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Full-Length Research Paper

Principal Component Analysis in Inbred of Maize (*Zea mays* L.) in a Diallel Cross

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ABSTRACT: The Genetic diversity provides the capacity for plants to meet changing environments. Multivariate analysis is the most popular approach for genetic variability estimation to study patterns of variation and their genetic relationships. The objectives of the study were: (i) To assess the extent of genetic diversity in maize through Principle Component Analysis (PCA), (ii) To assess the relationship between grain yield and yield related traits of maize genotypes. Maize inbred lines were crossed in a full diallel fashion producing twenty hybrids. The hybrids and the inbred parents were evaluated in a randomized complete block design (RCBD) replicated 3 times in 2 locations *viz*: in the ATBU Research Farm and in the farmers' field in Misau as well in the Bauchi state in the 2019 rainy season. The PCA revealed that, 5 vectors accounted for 88.40 % and 90.30 % of the total variability produced by all the traits under study in Bauchi and Misau, respectively. The first canonical vector PCI accounted for 38.90 % and 40.80 % of the total variability followed by second vector PCII which accounted for 22.30 % and 21.90 % of total variability in Bauchi and Misau, respectively. On the other hand, the third vector PCIII accounted for 16.10 % and 18.40 % of the total variance while PCIV and PCV accounted for 6.00 %, 5.30 % and 5.20 %, 3.80 % of the total variability in Bauchi and Misau, respectively. Days to 50% tasseling, days to 50 % silking, anthesis silking interval, cob diameter, cob length followed by cob weight/plant, number of ear/plant, kernel weight/plant and yield/plant in that order are the major contributors to the total divergence suggesting their importance in maize improvement. Attention should be given to days to 50 % tasseling, days to 50% silking, anthesis silking interval, cob diameter, cob length in the improvement of maize by breeders and geneticists and that the traits mentioned correlated positively with grain yield and therefore need to be given due consideration in grain yield improvement.

Keywords: Maize, PCA, Diallel, Vector, Multivariate

INTRODUCTION

Maize (*Zea mays* L.) is an important cereal crop of the family *Poaceae* that belongs to the tribe *Maydeae*. The plant is native to South America. Worldwide maize is the most important cereal food crop after wheat and rice accounting for 9 % of the total food grain production. It has occupied a prominent place in Nigerian agriculture as it is widely grown in varied climatic situations throughout the year suggesting its wider adaptability Sandeep *et al.,* (2017). Nigeria in 2018 grew 4853349-hectare maize and produced about 10.155 million tons of grains; with an average yield of 2092 kg/ha FAOSTAT (2020). It is consumed as food by humans and as a feed for the livestock and poultry. It is also used as basic raw materials in numerous industrial products including starch, oil, protein, alcoholic beverages, food sweeteners, pharmaceuticals, cosmetics, films, textiles, gums, packages, paper industries and so on (Avinash and Mishra, 2016). Maize has high nutritive value as it contains 72% starch, 10% protein, 4.80% oil, 8.50% fiber, 30% sugar and 1.70% ash (Mustafa *et al.,* 2014).

The major objective of any maize breeding programmes is to develop high yielding hybrids than the existing cultivars as hybrids are popular among the farming community for their yield advantage over others. To develop high yielding hybrid s in maize, the development and evaluation of inbreds form major thrust area of plant breeding programmes. Hence, inbred lines developed through sib mating need to be evaluated for their genetic diversity and performance to plan an effective hybrid breeding programme as genetically diverse parents are known to produce high heterotic effects. Evaluation, characterization and classification of genotypes based on estimates of genetic diversity will help to identify diverse parental lines which can be used in hybrid breeding to develop potential hybrids or varieties. Several methods have been reported to decipher the pattern and magnitude of variability such as Mahalanobis D2 analysis, Principal Component Analysis and hierarchical cluster analysis based on Ward's minimum variance method (Mounika and Mishra, 2018). Multivariate analysis is the most popular approach for genetic variability estimation to study the patterns of variation and their genetic relationships among germplasm collections to enhance their use in crop breeding (Ahmed *et al.,* 2020). The PCA and cluster analysis is better utilized for studying the diversity among the genotypes in various crops. In view of the aforementioned, 5 inbred lines were used to study the nature and magnitude of genetic divergence for grain yield and its component traits to provide a basis for selection of parents in hybridization programme in maize hybridization program (Solanke *et al.,* 2013). Many researchers have used principal component analysis to assess genetic variability among maize genotypes because it retrieves small numbers of components that account for most of the variations in the data (Asare *et al.,* 2016). The aim of the study is to deduce the trait(s) in maize that should preferentially considered in maize breeding program improvement. The objectives of the study were: (i) To assess the extent of genetic diversity in maize through Principle Component Analysis, (ii) To assess the relationship between grain yield and yield related traits of maize genotypes.

