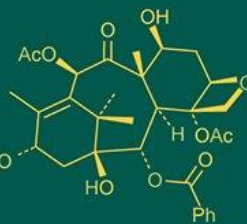
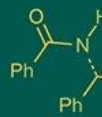
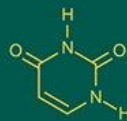
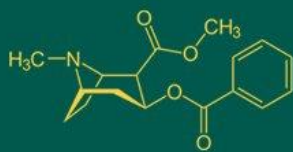


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(9): 1949-1955
www.biochemjournal.com
Received: 19-08-2025
Accepted: 22-09-2025

Ankita Kumari
M.Sc. Students, Department of
Genetics and Plant Breeding, College
of Agriculture, Vasantao Naik
Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

SM Umate
Wheat and Maize Breeder, Wheat and
Maize Research Station, Vasantao
Naik Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

DK Zate
Associate Professor, Department of
Genetics and Plant Breeding,
Vasantao Naik Marathwada Krishi
Vidyapeeth, Parbhani, Maharashtra,
India

HV Kalpande
Head, Department of Genetic and
Plant Breeding, Vasantao Naik,
Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

G Praveenkumar
Young Professional (CIMMYT-BISA)
Vasantao Naik Marathwada Krishi
Vidyapeeth, Parbhani, Maharashtra,
India

Mohit Kumar Dagar
M.Sc. Student, Department of
Genetics and Plant Breeding, College
of Agriculture, Vasantao Naik
Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

VR Ghuge
Assistant Professor, AICRP on
soybean, Vasantao Naik Marathwada
Krishi Vidyapeeth, Parbhani,
Maharashtra, India

AW More
Associate Professor, Department of
Genetics and Plant Breeding,
Vasantao Naik Marathwada Krishi
Vidyapeeth, Parbhani, Maharashtra,
India

JD Deshmukh
Assistant Professor, Department of
Genetics and Plant Breeding,
Vasantao Naik Marathwada Krishi
Vidyapeeth, Parbhani, Maharashtra,
India

Corresponding Author:
Ankita Kumari
M.Sc. Students, Department of
Genetics and Plant Breeding, College
of Agriculture, Vasantao Naik
Marathwada Krishi Vidyapeeth,
Parbhani, Maharashtra, India

Characterization and evaluation of maize (*Zea mays* L.) inbred lines 4

Ankita Kumari, SM Umate, DK Zate, HV Kalpande, G Praveenkumar, Mohit Kumar Dagar, VR Ghuge, AW More and JD Deshmukh

DOI: <https://www.doi.org/10.33545/26174693.2025.v9.i9Sy.5807>

Abstract

An investigation was conducted during *Rabi* 2024-25 at Wheat and Maize research Unit, VNMKV, Parbhani, entitled "Characterization and Evaluation of Maize (*Zea mays* L.) inbred lines". The experiment was conducted using source material of fifty maize inbreds and three checks using ten morphological traits. A study was conducted on fifty-three maize inbred lines to assess genetic diversity, correlation coefficients, and path coefficient analysis for grain yield and its contributing traits. Analysis of variance revealed significant differences among genotypes for all traits indicating considerable genetic variability within the population. Grain yield per plant exhibited significant positive correlations with plant height(cm), ear height(cm), number of grains per ear, and 100-grain weight(g), suggesting that these traits are crucial for improving yield through selection. Path coefficient analysis indicated that 100-grain weight (g) exerted the highest direct effect on grain yield followed by plant height (cm), ear height (cm), days to 50% tasseling, and number of grains per ear.

Genetic divergence assessed using Mahalanobis D^2 statistics across ten morphological and physiological traits, grouped the genotypes into seven distinct clusters. Cluster I comprised 44 genotypes, Cluster II included 4, while the remaining clusters each contained a single genotype. The inter-cluster distances ranged from 27.78 to 176.00 and intra-cluster distances varied from 0.00 to 23.49 reflecting a high degree of genetic variability both within and between clusters. Among the traits studied number of grains per ear contributed the most to total divergence followed by plant height, 100-grain weight, grain yield per plant and other related traits. These findings underscore the importance of these traits in selecting genetically diverse and high-yielding parental lines for maize improvement programs.

Keywords: Diversity, correlation, path coefficient, genotypic, grain yield, phenotypic, *Zea mays* L.)

