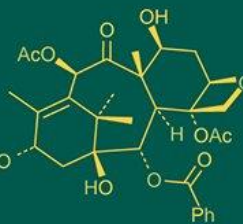
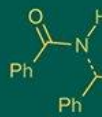


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## Principal component and cluster analysis of the F<sub>2</sub> segregating generation of maize (*Zea mays* L.) based on yield and related traits

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### Abstract

The present study was undertaken to assess multivariate diversity and characterize segregants in a maize F<sub>2</sub> population developed from contrasting parental lines differing for multiple yield and yield-related traits. A total of 212 entries comprising F<sub>2</sub> segregants along with parental lines and F<sub>1</sub> were evaluated for twelve yield and yield-attributing traits viz., days to tasseling (DTT), days to silking (DTS), anthesis-silking interval (ASI), plant height (PH), ear height (EH), cob length (CL), cob girth (CG), kernel row number (KRN), number of kernels per row (NKR), shelling percentage (SP), test weight (TW) and grain yield per plant (GYP). Principal component analysis (PCA) and cluster analysis were employed to characterize the variability among segregants. PCA revealed that the first four principal components possessed eigen values greater than unity and together explained 69.23% of the total variation. PC1 contributed 28.40% of the total variation and was mainly associated with flowering traits, whereas PC2 explained 16.57% of the variation and was predominantly influenced by plant architecture traits. Cluster analysis grouped the segregants into five distinct clusters, indicating substantial genetic diversity within the segregating population. Cluster III exhibited superior mean performance for grain yield, kernel row number, number of kernels per row and test weight, indicating the presence of elite segregants with favourable trait combinations. PCA biplot analysis revealed strong positive association among yield-contributing traits such as kernel row number, number of kernels per row and grain yield. Several superior segregants possessing desirable combinations of yield and related traits were identified and may serve as valuable breeding material for future maize improvement programs.

**Keywords:** Maize, F<sub>2</sub> population, principal component analysis, cluster analysis, multivariate diversity

### Introduction

Maize (*Zea mays* L.) is one of the most important cereal crops cultivated worldwide owing to its high productivity, wide adaptability and diverse industrial utilization. Improvement in grain yield remains the primary objective in maize breeding programs. Since grain yield is a complex quantitative trait governed by several interacting component traits, simultaneous evaluation of multiple traits becomes essential for effective selection. Grain yield in maize is a complex quantitative trait governed by several interrelated component traits including flowering behaviour, plant architecture, ear traits and grain characteristics. Simultaneous evaluation of these yield and yield-attributing traits is essential for identifying superior recombinants in segregating populations. Understanding the relationship among these traits facilitates effective selection and accelerates genetic improvement in maize breeding programs.

Segregating generations such as F<sub>2</sub> populations provide immense opportunity for studying recombination patterns, trait associations and genetic diversity. Early generation evaluation is particularly important in crop improvement programs because identification of superior genotypes during segregating generations helps breeders to reduce the population size to be advanced in subsequent generations. Effective selection at early stages minimizes the maintenance of undesirable segregants and improves selection efficiency by concentrating only on promising recombinants possessing favourable trait combinations. However, conventional univariate approaches may not adequately explain the complex interactions among several correlated traits. Multivariate statistical techniques such as principal

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component analysis (PCA) and cluster analysis are effective tools for studying genetic variability and classifying genotypes based on multiple traits (Mohammadi and Prasanna, 2003) [7]. The selection of genetically diverse inbred lines is essential for maximizing heterosis and enhancing the efficiency of hybrid breeding programs (Hallauer *et al.*, 2010) [5].

Principal component analysis (PCA) is highly useful in genetic studies as it reduces redundancy among correlated traits and provides a clearer understanding of the variability present among maize inbred lines (Nwangburuka *et al.*, 2011) [9]. Similarly, cluster analysis facilitates grouping of segregants into distinct classes based on trait similarity and genetic divergence. Genetic clustering facilitates the identification of diverse inbred lines, as genotypes belonging to different clusters exhibit higher genetic divergence, whereas those grouped within the same cluster possess comparatively lower diversity (Nyombayire *et al.*, 2018) [10].

Therefore, the present study was undertaken to assess multivariate diversity among maize F<sub>2</sub> segregants, identify major traits contributing to variation, classify segregants using cluster analysis and characterize segregants possessing desirable combinations of yield and related traits.