MATERIALS AND METHODS

The nursery was conducted at the Abubakar Tafawa Balewa University Bauchi Experimental Farm with on latitude 10.31° and longitude 9.85° at an altitude of 628 m above sea level in the 2018 rainy season. Maize inbred lines (OBATANPA 14, SAMAZ 15, SAMAZ 16, SAMAZ 32, and SAMAZ 33) obtained from the International Institute for Tropical Agriculture (IITA) was crossed in a diallel fashion (Table 1).

Maize is a diclinous plant because it has separate male and female flowers (efflorescence) and it is also monoecious crop because it has both the male and female flowers on same plant. The male efflorescence that produce the pollen or male gametic cells are formed at the apex or tip of the plant borne on a structure known as tassel where anthers are borne. The tassel begins to produce pollen immediately it blooms and normally the pollen is dispersed by wind to aid cross pollination. The female efflorescence that produce the kernel are produce at the side of the plant on a structure called the ear which is having long special stigmas on a style called the silk where each silk leads to a single ovary that grows from individual maize kernel.

Controlled crossing was achieved using parchment paper bags, stapler, marker, small knife and small white glossy bags. The inbred lines of SAMAZ 14, SAMAZ 15 and SAMAZ 16 were sown on June 26th, 2018 after proper soil tillage with inter and intra row spacing of 75 × 75 cm. The planting pattern were oriented so that particular cross can be obtained in a specific plot having the male intended plants on the outer row with the female intended plants occupied the inner rows. On July 10th SAMAZ 32 and SAMAZ 33 were stagger planted or sown 15 days after to allow for nicking to take place. The nursery was well spaced to allow for proper observation as well as ease of pollination.

After emergence of the ear and before silk emergence, the ears were covered. Blooming started in tassels near the tip of the central axils and it produces downward. It takes nearly 14 days to complete. The pollen grains become viable for 24 h when mature. The male efflorescence that produces the pollen was covered with brown envelopes that were well labeled. The opening of the inverted envelopes was then folded and stapled to prevent pollen from falling off. The glossy bags were slipped to cover the entire ear and fixed firmly in-between the ear and the stem. In cases where the silk took too long to emerge, the tips of the ear husks were cut to accelerate silk emergence. After making sure of silk emergence, pollens were collected from particular plant tassels that were covered a day before with brown envelopes by bending the stems of the plants with covered tassels and gently taping the envelopes to drop pollen.

The envelopes were gently removed in erect position to prevent pollen from falling. The envelopes containing the pollen were then taken to appropriate plants where the pollens are dusted on the silks (receptive stigmas) after the glossy white bags covering the ear were removed. Immediately after dusting, the ears were covered with the envelopes that conveyed pollen to allow for fertilization to take place without contamination by unknown pollen.

Table 1: Inbred lines, their traits and source.

Maize inbred line	Features of inbred lines	Source
OBATANPA14	white kernel, quality protein (QPM) maize, medium maturing (110 days),yield potential 3 to 4.5 tone/hectare	International Institute for Tropical Agriculture (IITA)
SAMAZ15	White normal kernel, tolerant to *Striga hermonthica*, medium maturing (110 days), yield potential 6.9 tone/hectare	International Institute for Tropical Agriculture (IITA)
SAMAZ16	White normal kernel, tolerant to *Striga hermonthica*, late maturing (120 days),yield potential 6.4 tone/hectare	International Institute for Tropical Agriculture (IITA)
SAMAZ32	Yellow seeded kernel, extra early, drought tolerant, yield potential 3-4 tone/hectare	International Institute for Tropical Agriculture (IITA)
SAMAZ33	White seeded kernel, extra early, drought tolerant, quality protein maize (QPM) yield potential 3-4 tone/hectare	International Institute for Tropical Agriculture (IITA)

After maturing, the kernels from each cross were harvested separately where they were manually threshed and stored in a cool dry place. A total of 20 hybrids were produced from 5 parents that were evaluated at the following season.

Evaluation of the trial was conducted in 2 locations in Sudan savannah zone of Nigeria i.e. Abubakar Tafawa Balewa University Bauchi, Experimental Farm and Misau Farmers Training Field at Kukadi, in 2019 rainy season. The 25 treatments were laid out in a randomized complete block design (RCBD) replicated 3 times. The seeds were sown manually by hand on the July 10th, 2019 in Bauchi and on July 17th, 2019 in Misau and after germination were thinned to 2 plants per hill, at 2 weeks after sowing. Any hill that did not have plants was gap-filled during the first weeding. The plot consisted of 4 ridges 3 m long and 75 cm apart, interplant spacing on the rows were 50 cm having 7 ridges with a plot length of 3.5 m. Each sub plot had an area of 10.50 m^2.