Introduction

Maize (*Zea mays* L. $2n=20$) is monoecious with protandrous nature and cross pollinated crop as about 95% of the pistillate flowers on a cob receive pollen from nearby other plants and about 5% of the kernels are as a result of self-pollination. It has got the sobriquet "Queen of Cereals" because of its high yield potential and wider adaptability. It belongs to the tribe maydeae, family poaceae and Genus *Zea*. It ranks as one of the most versatile cereal crops globally following wheat and rice in terms of importance. It serves as a crucial food source for both humans and livestock and is also a key raw material in the production of various products, including cornmeal, corn syrup, ethanol and biofuels. In addition maize plays a vital role in the feed industry providing essential nutrients to livestock, poultry and fish.

Among cereal crops, maize exhibits the highest average yield per hectare and ranks third in global total area and production, following wheat and rice. It is cultivated in a wide range of environmental conditions with altitudinal variations ranging from 0 to 3000 meters above sea level (Dowswell *et al.*, 1996) [6]. The growing utilization of maize as a staple food is attributed to its higher yields per hectare compared to wheat, rye and barley. Due to its affordability maize has become the primary source of dietary energy and protein particularly for impoverished populations in rural and underprivileged areas. Maize is grown throughout the year in India as *kharif*, *rabi* and *zaid* crop due to the availability of thermo and photo insensitive varieties.

Among the maize growing countries India rank 4th in area and 7th in production representing around 4% of the world maize area and 2% of total production. In India maize is the third

most important crop after rice and wheat. According to the second advance estimates 2024-25, the production of total (*kharif and rabi*) maize in India is 372.50 lakh tonnes (Anonymous). In India Kharif maize has been sown in around 88.5 lakh hectares (218.69 lakh acres) as on 27th September 2024 which is higher than 84.65 lakh hectares (209.17 lakh acres) covered during corresponding period of last year. Among the major maize growing state, Maharashtra stands 3rd in maize production with 42.66 lakh tonnes after Madhya Pradesh and Karnataka. Major maize growing states are Madhya Pradesh, Karnataka, Maharashtra, Rajasthan, Uttar Pradesh, Bihar, Gujarat and Telangana.

Genetic diversity involves assessing variation among individuals or populations typically using specific or combined analytical methods. Multivariate techniques, such as Mahalanobis D² statistics are key tools for quantifying genetic divergence at the genotypic level in crop species. Understanding the correlation coefficients between grain yield and its component traits is crucial for effective yield improvement. Both genotypic and phenotypic associations reveal the extent of relationships between various traits facilitating the selection of both yield and yield contributing characteristics. Additionally path coefficient analysis offers valuable insights into the direct and indirect effects of different yield component traits on grain yield thereby helping identify effective selection criteria for enhancing yield.

Material and Method

The present investigation entitled “Characterization and Evaluation of Maize (*Zea mays* L.) inbred Lines” was carried out during the *Rabi* season of 2023-2024 at the Wheat and Maize Research Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani. The experimental site is situated at a latitude of 19.2608°N and a longitude of 76.7748°E, at an elevation of 357 meters above sea level and the soils are loamy type with clay. The material was evaluated in Randomized Block Design (Fisher, 1925). The experimental material comprised 50 maize accessions along with three check varieties. The data were subjected to statistical analysis for analysis of variance (as per Panse and Sukhatme 1967) ^[17] and estimation of correlation coefficients (as per Johnson *et al.* 1955) ^[10] and path analysis as per Wright 1921 and Dewey and Lu 1959. D² statistics as proposed by Mahalanobis (1936) ^[12], was used to analyse genetic divergence among the considered 53 genotypes of maize under study and Tocher's approach, as suggested by Rao (1952) ^[21] grouped them into distinct clusters. The source of germplasm is given in (Table 1).

