, 2011). This approach enables a comprehensive understanding of the underlying genetic structure and relationships among the different inbred lines.

In this study, we aim to investigate the genetic diversity and population

structure of maize inbred lines under low moisture stress areas in Ethiopia using cluster analysis and PCA. By employing these analytical approaches, we seek to identify genetically distinct clusters within the population and determine the key factors contributing to the genetic variation.

The findings from this research will provide valuable insights for maize breeding programs, enabling the development of drought-tolerant maize varieties tailored to the specific low moisture and heat stress conditions in Nigeria. Overall, this study aims to contribute to the advancement of maize breeding efforts in Nigeria, enhancing the resilience and productivity of maize crops under low moisture and heat stress. By understanding the genetic diversity and relationships among maize inbred lines, breeders can make informed decisions to develop improved varieties that address the challenges posed by low moisture and heat stresses, ultimately benefiting maize farmers and ensuring food security in Nigeria.

Additionally, the findings of this manuscript will have practical implications for maize breeding programs and agricultural practices in low moisture and heat stress areas. By identifying genetically diverse maize inbred lines with desirable traits, the paper provides valuable guidance for the development of improved maize varieties that can withstand low moisture coupled with heat stress conditions. This information is crucial for enhancing crop productivity and ensuring food security in regions facing water scarcity more especially when it coincides with high temperature during reproductive stage.

It contributes to the broader field of agricultural research by expanding the knowledge base on maize breeding and adaptation to low moisture and heat stresses. It adds to the limited literature on the genetic diversity of maize inbred lines in Nigeria and provides a valuable reference for future studies in similar environments. The paper's insights can also stimulate further research and collaboration among scientists and

breeders working on maize improvement in low moisture and high temperature production areas.

Materials and methods

The experiment was conducted during the 2022 at Aliko Dangote University of Science and Technology teaching and research field, Wudil Kano Nigeria

64 maize inbred lines were used in this study. These inbred lines were chosen based on their tolerance to low moisture and high heat stress and their potential for yield improvement.

Experimental design and data collection

A Total of 64 inbred lines were planted 8 x 8 alpha lattice design (Patterson and Williams, 1976) with checks as replications and one row plot. The plot length was four (4) meters and 75 x 25 cm spacing between rows and plants used, respectively.

Thinning was done at the three to five leaf stages to attain a final plant density of 53,333 plants ha⁻¹. All management practices including planting, fertilization, weeding, and harvest were as performed as per the recommendations for the location.

Collected data

Ten plants were selected randomly for recording observations of all the quantitative traits except for days to 50 % tasselling and silking. The mean of ten plants for each entry in each replication was worked out for each trait using statistical analysis. The data recording was done for each quantitative trait (Days to 50% Anthesis, Days to 50% silking, Days to Maturity, Plant height (cm), Ear height (cm), Tassel Blast, Baren Plant, Leaf Death Score, Grain Yield (kg/ ha).

Result and discussion

Principal component analysis

Principal Component Analysis analyzes a data table representing observations described by several dependent variables, which are, in general, inter-correlated. Its goal is to extract the important information

from the data table and to express this information as a set of new orthogonal variables called principal components.

According to the principle of Syafi i, *et al.* (2015), the first principal component accounts for maximum variability in the data concerning succeeding components. The principal component analysis showed that the gross variability observed among the 121 test genotypes can be explained with four principal components with eigen values greater than one as shown (Table 1). The first four components together accounted for about 70.1% of the total variation among the genotypes concerning all the 10 traits evaluated and showed the presence of considerable genetic diversity among the genotypes for most of the traits under consideration. Individually, PC1, PC2, PC3 and PC4 in that order accounted for about 44.57%, 15.46%, 12.1%, and 10.07% of the gross variation among the 121 maize genotypes evaluated for 10 traits.

