

PHENOTYPIC DIVERSITY ANALYSIS OF MAIZE INBRED LINES USING PRINCIPAL COMPONENT ANALYSIS

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(Received 28 April, 2021; Accepted 17 June, 2021)

Key words : Principal component analysis (PCA), Cluster analysis, ANOVA, Inbred lines, PCA Biplot

Abstract– In the current study, thirty maize inbred lines were evaluated for various morphological traits and phenotypic diversity was estimated based on these traits using the Principal Component Analysis. The trial was carried out with thirty maize inbred lines and three replications laid in RCBD design. Analysis of variance showed that all the traits are significantly varied among the maize lines and the maize line, MGC 137 was found to be the best in terms yield and yield related attributes. The first two components of PCA, PC1 (39.87) and PC2 (21.26) explained the maximum variation with Eigen values of 4.39 and 2.34, respectively. The PCA biplot did not differentiate the maize lines into prominent groups except the lines, PFSR 49 and MGC 137, which lied far away from the other lines. The research concludes that prominent morphological variation exists among the maize germplasm and can be utilized for maize breeding.

INTRODUCTION

Maize is termed as the queen of cereal crops and is the third most popular cereals grown all over the world after wheat, and rice (Dass, 2012). It is exploited for various purposes such as animal feed, human food and for a large number of many other industrial products like oil, starch, glucose etc, (Ranum *et al.*, 2014). India is one of the leading corn-producing countries in the world. Production of maize has increased drastically over the last few years and a major breakthrough was noticed at the beginning of the 21st century with the development of new hybrids (Ali *et al.*, 2020)

Estimation of phenotypic and genetic variation among the germplasm is the initial step in maize breeding. Extraction of the maximum genetic variation present in germplasm depends upon the different biometrical techniques used for its estimation and different morphological and physiological traits used for variability estimation (Bajracharya *et al.*, 2006). Diversity studies based on principal component analysis (PCA), Mahalanobis's D2 statistics (MDS), and principal coordinate analysis (PCoA) are some of the most popular

methods used to evaluate genetic and phenotypic diversity among the germplasm (Brown-Guedira *et al.*, 2000). Several authors suggested principal component analysis (PCA) as one of the best biometrical methods for the clustering process (Mujaju and Chakauya, 2008). Hierarchical cluster analysis is also one of the key multivariate analysis methods that have been suggested for the division of germplasm collections into multiple groups based on the degree of similarity and dissimilarity. A combination of PCA and Hierarchical cluster method was used by Kandel *et al.*, 2018 to categorise maize (*Zea mays* L.) accessions. Several scientific investigations have reported comparing the cluster analysis algorithms, including those used for classification of germplasm collections (Peeters and Martinelli, 1989), and classification of maize inbreds (Mumm and Dudley, 1994).

Among these biometrical procedures, the main advantage of principal component analysis (PCA) is that each genotype can be assigned to only one group and it also reflects the significance of the largest contributor to the total variability at each axis of differentiation (Sharma, 1998). Genetic variation for morphological traits has been estimated using

principal component analysis, which differentiated the maize inbred lines into various groups. (Esmail *et al.*, 2008; Li *et al.*, 2008). The purpose of the present study was to evaluate the morphological diversity among maize inbred lines using Principal Component Analysis. This is expected to divide the maize lines into different groups and this research can be used in future breeding programmes.

MATERIALS AND METHODS

The experiment was conducted during Rabi (2020 – 21) at Seed Research and Technology Center, PJTS Agriculture University Hyderabad. Thirty Maize inbred lines developed at Maize Research Centre (MRC), PJTSAU were sowed in the month of November in RCBD design with three replications. All the agronomic practices were followed as per recommendations for a healthy crop. Ten plants were randomly tagged before flowering and quantitative traits were phenotyped for those ten plants at different stages of the crop growth in all three replications.