Table 1: Experimental details

| Sr. no | Experimental Design | Randomized Block Design |
|--------|-------------------------|----------------------------------|
| 1. | Number of Treatments | 53 (50 Elite inbreds +03 Checks) |
| 2. | Number of Replications | Two |
| 3. | Spacing | 60 × 20 Cm |
| 4. | Plot size | 4.0 m × 0.60 m |
| 5. | Number of Rows per Plot | One |
| 6. | Date of Sowing | 28 nov 2024 |

Table 2: List of maize inbred lines used in present study

| S.N. | Genotype | S.N. | Genotype |
|-------------------|---------------------|------|-----------|
| 1. | EC 447939-1-1-1 | 26. | DLR 3-4 |
| 2. | EC 447969-B-1 | 27. | MIL 9-104 |
| 3. | EC 646061-1-B-1-1-1 | 28. | MIL 9-107 |
| 4. | BAJIM 08-26 | 29. | MIL 9-109 |
| 5. | CIMpdc-SW9bC444 | 30. | MIL 9-115 |
| 6. | CM 119 | 31. | MIL 9-119 |
| 7. | TAI-99-PTS 33 | 32. | MIL 9-120 |
| 8. | Bajim 17-20 | 33. | MIL 9-122 |
| 9. | P-S99TLYQ432 | 34. | MIL 9-125 |
| 10. | BAJIM 08-26-1 | 35. | MIL 9-127 |
| 11. | CIMpdc-SW9bC444-1 | 36. | MIL 9-128 |
| 12. | CM 119-1 | 37. | MIL 9-129 |
| 13. | TAI-99-PTS 33 | 38. | MIL 9-133 |
| 14. | CIMs-CLRCY 30 | 39. | MIL 9-135 |
| 15. | MIL 9-260 | 40. | MIL 9-139 |
| 16. | MIL 9-263 | 41. | MIL 9-140 |
| 17. | MIL 9-265PS | 42. | MIL 9-142 |
| 18. | MIL 9-268PS | 43. | MIL 9-148 |
| 19. | MIL 9-269 | 44. | MIL 9-158 |
| 20. | MIL 9-275 | 45. | MIL 9-174 |
| 21. | MIL 9-277 | 46. | MIL 9-186 |
| 22. | MIL 9-280 | 47. | MIL 9-191 |
| 23. | MIL 9-281 | 48. | MIL 9-196 |
| 24. | MIL 9-285 | 49. | MIL 9-201 |
| 25. | MIL 9-287PS | 50. | MIL 9-206 |
| Checks | | | |
| 1. Phule Champion | | | |
| 2. Rajeshree | | | |
| 3. Phule Maharshi | | | |

Results and Discussion

Analysis of Variance

Analysis of variance revealed that all the fifty three genotypes differed significantly high for all the ten characters *viz.*, days to 50% tasseling, days to 50% silking, silk tassel interval, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of grains per ear, 100 grain weight (gm), grain yield per plant (gm). (Table 3)

Estimates of Phenotypic and Genotypic Correlation Coefficients

A. Genotypic correlation coefficient

Estimation of genetic and phenotypic correlation coefficients were calculated among all characters under investigation (Table 4). Character association studied at genotypic level showed that grain yield per plant had highly significant and positive correlation with plant height (cm), ear height (cm), number of grain per ear and 100 grain weight (gm). Days to 50% tasseling was positively correlated with days to 50% silking, ear length (cm). Days to 50% silking showed significant positive correlation with days to 50% tasseling, ear length (cm). Silk tassel interval showed negative significant correlation with days to 50% tasseling. Plant height (cm) showed positive and significant association with ear height (cm), number of grain per ear and 100 grain weight (gm). Ear height showed significant and positive correlation with plant height (cm), number of grain per ear and 100 grain weight (gm). Ear length showed positive and significant association with days to 50% tasseling, days to 50% silking, ear girth (cm). On the other hand number of grain per ear showed positive and significant correlation plant height (cm), ear height (cm) and 100 grain weight (gm). 100 grain weight (g) manifested positive and significant correlation with plant height (cm),

ear height (cm) and number of grains per ear. Likewise, the association of grain yield with either one or more than one trait has also been reported by Bisen *et al.* (2018) [3], Rajwade *et al.* (2018) [20], Jagadev *et al.* (2021) [8], Grace *et al.* (2018) [7], Singh *et al.* (2017) [23], Pandey *et al.* (2017) [16], Niharika (2017) [15], Lad *et al.* (2018) [11], Sukumar *et al.* (2018) [24], Premalatha and kalamani (2010) [18] and Munawar *et al.* (2013) [14].

Critical analysis of findings resulted from traits correlation indicated that selection for these characters could bring improvement in yield and yield contributing traits in maize.

B. Phenotypic correlation coefficient

At phenotypic level grain yield per plant showed significant and positive correlation with plant height (cm), ear height (cm), number of grains per plant ear and 100 grain weight (gm) while negatively correlated with Days to 50% tasseling, days to 50% silking and ear length (cm).