## Materials and Methods

The plant material comprised two contrasting maize parental lines, namely DHKN 563 and CM 111, their F<sub>1</sub> cross and an F<sub>2</sub> population consisting of 212 segregants. The experiment was conducted at a location situated in the Northern Transitional Zone of Karnataka, positioned at 15°15' N latitude and 74°40' E longitude, with an altitude of 697 m above mean sea level. The region receives an average annual rainfall of 1017 mm. The genetic material was evaluated in an unreplicated trial under a spacing of 60 × 20 cm following all the recommended agronomic practices. The observations were recorded from each F<sub>2</sub> plant for twelve traits viz., days to tasseling (DTT), days to silking (DTS), anthesis-silking interval (ASI), plant height (PH) (cm), ear height (EH) (cm), cob girth (CG) (cm), cob length (CL) (cm), kernel row number (KRN), number of kernels per row (NKPR), shelling per cent (SP), hundred grain weight (TW) (g) and grain yield per plant (GYP) (g). Genetic variability was evaluated by principal component analysis (PCA) and euclidean cluster analysis by grouping the similar genotypes into same clusters (Falconer and Mackay, 1996; Abdi and Williams, 2010) [4, 1]. PCA was performed with the *prcomp* function, and a biplot of PC1 vs. PC2 was generated using the *biplot* function (R Core Team, (2024).

## Results and Discussion

Principal component analysis revealed substantial variability among the maize F<sub>2</sub> segregants for yield and related traits. Twelve principal components corresponding to the twelve traits were generated, among which the first four principal components possessed eigen values greater than unity and together explained 69.23% of the total variation (Table 1). The first principal component (PC1) accounted for 28.40% of the total variation, followed by PC2 (16.57%), PC3 (12.97%) and PC4 (11.29%). The cumulative contribution of the first two principal components was 44.97%, indicating that these components effectively captured major variability present within the segregating population.

Similar observations were reported in earlier studies on maize multivariate diversity by Dutta *et al.* (2018) [3], Mounika *et al.* (2018) [8] and Sinana *et al.* (2023) [14], who also observed that the first few principal components explained a major proportion of total variability in maize populations.

PC1 was predominantly influenced by flowering-related traits such as days to tasseling and days to silking along with grain yield and cob girth, whereas PC2 was mainly associated with plant height and ear height. The positive contribution of plant architectural traits toward PC2 indicated the importance of structural characteristics in differentiating segregants. Kernel row number, number of kernels per row and grain yield also contributed substantially toward total variation, indicating their importance in identifying superior recombinants.

The scree plot (Figure 1) demonstrated a gradual decline in eigen values after the first few principal components, confirming that the majority of variability was concentrated within the initial components. The dimensionality reduction achieved through PCA indicated that yield-related and flowering traits played a major role in explaining variability among segregants. Similar findings were reported by Sandeep *et al.* (2015) [12] and Al-Naggar *et al.* (2020) [2], who emphasized the importance of yield and flowering traits in differentiating maize genotypes through principal component analysis.

The PCA biplot provided valuable information regarding relationships among traits and distribution of segregants within the multivariate space. Traits positioned close together exhibited positive association, whereas traits located in opposite directions showed negative association. Days to tasseling and days to silking were closely associated, indicating strong positive correlation between flowering traits. Similarly, plant height and ear height showed positive association, suggesting coordinated contribution of plant architectural traits. Kernel row number, number of kernels per row and grain yield were grouped closely, indicating their positive influence on yield potential. Similar associations among yield-related traits were reported by Suryanarayana *et al.* (2017) [17] and Gupta *et al.* (2019), who observed strong positive relationships among kernel traits and grain yield in maize.

The PCA loading biplot also revealed that segregants possessing higher kernel row number and grain yield were positioned separately from early flowering segregants. This suggested that flowering behaviour and yield traits contributed differentially toward total variability. The PCA score plot illustrated distinct grouping and clustering pattern among segregants. Several segregants located in favourable quadrants exhibited superior combinations of kernel row number, cob traits and grain yield and may therefore be considered as promising recombinants for future breeding programs.