The traits which contributed more to PC1, were Days to 50% silking, Anthesis Silking Interval, Tassel Blast, Barren Plant and Leaf Death Score. Whereas for PC2 Tassel Blast, Barren Plant and Leaf Death Score plant height, Ear Height and Grain Yield, For PC3, Days to 50% Flowering, Days to Maturity, Tassel Blast, Barren Plant and Leaf Death Score plant height, Ear Height and Grain Yield. The first three principal components PC1 PC2 and PC3 with values of 44.57%, 15.46% and 12.1%, respectively contributed more.

The present study confirmed that the Maize genotypes showed significant variations for the characters studied and it

suggested many opportunities for genetic improvement through selection. Similar works have been done by (Bhusal., 2016, Dawit, *et al.* (2012) and (Vol. 2016, Shazia, 2017) for grouping genotypes by principal component analysis

Conclusion

The study on the principal component analysis of maize inbred lines in low moisture and high temperature stress areas in Nigeria aimed to identify distinct groups among the lines and explore relationships among variables. The findings provide insights into genetic diversity and potential drought and heat tolerance of maize inbred lines

Principal Component Analysis (PCA) identified key variables influencing drought and heat tolerance. PCA results revealed relationships between important drought and heat related traits. This study guides breeders in selecting suitable inbred lines for breeding programs, promoting genetically diverse clusters. The research contributes to developing resilient maize varieties, benefiting farmers and enhancing food security. Further research and utilization of identified inbred lines and influential traits are recommended for ongoing maize breeding efforts.

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Table 1 Eigenvectors and eigenvalues of the Twelve principal components of 64 Maize inbred lines evaluated for 10 traits at Aliko Dangote University of Science and Technology, Wudil during 2022 dry season

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
DFE	-0.057	-0.053	0.303	-0.7088	0.3299	0.0218	0.0575	0.0686	0.0199	-0.019	-0.5306	-0.0138
DFS	0.1071	-0.1371	-0.3394	-0.676	-0.1798	-0.089	-0.0364	0.0308	0.0049	0.0373	0.5945	0.0138
ASI	0.1552	-0.0845	-0.5945	-0.0423	-0.4684	-0.1404	-0.1082	-0.0208	0.008	-0.0319	-0.6009	-0.0107
DM	-0.2748	-0.0828	0.3468	-0.0989	-0.3669	-0.1402	-0.3089	-0.7264	-0.03	-0.0955	0.0086	0.0095
TB	0.3197	0.116	0.2569	-0.0576	-0.3729	0.2672	0.2906	0.0043	0.1399	-0.0023	-0.0064	0.0222
BP	0.3197	0.116	0.2569	-0.0576	-0.3729	0.2672	0.2906	0.0043	0.1399	-0.0023	-0.0064	0.0222
LSD	0.3506	0.1126	0.1909	-0.0229	-0.0843	-0.0634	-0.2438	0.142	-0.8582	0.0065	-0.0051	0.0121
PH	-0.1657	0.5741	-0.0331	-0.0723	-0.065	-0.3051	0.1871	-0.0881	-0.0312	0.7032	-0.0319	-0.0093
EH	-0.1097	0.6152	-0.0853	-0.0777	0.0007	-0.2641	0.1818	0.008	-0.0173	-0.7009	0.0399	0.0091
YIELD	-0.3647	0.0874	0.0895	-0.0374	-0.249	0.1498	-0.2616	0.3896	0.0461	0.0146	-0.013	0.7368
Eigenvalue	6.2393	2.1649	1.7234	1.4097	0.8794	0.6338	0.5288	0.2107	0.1323	0.0461	0.0301	0.0015
Cumulative variance explained (%)	44.57	60.03	72.34	82.41	88.69	93.22	96.99	98.5	99.44	99.77	99.99	100
Variance explained (%)	44.57	15.46	12.31	10.07	6.28	4.53	3.78	1.5	0.94	0.33	0.22	0.01
Difference	2.4979	1.4713	1.3128	1.1873	0.9378	0.7961	0.7272	0.459	0.3638	0.2146	0.1736	0.0393

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