Days to 50% tasseling were positively correlated with days to 50% silking, ear length (cm). Days to 50% silking manifested positive and significant association with Days to 50% tasseling ear length and ear girth (cm). Plant height (cm) showed positive and significant association with ear height (cm), number of grains per ear and 100 grain weight. Ear height (cm) showed positive and significant association with plant height (cm), number of grains per plant and 100 grain weight (gm). Ear length showed positive and significant association with days to 50% tasseling, days to 50% silking and ear girth (cm). Ear girth (cm) showed positive and significant association with days to 50% silking and ear length (cm). Number of grain per ear showed positive and significant correlation with silk tassel interval, plant height (cm), ear height (cm) and 100 grain weight (gm). 100 grain weight (gm) manifested positive and significant correlation with plant height (cm), Ear height (cm) and number of grains per ear. Likewise, the association of grain yield with either one or more than one trait has also been reported by Bisen *et al.* (2018) [3], Ambika *et al.* (2018) [1], Mani and Deshpande (2016) [13] and Rajitha *et al.* Sumalini and manjulata (2012) [19] and Jawaharlal *et al.* (2011) [9], Grace *et al.* (2018) [7], Lakshmi *et al.* (2018) and Sukumar *et al.* (2018) [24].

Estimates of path coefficient at phenotypic and genotypic levels

The path coefficient is a statistical tool that splits the correlation coefficient into measures of the direct and indirect effects of various component traits on a specific dependent variable. The direct effect of a trait on grain yield indicates how reliable it is to select for that trait indirectly in order to increase grain yield. Direct and indirect effects of yield contributing traits and their genotypic and phenotypic correlation with grain yield per plant was presented in Table 6 and Table 7.

At the genotypic level, estimates of direct effect were positive and high for days to 50% tasseling (0.0903), plant height, ear height, number of grains per ear, 100 grain weight. In contrast the negative direct effect on grain yield was observed in days to 50% silking, silk tassel interval, ear length and ear girth at genotypic level. These results were supported by the findings of Grace *et al.* (2018) [7] and Usha *et al.* (2017).

At phenotypic level, positive direct effect were shown by days to 50% tassel, plant height, ear height, number of

grains per ear and 100 grain weight. Whereas, negative direct effects were exerted by days to 50% silking, silk tassel interval, ear length and ear on the expression of grain yield per plant. The results are in close conformity to the findings of Saritha *et al.*, for Days to 50% Tasseling, number of grains per ear, 100 kernel wt (g) grain yield per plant in maize.

The significant indirect effects on grain yield per plant was exhibited by plant height, ear height, number of grains per ear and 100 grain weight at genotypic level. At the phenotypic level plant height, ear height, number of grains per ear and 100 grain weight, all showed significant indirect effects on grain yield per plant. A negative significant indirect effect on grain yield per plant was attributed to days to 50% tassel and days to 50% silking at both genotypic and phenotypic level whereas in ear length showed only at phenotypic level. According to findings of Satyanarayana *et al.* (2008) and Sukumar *et al.* (2019) [24], the results are congruent.

The residual factor at genotypic level was 0.6795 whereas phenotypic residual effect was 0.6937 revealed that there may be environmental component contributing towards yield and other characters.

Clustering pattern of genotypes

Non-hierarchical Euclidean cluster analysis was used to compute the generalized distance for each pair of genotypes.

Group constellation

All the 50 test genotypes and 3 checks were classified into 7 clusters in such a way that average intra cluster distance remained minimum. Table 8 showed the clustering pattern of these genotypes. Cluster I contained forty four genotypes, cluster II contained four genotypes and rest of the clusters contained 1 genotype each suggesting presence of diversity among them.

Average intra and inter cluster distances

The average intra and inter cluster distances have been presented in (Table 10). In the present study intra cluster values ranged from 0 to 23.49. The maximum intra cluster D^2 value (23.49) was observed for cluster II followed by cluster I (20.24). Whereas, all rest of the cluster were reported zero intra cluster values. Inter cluster values varies from 27.78 to 176.24. The maximum inter cluster distance ($D^2 = 176.24$) was observed between cluster IV and cluster VII which was followed by cluster I and cluster VII ($D^2 = 168.49$), cluster III and cluster VII ($D^2 = 164.29$). Whereas it was lowest in between cluster I and cluster III ($D^2 = 27.78$). The values are presented in Table 4.9. Similar findings were reported by Reddy *et al.* (2012) [22].