The statistical analysis of data was done using “R” software. A mixed model analysis of the raw data was performed to analyse the different effects underlying the data. The quantitative traits were subjected to mixed model analysis by following the Restricted Maximum Likelihood (REML) method with the help of the “lme4” package (Bates and Maechler, 2010). The model was run by using the “lmerTest ()” function, and ANOVA was performed by using the Kenward-Roger degrees of freedom approximation method. Marginal means were computed and used for PCA. Principal Component Analysis (PCA) was performed by using the “FactoMineR” package (Husson *et al.*, 2020). The model used for mixed model analysis is presented below. The Normal distribution test was performed on the raw data by using the Shapiro-Wilk normality test (Shapiro and Wilk, 1965). A heterogeneity test was performed by Levene’s test of heterogeneity.

$$Y_{ij} = \mu + G_i + B_j \quad (6)$$

Y_{ij} = observed value of the i_{th} entry in J_{th} block

μ = general effect

G_i = effect of the i_{th} entry

B_j = effect of the j_{th} block (block as a random effect)

RESULTS AND DISCUSSION

The present research was conducted to evaluate the variation and diversity that existed among the maize

inbred lines. All the traits were following normal distribution and satisfying the heterogeneity condition. Wide variation was noticed among the quantitative traits of maize inbred lines. Analysis of variance was carried out to partition the variances into their components. The analysis of variance showed that the variation among maize lines was significant for all the traits. The variation among the blocks was found to be non-significant in all the quantitative traits phenol typed. The mean squares and other descriptive statistics of the traits are presented in Table No 1. Among the tested inbred lines, PFSR 135 flowered earlier than others (days to tasseling – 69, days to silking – 71) whereas PFSR 32 and MGC 7 flowered late (days to tasseling – 77, days to silking – 79). Days to anthesis was more than expected in all the genotypes due to low temperatures during the growing season. Plant height was found to be highest in PFSR 90 (171cm) while the ear length is the highest in MGC 137 (14.4 cm). The number of rows per cob and number of kernels per row was

Table 1. Mean sum of squares (treatment, block, and error), Mean, CV% and Range of the quantitative traits of maize inbred lines.

	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of rows per cob	Number of kernels per row	10 cob yield (Kg)	10 cob grain yield (Kg)	100 Seed weight (gm)
Treatment	11.6	12.4	592.5	195.9	5.5	0.17	7.07	12.1	0.02	0.01	22.68
Block	4.03	6.07	29.30	261.0	3.7	0.04	0.04	18.4	0.01	0.01	5.62
Error	2.61	2.35	82.7	44.17	0.62	0.01	0.55	1.44	0.00	0.00	1.77
Mean	73	75	152.3	68.69	13.12	3.53	12	22.65	0.70	0.55	23.33
CV %	2.19	2.03	5.97	9.67	6.0	3.08	6.27	5.30	5.53	6.53	5.71
Range	69-78	71-79	120.4-171.3	52.7-79.8	11.15-14.40	3.25-4.0	10-16	21-29	0.60-1.03	0.42-0.79	17.3-27.97

recorded as the highest in MGC 137 (29) and PFSR 104 (42), respectively. The overall performance was found to be best in the inbred line, MGC 137. The 10-cob yield and 10-grain yield was found to be 1.03 Kg and 0.79 Kg in the entry MGC 137. This kind of variation among the maize inbreds is in alignment with the studies performed by Bhadru *et al.*, 2020. Such a prominent variation among the tested maize lines is accounted to its genetic variation and environmental factors (Shrestha, 2016). For the development of high yielding maize hybrids, such significant phenotypic variation is essential.

Principal Component Analysis

The phenotypic diversity was analysed on the morphological traits of maize inbred lines using principal component analyses. Principal component analysis reduces the large set of variables into few components that explain the variation among the observations (Jolliffe and Cadima, 2016). The study revealed that the maximum variation was held by PC 1 (39.87%) followed by PC 2 (21.26%). The Eigen values of PC1 and PC2 are recorded as 4.39 and 2.34 respectively. The Eigen values and factor loadings of each variable are presented in Table 2. A similar kind