Cluster analysis grouped the 214 entries comprising parental lines, F<sub>1</sub> and 212 F<sub>2</sub> segregants into five distinct clusters based on multivariate trait combinations (Table 2, Figure 2). Cluster II contained the highest number of genotypes (63), followed by Cluster I and Cluster IV containing 43 segregants each. Cluster III comprised 31 genotypes including parental line DHKN 563 and F<sub>1</sub>, whereas Cluster V consisted of 34 segregants. The distribution of segregants across different clusters indicated the presence of substantial diversity within the F<sub>2</sub> population. Similar clustering

patterns reflecting considerable genetic diversity among maize genotypes were also reported by Kumar *et al.* (2015) [6], Singh *et al.* (2019) [15] and Sinana *et al.* (2023) [14]. Cluster mean analysis further revealed considerable variation among clusters for different traits (Table 3). Cluster III recorded the highest mean values for cob length (14.5 cm), cob girth (4.7 cm), kernel row number (20.6), number of kernels per row (24.7), test weight (24.9 g) and grain yield per plant (99.8 g), indicating the presence of superior segregants with favourable yield attributes. In contrast, Cluster V recorded lower values for several yield-related traits, suggesting comparatively poor performance. Cluster I and Cluster IV exhibited higher mean values for plant height and ear height, while Cluster V showed delayed flowering and higher anthesis-silking interval. The variability observed among clusters suggested the presence of considerable divergence among segregants. Similar observations regarding cluster divergence in maize populations were reported by Suryanarayana *et al.* (2017) [17] and Nyombayire *et al.* (2018) [10], who emphasized the usefulness of cluster analysis in classifying genetically diverse maize genotypes.

The multivariate analyses effectively differentiated the segregants based on flowering behaviour, plant architecture, ear traits and grain yield components (Figure 3.). Segregants belonging to Cluster III demonstrated superior performance for most yield-related traits and may therefore serve as potential candidates for advancement and selection. The simultaneous consideration of grain yield, kernel row number, number of kernels per row and test weight enabled identification of promising segregants possessing desirable trait combinations. The PCA score plot and cluster analysis together revealed clear grouping patterns among the segregants, demonstrating the usefulness of multivariate statistical tools in understanding population structure and diversity in maize segregating generations. Studies by Dutta *et al.* (2018) [3] and Al-Naggar *et al.* (2020) [2] also reported positive association of flowering traits with plant architectural characters, wherein delayed flowering genotypes tended to exhibit increased plant height and ear length, which corroborates the present findings. Likewise, the importance of kernel row number and number of kernels per row in contributing toward variability and yield potential in maize populations has also been emphasized by Sinana *et al.* (2023) [14].

**Table 1:** Principal component analysis (PCA) loadings and variance explained for twelve traits in segregating population of maize

| Variable            | PC1   | PC2   | PC3   | PC4   | PC5   | PC6   | PC7   | PC8   | PC9   | PC10  | PC11   | PC12   |
|---------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|
| DTT                 | 0.30  | 0.40  | -0.27 | -0.10 | -0.26 | 0.06  | -0.44 | -0.19 | -0.04 | -0.04 | 0.15   | -0.58  |
| DTS                 | 0.36  | 0.34  | -0.41 | 0.15  | -0.17 | -0.04 | -0.03 | -0.04 | -0.02 | -0.01 | 0.06   | 0.72   |
| ASI                 | 0.23  | 0.04  | -0.37 | 0.43  | 0.07  | -0.18 | 0.62  | 0.22  | 0.02  | 0.05  | -0.11  | -0.38  |
| PH                  | -0.15 | 0.54  | 0.33  | 0.11  | 0.17  | 0.03  | 0.16  | 0.20  | 0.08  | 0.22  | 0.64   | 0.00   |
| EH                  | -0.10 | 0.61  | 0.28  | 0.03  | 0.09  | 0.08  | 0.02  | 0.10  | -0.17 | -0.16 | -0.68  | 0.00   |
| CL                  | -0.37 | 0.06  | -0.22 | 0.25  | 0.23  | 0.29  | 0.17  | -0.63 | -0.28 | -0.29 | 0.14   | 0.00   |
| CG                  | -0.41 | -0.03 | -0.21 | 0.00  | -0.37 | -0.11 | -0.06 | 0.52  | -0.47 | -0.34 | 0.16   | 0.00   |
| KRN                 | -0.29 | 0.16  | 0.00  | -0.28 | -0.59 | -0.10 | 0.40  | -0.25 | 0.46  | -0.10 | -0.04  | 0.00   |
| NKR                 | -0.27 | 0.06  | -0.46 | -0.12 | 0.29  | 0.46  | -0.14 | 0.35  | 0.51  | -0.06 | -0.07  | 0.00   |
| SP                  | 0.04  | 0.13  | -0.18 | -0.53 | 0.48  | -0.57 | 0.08  | -0.05 | -0.01 | -0.32 | 0.09   | 0.00   |
| TW                  | -0.22 | 0.01  | 0.08  | 0.58  | 0.03  | -0.48 | -0.39 | -0.06 | 0.40  | -0.25 | -0.03  | 0.00   |
| GYP                 | -0.42 | 0.09  | -0.30 | -0.04 | 0.03  | -0.30 | -0.13 | -0.13 | -0.16 | 0.74  | -0.17  | 0.00   |
| Eigen value         | 3.41  | 1.99  | 1.56  | 1.36  | 0.96  | 0.89  | 0.77  | 0.44  | 0.25  | 0.23  | 0.17   | 0.00   |
| Variance explained  | 28.40 | 16.57 | 12.97 | 11.29 | 7.99  | 7.39  | 6.39  | 3.63  | 2.09  | 1.88  | 1.40   | 0.00   |
| Cumulative Variance | 28.40 | 44.97 | 57.94 | 69.23 | 77.23 | 84.61 | 91.00 | 94.63 | 96.72 | 98.60 | 100.00 | 100.00 |