Cluster mean

Table 9 showed the average values of ten morpho-physiological and yield contributing traits for each of the seven clusters. The genetic differences between the clusters are reflected in the cluster means which differ from each other for one or more traits. Cluster VII had the highest cluster mean for grain yield per plot (629.10), followed by clusters V (198.50) and VI (96.75). Cluster IV had the lowest average grain yield per plot (24.00). The cluster mean for the character days to 50% tasseling was maximum for cluster III (78.00) followed by cluster I (76.31). While lowest cluster mean was noted in cluster V (66.00). The

highest cluster mean for days to 50% silking exhibited by cluster III (80.50) followed by cluster I (79.20) while Cluster V (71.00) showed minimum value for days to 50% silking. The highest cluster mean for days to 50% silking tassel interval was exhibited by cluster VI (4.55) followed by cluster II (3.30) while lowest cluster mean was noted in cluster VII (2.50). The highest cluster mean for plant height was exhibited by cluster VII (228.50) followed by cluster III (185.80), while, lowest cluster mean was noted in cluster IV (85.50). The highest cluster mean for ear height was exhibited by cluster VII (113.90) followed by cluster V (98.60) while lowest cluster mean for ear height was noted in cluster IV (44.40). The highest cluster mean for ear length was exhibited by cluster VI (26.90) followed by cluster I (20.51). The genotypes with minimum ear length were concentrated in cluster VII (16.10). The highest cluster mean for ear girth was exhibited by cluster VI (20.80) followed by cluster II (16.48). The genotypes with minimum ear girth were concentrated in cluster VII (13.20). The genotypes with highest cluster mean for number of grains per ear were grouped into cluster VI (425.70) followed by cluster V (369.50). The genotypes of cluster III (169.40) showed lowest cluster mean for number of grains per row. For the character 100 grain the cluster mean was highest in cluster VII (54.35) followed by cluster VI (47.95) while lowest cluster mean was recorded in cluster IV (20.55).

Contribution of different characters towards divergence

The relative per cent contribution of the individual trait to the genetic divergence among maize genotypes was presented in (Table 11). Among all the ten attributes under study number of grains per ear (48.26%) contributed maximum to the total divergence by 665 times followed by plant height (15.53%) by 214 times, 100 grain weight (14.51%) by 200, grain yield per plant (14.08%) by 194 times, ear height (6.46%) by 89 times, ear length (0.51%)

by 7, ear girth (0.29%) by 4 times, days to tasseling (0.22%) by 3 times, days to 50% silking (0.15%) by 2 times. Whereas silk tassel interval had no contribution towards genetic divergence and hence were of less importance. Suman *et al.*, observed maximum contribution towards genetic divergence by number of grains per ear. The results are in accordance with the reports of divergence studies by Azam *et al.* 2014 and Biswas *et al.* 2014^[2, 4].

Conclusion

Grain yield per plant was positively and significantly correlated with plant height, ear height, number of grains per ear and 100-grain weight which indicates that selection for these four traits will definitely lead to selection of better yielding inbreds and hybrids on crossing between them. Path coefficient analysis showed 100-grain weight had the highest positive direct effect on yield followed by ear height, plant height, days to 50% tasseling and number of grains per ear while, days to 50% silking had the highest negative direct effect followed by ear length, silk-tassel interval and ear girth.

Results of D^2 statistics and Tocher's dendrogram indicate about presence of genetic divergence among the fifty-three genotypes of maize which was clustered into seven groups for ten morpho-physiological traits. Cluster I contained forty-four genotypes, cluster II contained four genotypes and rest of the clusters contained one genotype each. On the basis of Mahalanobis D^2 statistics, fifty-three genotypes were grouped into seven clusters. Inter cluster values varied from 27.78 to 176.24. The maximum inter cluster distance ($D^2 = 176.24$) was observed between cluster IV and cluster VII which was followed by cluster I and cluster VII ($D^2 = 168.49$), cluster III and cluster VII ($D^2 = 164.29$). Whereas it was lowest in between cluster I and cluster III ($D^2 = 27.78$). This suggests that there was wide diversity available among different clusters and in hybrid development programs.