Ten plants were tagged from internal rows for recording observations for each entry/plot for all the quantitative characters except for days to 50 % tasseling, silking and anthesis silking interval. Mean of the 10 plants for each entry in each replication was computed for each character and used for statistical analysis. Observations on the following quantitative characters days to 50% tasseling, days to 50% silking, anthesis silking interval, number of tassel branch, number of ears per plant, number of days to maturity, cob weight per plant, number of rows/ear, number of kernel/row, cob length, cob diameter, 100 seed weight, kernel weight/ear, kernel weight/plant and yield/hectare were recorded at the appropriate stages of plant growth.

The set of data collected were subjected to a multivariate analysis specifically principal component analysis. Principal component analysis is a mathematical procedure that transforms a large number of possibly correlated variables into a smaller number of uncorrelated variables called the principal component. To compute for principal component from large different sets of data is simply the Eigen decomposition of covariance or correlation matrix.

Covariance (COV x, y) = $\frac{1}{n}\sum_{i=1}^{n}(X_i-\bar{X})(Y_i-\bar{Y})$

Correlation (rxy) = $\frac{\sum_{i=1}^{n}(X_i-\bar{X})(Y_i-\bar{Y})}{\sum_{i=1}^{n}\sqrt{(X_i-\bar{X})^2(Y_i-\bar{Y})^2}}$

Entries were fed in a matrix format to produce covariance matrix or correlation matrix. Eigen values and Eigenvectors was computed from the covariance or correlation matrix, state as follows

$A\bar{v} = \lambda\bar{v}$, $A\bar{v} - \lambda I\bar{v} = 0$, $(A - \lambda I)\bar{v} = 0$, $\det(A - \lambda I) = 0$

Where, A = is a covariance matrix, λ = is the Eigen value, $\bar{v}$ = is the eigenvector, I = identity matrix. The Eigen values and the eigenvectors give the foundation of PCA or by matrix method which is the products of a transpose of a matrix and the matrix itself.

Covariance Matrix = $X^T X$, Where; X = is a set of matrix of data, and $X^T =$ is the transpose of Matrix X

RESULTS AND DISCUSSION

The principal component analysis result for the 15 traits in Bauchi presented in (Table 2) were the Eigen values, % variance, % cumulative variance and factor loading of different traits are given. In canonical variant analysis, the number of variable is produce to linear function called canonical vector which account for most of the variation produce by these characters. The 5 vectors accounted for 88.40 % to the total variability produced by all maize

Table 2: Principal component analysis for 15 traits in Bauchi 2019.

Eigen components (EC)	**ECI**	**ECII**	**ECIII**	**ECIV**	**ECV**
Eigenvalue	5.835	3.342	2.411	0.896	0.7 75
Proportion	0.389	0.223	0.161	0.060	0.052
Cumulative	0.389	0.612	0.773	0.832	0.884
Principal components (PC) Variable	**PCI**	**PCII**	**PCIII**	**PCIV**	**PCV**
Days to 50 % tasseling	0.275	-0.117	0.338	0.080	-0.486
Days to 50 % silking	0.309	-0.141	0.308	0.050	-0.394
Anthesis silking interval	0.345	-0.191	0.100	-0.078	0.075
Number of tassel branch	0.178	-0.287	0.090	-0.411	-0.107
Number of ears/plant	0.155	0.289	0.396	-0.142	0.409
Number of days to maturity	0.251	-0.131	0.261	0.133	0.423
Cob weight/plant	0.278	0.392	0.025	-0.174	0.047
Number of rows/ear	0.216	-0.347	-0.231	-0.110	0.259
Number of kernels/row	0.216	-0.251	-0.286	0.096	0.315
Cob length	0.199	0.138	0.037	0.819	0.048
Cob diameter	0.346	-0.231	-0.072	0.057	0.038
100 seed weight	0.255	-0.009	-0.427	-0.044	-0.136
Kernel weight/ear	0.208	0.185	-0.462	0.076	-0.232
Kernel weight/plant	0.278	0.390	-0.069	-0.152	0.004
Yield/ha	0.278	0.390	-0.069	-0.152	0.004