DTT - Days to tasseling, DTS - Days to silking, ASI - Anthesis-silking interval, PH - Plant height (cm), EH - Ear height (cm), CL - Cob length (cm), CG - Cob girth (cm), KRN - Kernel rows per cob, NKR - Number of kernels per row, SP - Shelling per cent (%), TW - Hundred grain weight (g), GYP - Grain yield per plant (g).

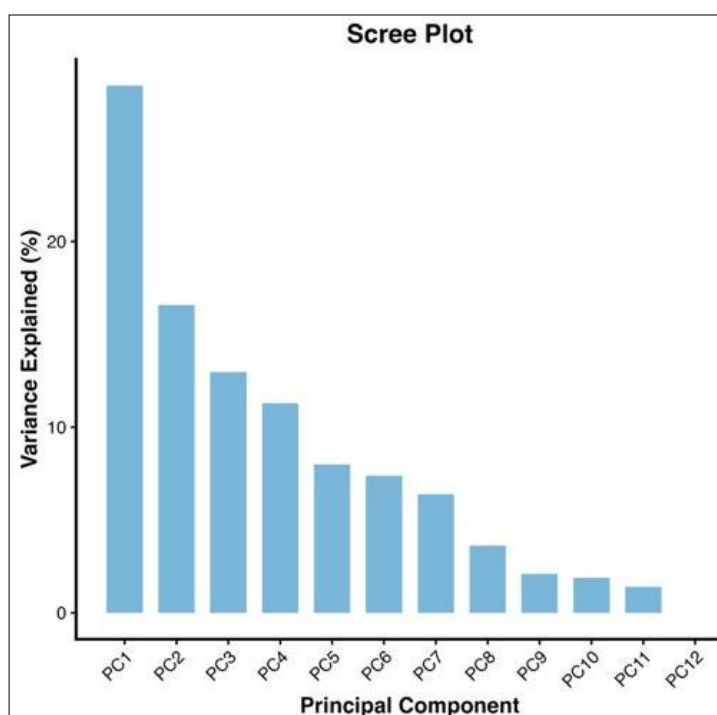
**Table 2:** Non-hierarchical clustering of 212 F<sub>2</sub> maize population along with parental lines and F<sub>1</sub> cross