Table 3: Analysis of variance for agro-morphological traits among 53 of genotypes of maize

| Source | df | DT | DS | STI | PH | EH | EL | EG | NGPE | 100 GW | GYPP |
|-------------|----|---------|---------|--------|-----------|----------|---------|---------|-----------|----------|------------|
| Replication | 1 | 31.74 | 24.54 | 0.00 | 2.09 | 46.49 | 1.46 | 0.24 | 0.14 | 2.24 | 38.35 |
| Genotype | 52 | 24.27** | 22.22** | 1.14** | 1721.33** | 692.18** | 22.90** | 10.07** | 7854.63** | 154.26** | 14639.51** |
| Error | 52 | 2.99 | 2.38 | 0.30 | 14.45 | 15.88 | 3.18 | 1.80 | 23.47 | 1.80 | 16.52 |

DT: Days to 50% Tasselling, **DS:** Days to 50% Silking, **PH:** Plant Height, **EH:** ear height, **EL:** Ear Length, **EG:** Ear girth, **NGPE:** Number of grain per ear, **100 GW:** 100 grain wt, **GYPP:** Grain yield per plant.

Table 4: Genotypic correlation coefficient for grain yield and its contributing characters in maize genotypes

| Cha. | DT | DS | STI | PH | EH | EL | EG | NGPE | 100 GW | GYPP |
|--------|----|---------|-----------|---------|-----------|-----------|-----------|------------|-----------|------------|
| DT | 1 | 0.98 ** | -0.2921 * | -0.2112 | -0.2577 | 0.5214 ** | 0.2428 | -0.5285 ** | -0.1936 | -0.4651 ** |
| DS | | 1 | -0.0843 | -0.2457 | -0.2648 | 0.5272 ** | 0.2613 | -0.4954 ** | -0.1713 | -0.4988 ** |
| STI | | | 1 | -0.1365 | 0.0103 | -0.1266 | 0.1128 | 0.2549 | 0.0538 | -0.0929 |
| PH | | | | 1 | 0.7684 ** | 0.0608 | 0.0965 | 0.3514 ** | 0.5152 ** | 0.572 ** |
| EH | | | | | 1 | 0.0142 | 0.0776 | 0.3257 * | 0.3197 * | 0.5194 ** |
| EL | | | | | | 1 | 0.4162 ** | -0.0452 | 0.071 | -0.236 |
| EG | | | | | | | 1 | -0.18 | -0.0161 | 0.1666 |
| NGPE | | | | | | | | 1 | 0.3164 * | 0.3912 ** |
| 100 GW | | | | | | | | | 1 | 0.4664 ** |
| GYPP | | | | | | | | | | 1 |

* and ** Significant at 5% and 1% levels of significance, respectively

DT: Days to 50% Tasselling, **DS:** Days to 50% Silking, **STI:** Silk Tassel Interval, **PH:** Plant Height, **EH:** Ear height, **EL:** Ear Length, **EG:** Ear girth, **NGPE:** Number of grains/ ear, **100 GW:** 100 grain wt., **GYPP:** grain yield per, **cha :** character

Table 5: Phenotypic correlation coefficient for grain yield and its contributing characters in maize genotypes.

| Cha. | DT | DS | STI | PH | EH | EL | EG | NGPE | 100 GW | GYPP |
|--------|----|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|------------|
| DT | 1 | 0.9703 ** | -0.2717 ** | -0.1975 | -0.2353 * | 0.4611 ** | 0.2121 | -0.4690 ** | -0.1773 | -0.4339 ** |
| DS | | 1 | -0.0537 | -0.2344 * | -0.2491 * | 0.4763 ** | 0.2247 * | -0.4683 ** | -0.1582 | -0.4695 ** |
| STI | | | 1 | -0.1273 | -0.0107 | 0.0432 | 0.0509 | 0.2182 * | 0.0451 | -0.0816 |
| PH | | | | 1 | 0.7546 ** | 0.0515 | 0.0856 | 0.3489 ** | 0.5084 ** | 0.5698 ** |
| EH | | | | | 1 | 0.0137 | 0.0804 | 0.3219 ** | 0.3130 ** | 0.5130 ** |
| EL | | | | | | 1 | 0.3203 ** | -0.0445 | 0.0725 | -0.2199 * |
| EG | | | | | | | 1 | -0.1624 | -0.0176 | 0.1491 |
| NGPE | | | | | | | | 1 | 0.3144 ** | 0.3905 ** |
| 100 GW | | | | | | | | | 1 | 0.4625 ** |