genotypes for yield. The results indicated that all the traits showed positive loading on PCI which contributed to 38.9 % of the total variation having an Eigen value of 5.8349 with the highest loadings coming from days to 50% tasseling, anthesis silking interval and cob diameter with values of 0.309, 0.345 and 0.346, respectively. The least contribution came from number of ear/plant with value of 0.155. The PCII which contributed to 22.30% of the total variability with Eigen value of 3.3421 showed maximum positive loadings on cob weight/plant (0.392), number of ears/plant (0.289), kernel weight/plant (0.390) and yield/ha (0.390), while number of tassel branch (-0.287), number of rows/ear (-0.347), number of kernels/row (-0.231) had the higher negative values. The PCIII which contributed to 16.10 % of total variability with an Eigen value of 2.411 showed maximum positive loadings on days to 50 % tasseling, days to 50 % silking and number of ears/plant, with the corresponding values of 0.338, 0.308 and 0.396, respectively with the highest negative values on 100 seed weight (-0.427) and kernel weight/ear (-0.462). The PCIV which contributed to 8.32% of the total variability with an Eigen value of 0.8957 showed maximum positive loadings on cob length (0.819), with the least value of -0.411 from number of tassels/branch. The PCV which contributed to 5.20% of the total variability with an Eigen value of 0.7747 showed maximum positive loadings on number of ears/plant, number of days to maturity and number of kernels/row with loading factors of 0.409, 0.423 and 0.315, respectively with the least values of -0.486, and -0.394, for 50 % tasseling and days to 50 % silking, respectively.

The principal component analysis result for the 15 traits in Misau in (Table 3) indicated that Eigen value, % variance, % cumulative variance and factor loading of different traits. In canonical variant analysis, the number of variable was produced to linear function called canonical vector which accounted for most of the variation among traits. Vectors accounted for 90.30 % of total variability produced by all the genotypes for yield. The results indicated that all the traits showed positive loading on PCI which contributed to 40.80 % of the total variation having an Eigen value of 6.1247 with the highest loadings coming from days to 50% tasseling, days to 50 % silking, anthesis silking interval, cob length and cob diameter with values of 0.329, 0.321, 0.339 and 0.340, respectively. The least contribution came from number of ears/plant and 100 seeds weight with 0.161 and 0.167, respectively. Principal component 2 which contributed to 21.90 % of the total variability with an Eigen value of 3.2907 showed maximum positive loadings on number of ears/plant (0.369), cob weight/plant (0.456) while number of tassel branch (-0.209) and number of rows/ear (-0.282) had higher negative values.

Principal component 3 which contributed to 18.4% of total days to 50 % tasseling variability with an Eigen value of 2.7626 showed maximum positive loadings on cob length, kernels/row, and number of rows/ear with values of 0.200, 0.251 and 0.195. PCIV on the other hand contributed to 5.30% of the total variability with an Eigen value of 0.7997 had maximum positive loadings on 100 seeds weight, number of days to maturity, number of tassel branch and anthesis silking interval, with corresponding values of 0.235, 0.242, 0.231 and 0.0.247 with the least value of -0.506 from kernels/row. PCV contributed to 3.80% of total variability with an Eigen

Table 3: Principal Component Analysis for 15 traits in Kukadi 2019.

Eigen components (EC)	**ECI**	**ECII**	**ECIII**	**ECIV**	**ECV**
Eigenvalue	6.1247	3.2907	2.7626	0.7997	0.5722
Proportion	0.408	0.219	0.184	0.053	0.038
Cumulative	0.408	0.628	0.812	0.865	0.903
Principal components (PC) Variable	**PCI**	**PCII**	**PCIII**	**PCIV**	**PCV**
Days to 50% tasseling	0.329	-0.102	-0.262	0.107	-0.131
Days to 50% silking	0.321	-0.054	-0.273	0.104	-0.207
Anthesis silking interval	0.339	-0.129	-0.160	0.247	0.180
Number of tassel branch	0.264	-0.209	-0.130	0.231	0.721
Number of ear/plant	0.161	0.369	-0.288	-0.387	-0.016
Number of days to maturity	0.261	-0.015	-0.284	0.242	-0.258
Cob weight/plant	0.222	0.456	0.013	-0.021	0.060
Number of row/ear	0.261	-0.282	0.195	-0.326	-0.062
Number of kernel/row	0.211	-0.150	0.251	-0.506	0.373
Cob length	0.317	-0.168	0.200	-0.203	-0.344
Cob diameter	0.340	-0.164	0.126	-0.071	-0.164
100 seed weight	0.167	-0.011	0.478	0.235	-0.119
Kernel weight/ear	0.091	0.136	0.494	0.436	0.000
Kernel weight/plant	0.218	0.451	0.102	-0.019	0.085
Yield/ha	0.218	0.451	0.102	-0.019	0.085

value of 0.5722 showing maximum positive loadings on kernels/row and number of tassel branch with values of 0.373 and 0.721, respectively, while the least values are -0.344, -0.258 and -0.207 for cob length, number of days to maturity and days to 50% silking