| Cluster   | No. of Genotypes | Genotypes                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|-----------|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Cluster_1 | 43               | F2-3, F2-4, F2-7, F2-22, F2-41, F2-43, F2-63, F2-65, F2-74, F2-76, F2-77, F2-82, F2-85, F2-88, F2-92, F2-95, F2-99, F2-102, F2-103, F2-107, F2-114, F2-117, F2-119, F2-126, F2-128, F2-131, F2-136, F2-137, F2-138, F2-142, F2-145, F2-154, F2-163, F2-167, F2-168, F2-175, F2-179, F2-180, F2-185, F2-189, F2-190, F2-194, F2-208                                                                                                                                                        |
| Cluster_2 | 63               | P2 (CM 111), F2-1, F2-9, F2-10, F2-12, F2-14, F2-16, F2-19, F2-21, F2-23, F2-27, F2-28, F2-31, F2-35, F2-38, F2-39, F2-47, F2-48, F2-49, F2-50, F2-51, F2-54, F2-58, F2-59, F2-60, F2-61, F2-66, F2-69, F2-70, F2-72, F2-73, F2-83, F2-94, F2-104, F2-110, F2-113, F2-118, F2-121, F2-122, F2-125, F2-130, F2-132, F2-139, F2-141, F2-152, F2-153, F2-155, F2-164, F2-176, F2-178, F2-181, F2-182, F2-183, F2-184, F2-186, F2-188, F2-191, F2-195, F2-199, F2-204, F2-205, F2-207, F2-209 |
| Cluster_3 | 31               | P1 (DHKN 563), F1, F2-17, F2-18, F2-24, F2-25, F2-26, F2-32, F2-37, F2-46, F2-56, F2-62, F2-78, F2-100, F2-105, F2-111, F2-115, F2-124, F2-129, F2-133, F2-140, F2-150, F2-161, F2-162, F2-166, F2-169, F2-170, F2-171, F2-202, F2-206, F2-210                                                                                                                                                                                                                                            |
| Cluster_4 | 43               | F2-2, F2-5, F2-8, F2-20, F2-29, F2-33, F2-36, F2-40, F2-42, F2-52, F2-53, F2-55, F2-57, F2-71, F2-75, F2-80, F2-81, F2-86, F2-89, F2-90, F2-93, F2-97, F2-98, F2-106, F2-109, F2-116, F2-123, F2-127, F2-135, F2-143, F2-144, F2-147, F2-156, F2-157, F2-158, F2-159, F2-160, F2-165, F2-173, F2-174, F2-187, F2-200, F2-203                                                                                                                                                              |
| Cluster_5 | 34               | F2-6, F2-11, F2-13, F2-15, F2-30, F2-34, F2-44, F2-45, F2-64, F2-67, F2-68, F2-79, F2-84, F2-87, F2-91, F2-96, F2-101, F2-108, F2-112, F2-120, F2-134, F2-146, F2-148, F2-149, F2-151, F2-172, F2-177, F2-192, F2-193, F2-196, F2-197, F2-198, F2-201, F2-211                                                                                                                                                                                                                             |

**Table 3:** Cluster mean and standard deviation for twelve traits in segregating population of maize

| Cluster |      | Cluster_1 | Cluster_2 | Cluster_3 | Cluster_4 | Cluster_5 |
|---------|------|-----------|-----------|-----------|-----------|-----------|
| DTT     | Mean | 71.1      | 68.2      | 67.2      | 70.3      | 72.2      |
|         | SD   | 1.6       | 2.2       | 2.3       | 1.6       | 1.9       |
| DTS     | Mean | 74.8      | 71.4      | 69.4      | 73        | 76.5      |
|         | SD   | 2.4       | 2.5       | 2.2       | 2.2       | 2.3       |
| ASI     | Mean | 3.7       | 3.2       | 2.2       | 2.7       | 4.3       |
|         | SD   | 1.7       | 1.6       | 1.3       | 1.6       | 1.6       |
| PH      | Mean | 220       | 183.5     | 212.1     | 220.7     | 188.6     |
|         | SD   | 14.3      | 23.0      | 18.6      | 12.9      | 20.8      |
| EH      | Mean | 137.8     | 99.9      | 121.9     | 137.2     | 109.5     |
|         | SD   | 16.3      | 16.5      | 15.1      | 17.2      | 15.7      |
| CL      | Mean | 11.7      | 12        | 14.5      | 13.1      | 10.2      |
|         | SD   | 1.6       | 1.6       | 1.6       | 1.6       | 1.5       |
| CG      | Mean | 3.7       | 4         | 4.7       | 4.3       | 3.6       |
|         | SD   | 0.5       | 0.4       | 0.3       | 0.3       | 0.3       |
| KRN     | Mean | 17.6      | 17.4      | 20.6      | 19.3      | 15.6      |
|         | SD   | 2.0       | 2.4       | 3.1       | 2.3       | 1.8       |
| NKR     | Mean | 20.2      | 20.3      | 24.7      | 23.3      | 16.7      |
|         | SD   | 4.5       | 5.0       | 4.8       | 4.8       | 4.5       |
| SP      | Mean | 81.7      | 79.3      | 79.7      | 80.7      | 80.6      |
|         | SD   | 4.0       | 4.0       | 4.2       | 5.8       | 2.8       |
| TW      | Mean | 20.8      | 21.9      | 24.9      | 22.7      | 20.6      |
|         | SD   | 3.3       | 3.7       | 4.2       | 3.5       | 3.4       |
| GYP     | Mean | 58.9      | 61        | 99.8      | 70.9      | 50.9      |
|         | SD   | 9.7       | 14.0      | 20.2      | 14.7      | 9.4       |