* and ** Significant at 5% and 1% levels of significance, respectively

DT: Days to 50% Tasselling, **DS:** Days to 50% Silking, **STI:** Silk Tassel Interval, **PH:** Plant Height, **EH:** Ear height, **EL:** Ear Length, **EG:** Ear girth, **NGPE:** Number of grains/ ear, **100 GW:** 100 grain wt., **GYPP:** grain yield per plant, **Cha:** character

Table 6: Direct and indirect effects of yield components on grain yield at genotypic level in maize genotypes

| Cha. | DT | DS | STI | PH | EH | EL | EG | NGPE | 100 GW | GYPP |
|--------|---------------|----------------|----------------|---------------|---------------|----------------|----------------|---------------|---------------|------------|
| DT | 0.0903 | 0.0885 | -0.0264 | -0.0191 | -0.0233 | 0.0471 | 0.0219 | -0.0477 | -0.0175 | -0.4651 ** |
| DS | -0.3271 | -0.3338 | 0.0282 | 0.0820 | 0.0884 | -0.1760 | -0.0872 | 0.1654 | 0.0572 | -0.4988 ** |
| STI | 0.0333 | 0.0096 | -0.1140 | 0.0156 | -0.0012 | 0.0144 | -0.0129 | -0.0291 | -0.0061 | -0.0929 |
| PH | -0.0392 | -0.0456 | -0.0253 | 0.1856 | 0.1426 | 0.0113 | 0.0179 | 0.0652 | 0.0956 | 0.572 ** |
| EH | -0.0551 | -0.0567 | 0.0022 | 0.1644 | 0.2140 | 0.0030 | 0.0166 | 0.0697 | 0.0684 | 0.5194 ** |
| EL | -0.0672 | -0.0680 | 0.0163 | -0.0078 | -0.0018 | -0.1289 | -0.0536 | 0.0058 | -0.0091 | -0.236 |
| EG | -0.0127 | -0.0137 | -0.0059 | -0.0050 | -0.0041 | -0.0218 | -0.0523 | 0.0094 | 0.0008 | -0.1666 |
| NzPE | -0.0380 | -0.0357 | 0.0183 | 0.0253 | 0.0234 | -0.0033 | -0.0130 | 0.0720 | 0.0228 | 0.3912 ** |
| 100 GW | -0.0492 | -0.0436 | 0.0137 | 0.1311 | 0.0813 | 0.0180 | -0.0041 | 0.0805 | 0.2544 | 0.4664 ** |

Residual effect = 0.6795, Bold figure = Direct effects, Normal figures = Indirect effects

DT: Days to 50% Tasselling, **DS:** Days to 50% Silking, **STI:** Silk Tassel Interval, **PH:** Plant Height, **EH:** Ear height, **EL:** Ear Length, **EG:** Ear girth, **NGPE:** Number of grains/ ear, **100 GW:** 100 grain wt., **GYPP:** grain yield per plant, **cha :** character

Table 7: Direct and indirect effects of yield components on grain yield at phenotypic level in maize genotypes

| Cha. | DT | DS | STI | PH | EH | EL | EG | NGPE | 100 GW | GYPP |
|--------|---------------|----------------|----------------|---------------|---------------|----------------|----------------|---------------|---------------|------------|
| DT | 0.1979 | 0.1921 | -0.0538 | -0.0391 | -0.0466 | 0.0913 | 0.0420 | -0.0982 | -0.0351 | -0.4339 ** |
| DS | -0.4074 | -0.4198 | 0.0225 | 0.0984 | 0.1046 | -0.1999 | -0.0943 | 0.1966 | 0.0664 | -0.4695 ** |
| STI | 0.0129 | 0.0025 | -0.0474 | 0.0060 | 0.0005 | 0.0020 | -0.0024 | -0.0103 | -0.0021 | -0.0816 |
| PH | -0.0432 | -0.0512 | -0.0278 | 0.2186 | 0.1649 | 0.0113 | 0.0187 | 0.0763 | 0.1111 | 0.5698 ** |
| EH | -0.0467 | -0.0495 | -0.0021 | 0.1499 | 0.1986 | 0.0027 | 0.0160 | 0.0639 | 0.0622 | 0.5130 ** |
| EL | -0.0543 | -0.0561 | 0.0051 | -0.0061 | -0.0016 | -0.1177 | -0.0377 | 0.0052 | -0.0085 | -0.2199 * |
| EG | -0.0161 | -0.0171 | -0.0039 | -0.0065 | -0.0061 | -0.0244 | -0.0760 | 0.0123 | 0.0013 | -0.1491 |
| NGPE | -0.0334 | -0.0315 | 0.0147 | 0.0235 | 0.0217 | -0.0030 | -0.0109 | 0.0673 | 0.0212 | 0.3905 ** |
| 100 GW | -0.0436 | -0.0389 | 0.0111 | 0.1251 | 0.0770 | 0.0178 | -0.0043 | 0.0773 | 0.2460 | 0.4625 ** |