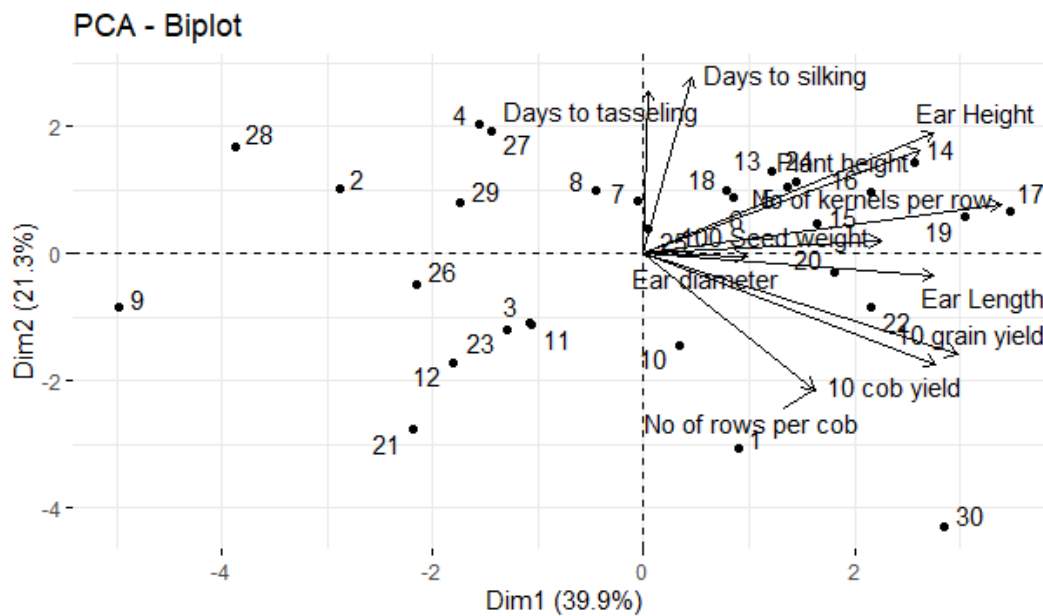


Fig. 1. PCA biplot constructed on the basis of PCA scores of eleven morphological characters.

Table 2. Eigen value, the proportion of the total variance represented by the first ten principal components, cumulative percent variance and component loading of Different characters in maize inbred lines.

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9	PC 10
Eigen Value	4.39	2.34	1.81	1.21	0.91	0.21	0.09	0.03	0.02	0.00
% Var. Exp.	39.87	21.26	16.41	10.96	8.27	1.90	0.86	0.26	0.20	0.01
Cum. Var. Exp.	39.87	61.13	77.54	88.50	96.77	98.67	99.53	99.79	99.99	100.00
Days to tasseling	0.01	0.70	0.68	-0.15	0.10	0.01	0.70	0.68	-0.15	0.10
Days to silking	0.12	0.76	0.61	-0.11	0.09	0.12	0.76	0.61	-0.11	0.09
Plant height (cm)	0.72	0.44	-0.44	0.05	-0.30	0.72	0.44	-0.44	0.05	-0.30
Ear height (cm)	0.75	-0.09	0.02	-0.28	0.50	0.75	-0.09	0.02	-0.28	0.50
Ear length (cm)	0.75	0.52	-0.33	0.01	-0.24	0.75	0.52	-0.33	0.01	-0.24
Ear diameter (cm)	0.27	-0.01	0.42	0.82	-0.14	0.27	-0.01	0.42	0.82	-0.14
Number of rows	0.44	-0.58	0.36	-0.50	-0.22	0.44	-0.58	0.36	-0.50	-0.22
Number of kernels per row	0.92	0.21	-0.14	-0.20	-0.18	0.92	0.21	-0.14	-0.20	-0.18
10 cob yield (Kg)	0.76	-0.48	0.36	0.18	-0.05	0.76	-0.48	0.36	0.18	-0.05
10 cob grain yield (Kg)	0.81	-0.43	0.31	0.09	-0.04	0.81	-0.43	0.31	0.09	-0.04
100 Seed weight (g)	0.61	0.06	-0.33	0.27	0.62	0.61	0.06	-0.33	0.27	0.62

of results was noticed in the research conducted by Al-Naggar *et al.*, (2020). The factor loadings of the variables on each component revealed that all the traits contributed to the first component significantly except the traits days to tasseling and silking, which contributed to the second component.

The PCA biplot constructed based on PCA scores (Fig. 1) showed that all the genotypes are grouped except the maize lines PFSR 49 and MGC 137, which lied far away from other maize lines. Comparisons among the tested lines revealed that this line outnumbered all the other lines in most of the traits and stood as the best line. The PCA plot also denotes that all the traits which are contributing to PC1 are in strong correlation similar to the traits contributing to PC2. Such a strong correlation among the traits aids in the indirect selection of traits (Nascimento-Júnior *et al.*, 2018).

CONCLUSION

Even though PCA biplot did not reveal any prominent grouping, tested maize inbred lines have a considerable morphological variation that can be used in hybrid breeding programmes. The maize line, MGC 137 was found to be best among all the lines and also phenotypically divergent from all the other lines. This line is expected to play a prominent role in hybrid breeding programmes.