DTT - Days to tasseling, DTS - Days to silking, ASI - Anthesis-silking interval, PH - Plant height (cm), EH - Ear height (cm), CL - Cob length (cm), CG - Cob girth (cm), KRN - Kernel rows per cob, NKR- Number of kernels per row, SP - Shelling per cent (%), TW - Hundred grain weight (g), GYP - Grain yield per plant (g), SD - Standard deviation

**Fig 1:** Scree plot of principal component analysis for F<sub>2</sub> segregating population of maize between the% of variances explained and principal components

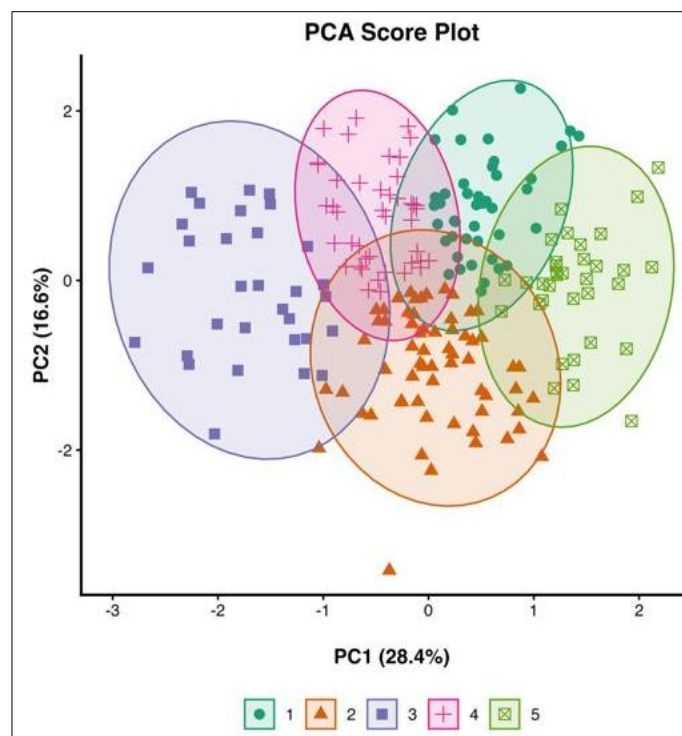
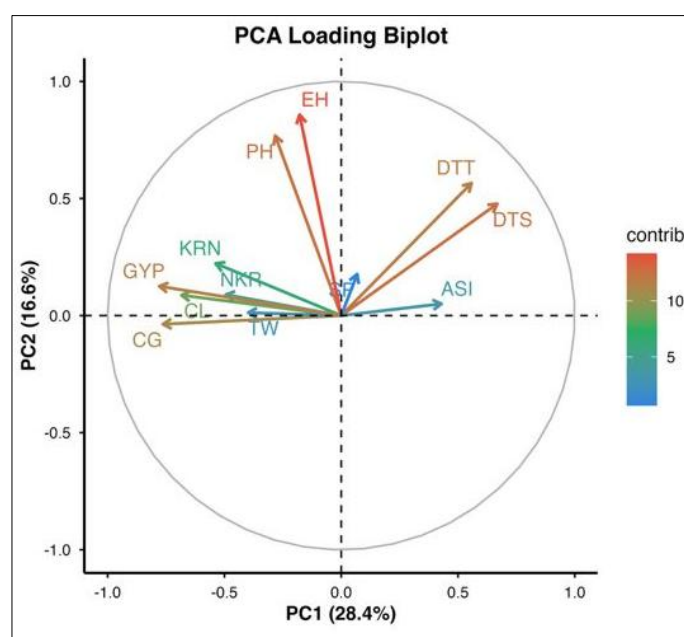


**Fig 2:** Principal Component Analysis (PCA) biplot showing genotypic distribution and clustering



DTT - Days to tasseling, DTS - Days to silking, ASI - Anthesis-silking interval, PH - Plant height (cm), EH - Ear height (cm), CL - Cob length (cm), CG - Cob girth (cm), KRN - Kernel rows per cob, NKR- Number of kernels per row, SP - Shelling per cent (%), TW - Hundred grain weight (g), GYP - Grain yield per plant (g).