Agro-morphological diversity was the outcome of several factors along with a factor geographic diversity, the results of this research showed the same pattern in Eigen component as well as factor loadings for the characters between the 2 locations (Bauchi and Misau), this indicated that the diversity noticed is as a result of genetic diversity. Hence, selection for hybridization should be more based on genetic diversity than geographic diversity. The Principal Component Analysis sorted out the total characters into 5 main principal components. By PCA, the in-depth analysis for genetic diversity can be made. Principal Components revealed characters viz., days to 50 % tasseling, anthesis silking interval and cob diameter in PCI and cob weight/plant, number of ears/plant, kernels weight/plant and yield/ha were loaded in PCII, while days to 50 % tasseling, days to 50 % silking and number of ear/plant in PCIII, the characters mentioned instantly contributed more towards variability and thus, the characters should be given more attention in selection for hybridization. The contribution of the main characters for variance easily identified by the characters loaded on PC1 as it explained maximum variance are therefore, first and foremost considered in selection for hybridization followed in accordance by characters in the other vectors. In the present study, principal component analysis revealed that days to 50% tasseling, days to 50% silking, anthesis silking interval, cob diameter, cob weight/plant, number of ears/plant, and kernels weight/plant are the major contributors to the total divergence therefore, the characters easily affect maize yield positively and thus, the characters can be utilized in breeding programs. The results of principal components analysis corroborated with results obtained by Ahmed *et al.,* (2020), Hafiz *et al.,* (2015) Sandeep *et al.,* (2017)*,* Solanke *et al.,* (2013) and Worknesh *et al.,* (2019).

All the characters under the study positively correlated with yield in the first principal component this deduce that all the characters under the study are yield related characters. It was observed that days to 50 % tasseling, days to 50% silking, anthesis silking interval, cob diameter, cob weight/plant, number of ears/plant, and kernels weight/plant were identified as the mostly correlated characters with grain yield in all environments this deduce that the characters can be use simultaneously in a maize breeding program for yield improvement. This finding is in accordance with the result of Ahmed *et al.,* (2020). Morpho-agronomic characters, days to 50 % tasseling, days to 50% silking, anthesis silking interval, cob diameter, cob weight/plant, number of ears/plant, and kernels weight/plant that had high values in the first 5 components indicated their importance as maize descriptors and could be helpful for differentiation and characterization of maize genotypes. Overall, PCA enable to recognize the most crucial traits viz. according to their importance in breeding program to improve grain yield as follows days to 50 % tasseling, days to 50 % silking, anthesis silking interval, cob diameter, cob weight/plant, number of ears/plant, and kernels weight/plant, respectively for classifying the variability within the genotypes. This outcome is in accordance to the findings of Khodarahmpour and