REFERENCES

- Al-Naggar, A.M.M., Shafik, M.M. and Musa, R.Y.M. 2020. Genetic Diversity Based on Morphological Traits of 19 Maize Genotypes Using Principal Component Analysis and GT Biplot. *Annual Research & Review in Biology*. 35(2) : 68–85.
- Ali, A., Beshir Issa, A. and Rahut, D.B. 2020. Adoption and Impact of the Maize Hybrid on the Livelihood of the Maize Growers: Some Policy Insights from Pakistan. *Scientifica*. 2020.
- Bajracharya, J., Steele, K. A., Jarvis, D. I., Sthapit, B. R. and Witcombe, J.R. 2006. Rice landrace diversity in Nepal: Variability of agro-morphological traits and SSR markers in landraces from a high-altitude site. *Field Crops Research*. 95 (2–3).
- Bhadru, D., Swarnalatha, V., Mallaiiah, B., Sreelatha, D., Kumar, M. V. N. and Reddy, M. L. 2020. Study of Genetic Variability and Diversity in Maize (*Zea mays* L.) Inbred Lines. *Current Journal of Applied Science and Technology*. 31–39.
- Brown-Guedira, G.L., Thompson, J.A., Nelson, R.L. and Warburton, M.L. 2000. Evaluation of genetic diversity of soybean introductions and North American ancestors using RAPD and SSR markers. *Crop Science*. 40 (3).
- Dass, S.K.A.J.S.P.C.S.A.C.G. and J.M. 2012. Maize holds potential for diversification and livelihood security. *Indian Journal of Agronomy*. 57 (3s) : 32–37. <http://krishi.icar.gov.in/jspui/handle/123456789/14995>
- Esmail, R.M., Zhang, J. F. and Abdel-Hamid, A. M. 2008. Genetic Diversity in Elite Cotton Germplasm Lines Using Field Performance and Rapd Markers. *World Journal of Agricultural Sciences*. 4 (3) : 369–375.
- Husson, F., Josse, J., Le, S. and Maintainer, J.M. 2020. Package “FactoMineR” Title Multivariate Exploratory Data Analysis and Data Mining. <http://factominer.free.fr>
- Jolliffe, I.T. and Cadima, J. 2016. Principal component analysis: A review and recent developments. In *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences* (Vol. 374, Issue 2065). Royal Society of London.
- Kandel, M., Ghimire, S. K., Ojha, B. R. and Shrestha, J. 2018. Analysis of genetic diversity among the maize inbred lines (*Zea mays* L.) under heat stress condition. *Journal of Maize Research and Development*. 3 (1) : 86–97.
- Li, Z., Wang, X., Zhang, Y., Zhang, G., Wu, L., Chi, J. and Ma, Z. 2008. Assessment of genetic diversity in glandless cotton germplasm resources by using agronomic traits and molecular markers. *Frontiers of Agriculture in China*. 2 (3) : 245–252.
- Mujaju, C. and Chakauya, E. 2008. Morphological variation of sorghum landrace accessions on-farm in semi-arid areas of Zimbabwe. *International Journal of Botany*. 4(4).
- Mumm, R. H. and Dudley, J. W. 1994. A classification of 148 U.S. maize inbreds: I.Cluster analysis based on RFLPs. *Crop Science*. 34 (4) : 842–851.
- Nascimento-Júnior, I., Môro, G.V. and Môro, F.V. 2018. Indirect selection of maize genotypes based on associations between root agronomic and anatomical characters. *Chilean Journal of Agricultural Research*. 78 (1) : 39–47.
- Peeters, J.P. and Martinelli, J.A. 1989. Hierarchical cluster analysis as a tool to manage variation in germplasm collections. *Theoretical and Applied Genetics*. 78 (1) : 42–48.
- Ranum, P., Peña-Rosas, J. P. and Garcia-Casal, M.N. 2014. Global maize production, utilization and consumption. *Annals of the New York Academy of Sciences*. 1312 (1) : 105–112.
- Shapiro, S.S. and Wilk, M. 1965. An Analysis of Variance Test for Normality (Complete Samples). *Biometrika*. 52 (3/4) : 591.
- Shrestha, J. 2016. Cluster Analysis of Maize Inbred Lines. *Journal of Nepal Agricultural Research Council*. 2 : 33–36.