**Fig 3:** Biplot representation of Principal Component Analysis (PCA) showing trait contributions

### Conclusion

The present investigation revealed significant multivariate diversity among maize  $F_2$  segregants for yield and yield-related characters. Principal component analysis effectively explained the major sources of variability, while cluster analysis classified segregants into distinct groups based on multivariate trait combinations. The first four principal components explained a substantial proportion of total variation, indicating the effectiveness of PCA in characterizing segregating populations. Yield-attributing traits including cob girth, kernel row number, number of kernels per row, test weight and grain yield contributed

significantly toward total variability and may therefore serve as important selection criteria in maize breeding programs. Cluster III exhibited superior performance for grain yield and associated ear traits and contained promising segregants possessing favourable trait combinations. The results demonstrated the effectiveness of PCA and cluster analysis in assessing multivariate diversity and grouping patterns within maize  $F_2$  populations.

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## References

1. Abdi H, Williams LJ. Principal component analysis. Wiley Interdiscip Rev Comput Stat. 2010;2(4):433-459.
2. Al-Naggar AMM, Shafik MM, Musa RYM. Genetic diversity based on morphological traits of 19 maize genotypes using principal component analysis and GT biplot. Annu Res Rev Biol. 2020;35(2):68-85.
3. Dutta R, Kumar A, Chandra S, Ngachan SV. Genetic divergence, path coefficient, principal component and cluster analyses of maize genotypes in the mid-altitudes of Meghalaya. Maydica. 2018;62(1):5-5.
4. Falconer DS, Mackay TFC. Introduction to Quantitative Genetics. 4th ed. England: Longman Group Ltd.; 1996.
5. Hallauer AR, Carena MJ, Miranda Filho JB. Quantitative Genetics in Maize Breeding. 3rd ed. New York: Springer; 2010.
6. Kumar V, Singh SK, Bhati PK, Sharma A, Sharma SK, Mahajan V. Correlation, path and genetic diversity analysis in maize (*Zea mays* L.). Environ Ecol. 2015;33(2A):971-975.
7. Mohammadi SA, Prasanna BM. Analysis of genetic diversity in crop plants: salient statistical tools and considerations. Crop Sci. 2003;43:1235-1248.
8. Mounika K, Ahamed ML, Nafeez US. Principal component and cluster analysis in inbred lines of maize (*Zea mays* L.). Int J Curr Microbiol Appl Sci. 2018;7(6):3221-3229.
9. Nwangburuka CC, Denton OA, Kehinde OB, Ojo DK, Popoola AR. Genetic variability and relationships among yield components in maize. J Plant Breed Crop Sci. 2011;3(12):341-350.
10. Nyombayire A, Derera J, Sibiya J, Gasura E. Genetic diversity among maize inbred lines selected for the mid altitudes and highlands of Rwanda. Maydica. 2018;61(2):7-7.
11. R Core Team. R: A language and environment for statistical computing. Vienna: R Foundation for Statistical Computing; 2024.
12. Sandeep S, Bharathi M, Narsimha Reddy V, Eshwari KB. Principal component analysis in inbreds of maize (*Zea mays* L.). Int J Trop Agric. 2015;33(2):213-216.
13. Sharma JR. Statistical and Biometrical Techniques in Plant Breeding. New Delhi: New Age International Publishers; 2006.
14. Sinana HF, Ravikesavan R, Iyanar K, Senthil A. Study of genetic variability and diversity analysis in maize (*Zea mays* L.) by agglomerative hierarchical clustering and principal component analysis. Electron J Plant Breed. 2023;14(1):43-51.
15. Singh R, Sinha SK, Thakur D, Tigga K. Genetic variability and diversity analysis for the selection of diverse inbred lines in maize (*Zea mays* L.) crop. Int J Genet. 2019;11(4):578-582.
16. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic Analysis. New Delhi: Kalyani Publishers; 1985.
17. Suryanarayana L, Reddi Sekhar M, Ratna Babu D, Ramana AV, Srinivasa Rao V. Cluster and principal component analysis in maize. Int J Curr Microbiol Appl Sci. 2017;6(7):354-359.