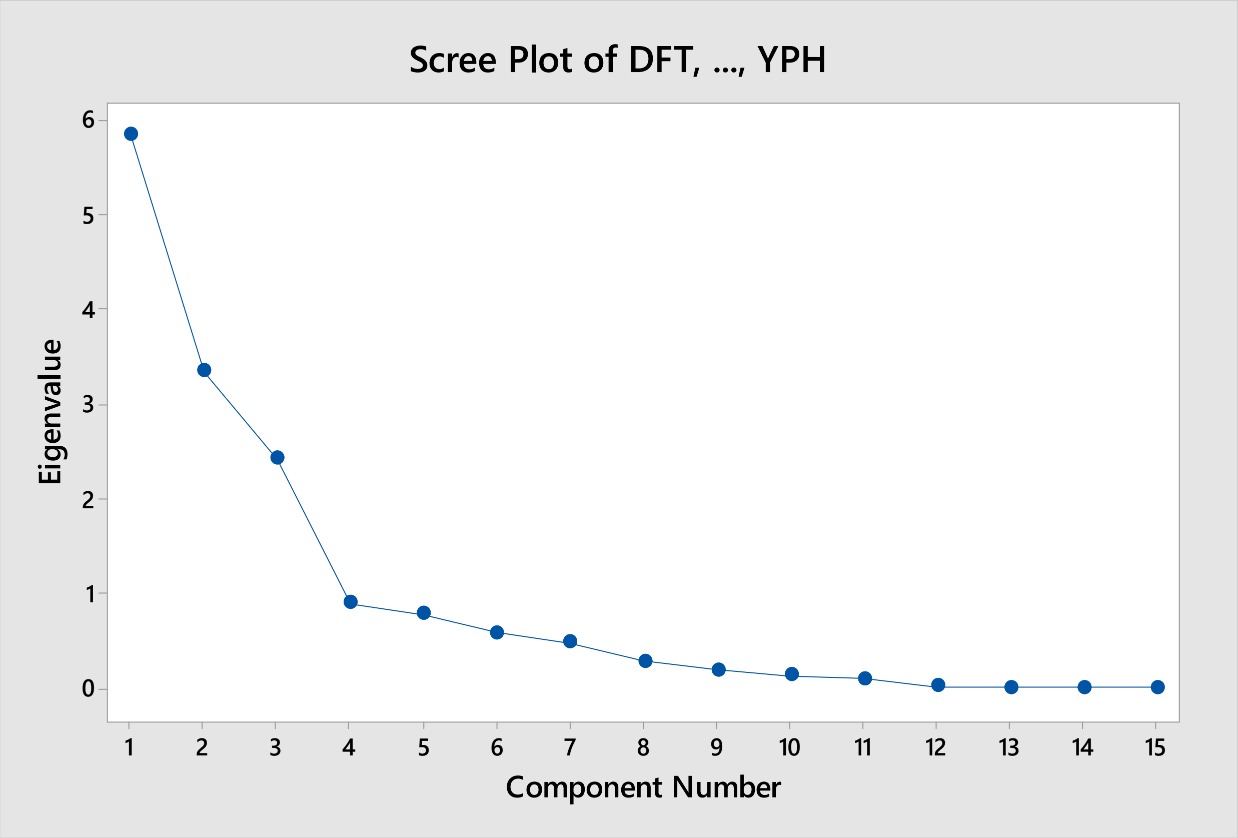

Figure 1: Screen plot for 15 traits in principal component analysis Bauchi location.
DFT = Days to 50 % tasseling
DFS = Days to 50 % silking
ASI = Anthesis silking interval
NTB = Number of tassel branch
NEPP = Number of ears/plant
NDM = Number of days to maturity
CWPP = Cob weight/plant
NRPE = Number of rows/ear
NKPR = Number of kernels/row
CLT = Cob length

Hamidi (2012), Hafiz *et al.,* (2015), Solanke *et al.,* (2013) and Worknesh *et al.,* (2019).

Figures 1 and 2 reveals the graph of screen plot plotted for Eigen values on vertical axis against principal component number the graph indicated sharp decline in Eigen values from principal components one (PCI) to principal component 5 (PCV) accounted for 88.40 % and 90.30 % of the total decline on Bauchi and Misau locations, respectively on (Figures 1 and 2) accordingly. Thus, is sufficiently enough to explain quick and immediate level of change in the diversity of the traits. The vector loadings ranging from PCI – PCV is therefore sufficient and significantly enough to explain the diversity of the different traits. The graphs show the magnitude of change in diversity loaded on the various principal components which provided the level of magnitude in the principal component that sufficiently explain the diversity.

Figures 3 and 4 are the graphs of factor loadings for the traits under the study with PCII on vertical axis and PCI on horizontal axis indicated the magnitude and direction to which each trait contributed to on either positive or negative variable loadings on PCI and PCII which explain 61.20 % and 62.80 % of the total magnitude of the diversity loaded by the traits under the study. All the traits under the study loaded on to positive direction on PCI in both locations with the highest magnitude of 38.90 % and 40.80 %, respectively. The graph of plot loadings for the traits identifies the importance of characters' number of ears/plant, kernel weight per ear, cob weight per plant, and kernel

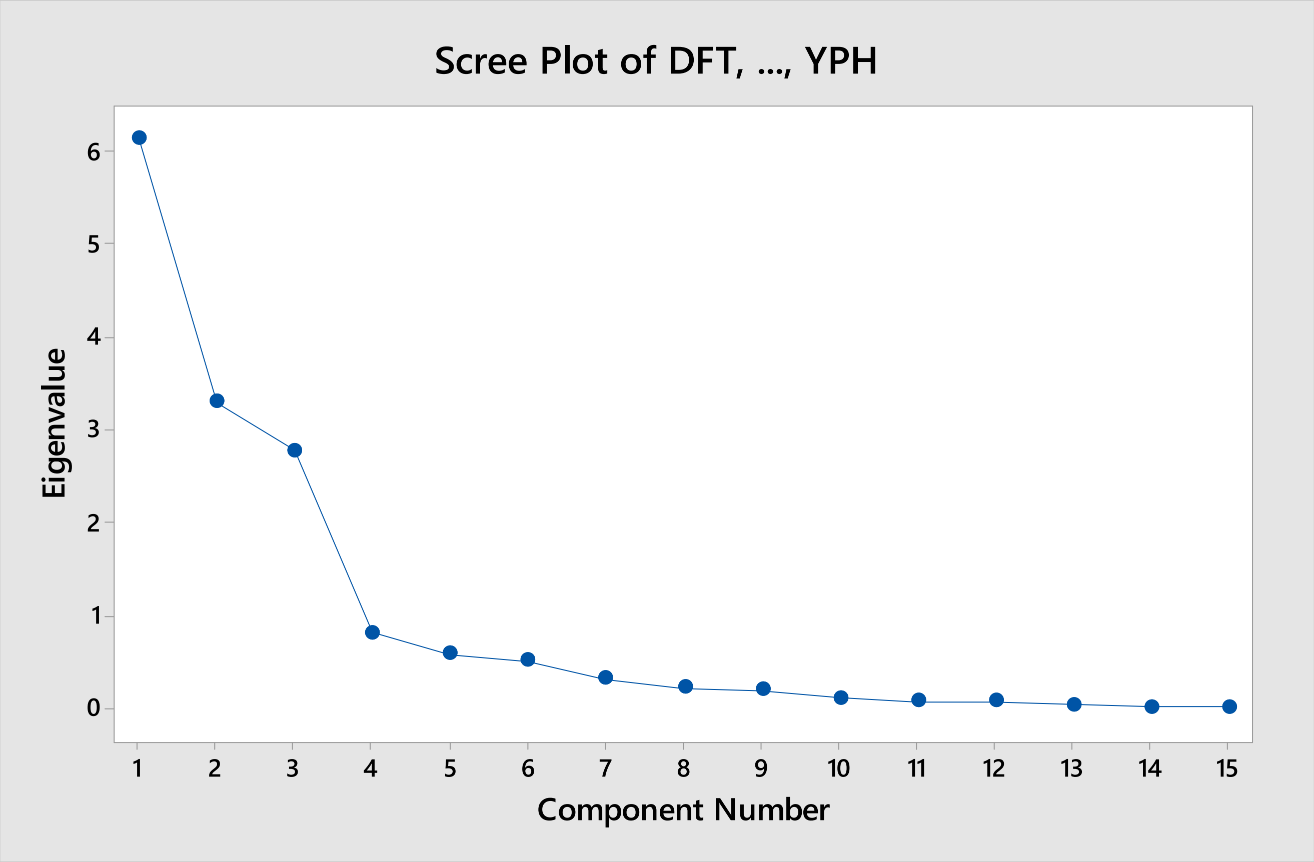

Figure 2: Screen plot for 15 traits in principal component analysis Bauchi location
DFT = Days to 50 % tasseling
DFS = Days to 50 % silking
ASI = Anthesis silking interval
NTB = Number of tassel branch
NEPP = Number of ears/plant
NDM = Number of days to maturity
CWPP = Cob weight/plant
NRPE = Number of rows/ear
NKPR = Number of kernels/row
CLT = Cob length
CDM = Cob diameter
100SW = 100 seed weight
KWPE = Kernel weight/ear
KWPP= Kernel weight/plant
YHP = Yield/ha

weight/plant as they load in positive direction on PCI and PCII axis together with yield/hectare in both locations. Principal component II on vertical axis indicated negative loadings for all the traits under the study except for number of ears per plant, cob weight per plant, cob length, kernels weight per ear, kernels weight per plant and grain yield of the 2 locations. The loading plot graph indicated the magnitude and direction of the various traits under the study thus, revealed the use fullness of number of ears/plant, cob weight/plant, cob length, kernels weight/ear, kernels weight/plant as preferred traits in yield improvement as they positive correlated with yield on the factor loadings of both PCI and PCII with the highest loadings revealed by kernels weight/ear and kernels weight/plant been the most important traits to be considered by breeders and geneticist in the improvement of grain yield in maize breeding program. The results of principal components analysis

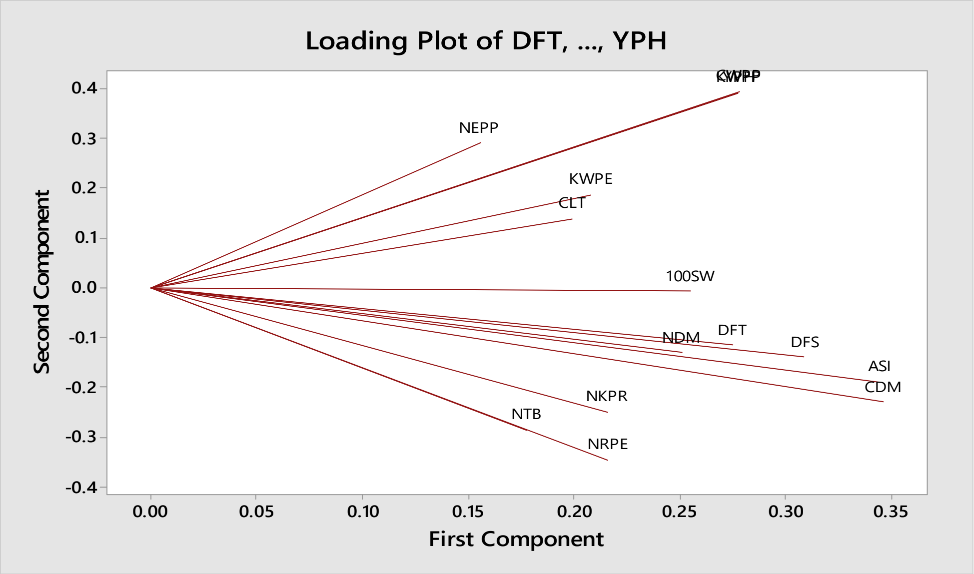

Figure 3: Loading plot for 15 traits on PCI and PCII Bauchi location

DFT = Day to 50 % tasseling
DFS = Day to 50 % silking
ASI = Anthesis silking interval
NTB = Number of tassel branch
NEPP = Number of ears/plant
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KWPP= Kernel weight/plant
YHP = Yield/ha

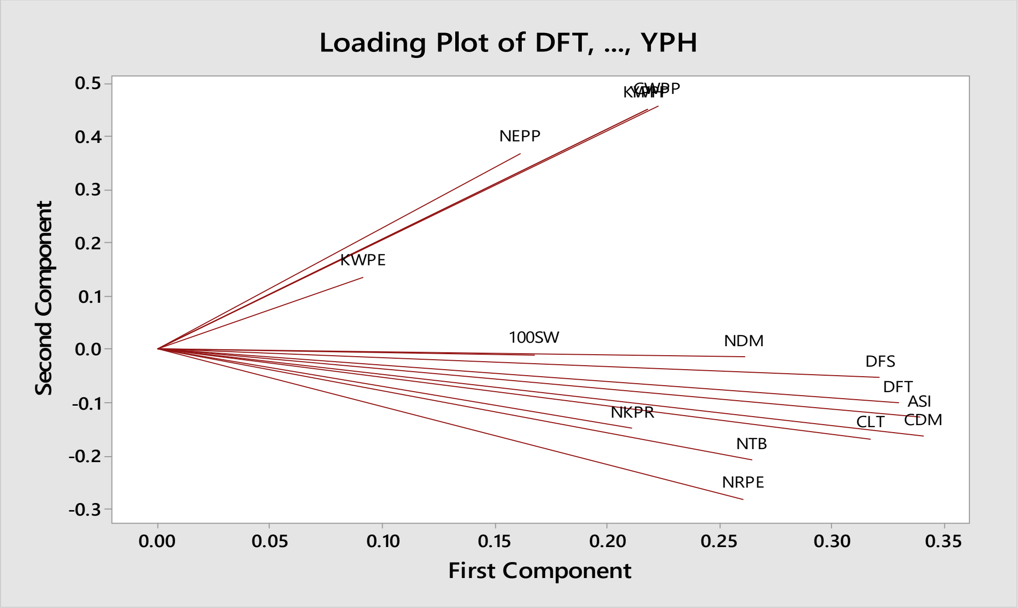

Figure 4: Loading plot for 15 traits on PCI and PCII Misau location

DFT = Day to 50 % tasseling
DFS = Day to 50 % silking
ASI = Anthesis silking interval
NTB = Number of tassel branch
NEPP = Number of ears/plant
NDM = Number of days to maturity
CWPP = Cob weight/plant
NRPE = Number of rows/ear
NKPR = Number of kernels/row
CLT = Cob length
CDM = Cob diameter
100SW = 100 seed weight
KWPE = Kernel weight/ear
KWPP= Kernel weight/plant
YHP = Yield/ha

corroborated with results obtained by Ahmed *et al.,* (2020)*,* Hafiz *et al.,* (2015)*,* Sandeep *et al.,* (2017) and Solanke *et al.,* (2013)*.*

Conclusion

The results indicated that the characters' days to 50 % tasseling, days to 50% silking, anthesis silking interval, cob diameter, cob length showed the maximum positive contribution to the divergence on PCI in both locations followed by cob weight/plant, number of ears/plant, kernel weight/plant and yield/plant are major contributors to the total divergence on PCII having the maximum positive contribution. PCIII had 100 seed weight and kernels weight, ears with the maximum positive contribution suggesting their importance in maize improvement. The traits were also found to positively contribute to diversity as reported by Hafiz *et al.,* (2015), Manoj *et al.,* (2017) and Worknesh *et al.,* (2019). Positive correlations existed among the traits to up to 38.90 % and 40.80 % in both locations. This therefore, means that improvement in one of the traits can bring about improvement of other traits and that the traits can be simultaneously improved with 40.80 and 38.90 % success. Number of ears/plant, cob weight/plant, kernels weight/plant, kernel weight/ear, cob length and yield/ha positively correlate up to 81.20 %. This study identified the importance of traits like days to 50 % tasseling, days to 50 % silking, anthesis silking interval, cob diameter, cob length that can be beneficial for the improvement of grain yield in maize by breeders and geneticists. These traits need to be given due consideration in maize breeding programs targeted for grain yield. Also, this study will help breeders and geneticists to uncover the critical traits in maize which contribute positively and most significantly to grain yield in northern guinea and Sudan savanna of Nigeria.

Disclosure of conflict of interest

None

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