Residual effect = 0.6937, Bold figure = Direct effects, Normal figures = Indirect effects

DT: Days to 50% Tasselling, **DS:** Days to 50% Silking, **STI:** Silk Tassel Interval, **PH:** Plant Height, **EH:** Ear height, **EL:** Ear Length, **EG:** Ear girth, **NGPE:** Number of grains per ear, **100 GW:** 100 grain wt., **GYPP:** grain yield per plant, **cha :** character

Table 8: Distribution of fifty three maize genotypes into nine clusters based on D² statistics (Tocher's Method)

| Cluster | No. of entries | Name of entries |
|---------|----------------|--|
| I | 44 | EC 447939-1-1-1, EC 447969-B-1, EC 646061-1-B-1-1-1, CIMpdc-SW9bC444, CM 119, TAI-99-PTS 33, Bajim 17-20, P-S99TLYQ432, BAJIM 08-26, CM 119, TAI-99-PTS 33, CIMs-CLRCY 30, MIL 9-260, 118944, MIL 9-275, MIL 9-277, MIL 9-280, MIL 9-281, MIL 9-285, MIL 9-287PS, DLR 3-4, MIL 9-104, MIL 9-107, MIL 9-109, MIL 9-115, MIL 9-119, MIL 9-120, MIL 9-122, MIL 9-125, MIL 9-127, MIL 9-128, MIL 9-133, MIL 9-135, MIL 9-139, MIL 9-140, MIL 9-142, MIL 9-142, MIL 9-158, MIL 9-174, MIL 9-186, MIL 9-191, MIL 9-196, MIL 9-201 and 119097 |
| II | 4 | BAJIM 08-26, CIMpdc-SW9bC444, MIL 9-268PS, Phule champion |
| III | 1 | MIL 9-263 |
| IV | 1 | MIL 9-129 |
| V | 1 | Rajeshree |
| VI | 1 | MIL 9-265PS |
| VII | 1 | Phule maharshi |

Table 9: Cluster means of grain yield and its contributing traits in maize inbreds

| Cluster Means | DT | DS | STI | PH | EH | EL | EG | NGPE | 100 GW | GYPP |
|---------------|-------|-------|------|--------|--------|-------|-------|--------|--------|--------|
| Cluster I | 76.31 | 79.20 | 3.00 | 125.03 | 58.60 | 20.51 | 15.61 | 214.73 | 26.36 | 38.44 |
| Cluster II | 73.25 | 76.50 | 3.30 | 162.40 | 70.97 | 19.20 | 16.48 | 294.23 | 37.94 | 85.42 |
| Cluster III | 78.00 | 80.50 | 3.20 | 185.80 | 85.50 | 18.30 | 15.60 | 169.40 | 33.50 | 39.50 |
| Cluster IV | 71.50 | 74.50 | 3.00 | 85.50 | 44.40 | 20.00 | 15.60 | 346.70 | 20.55 | 24.00 |
| Cluster V | 66.00 | 69.00 | 3.00 | 179.00 | 98.60 | 16.35 | 13.70 | 369.50 | 37.50 | 198.50 |
| Cluster VI | 73.50 | 77.50 | 4.55 | 179.10 | 83.00 | 26.90 | 20.80 | 425.70 | 47.95 | 96.75 |
| Cluster VII | 68.50 | 71.00 | 2.50 | 228.50 | 113.90 | 16.10 | 13.20 | 324.40 | 54.35 | 629.10 |

DT: Days to 50% Tasselling, **DS:** Days to 50% Silking, **STI:** Silk Tassel Interval, **PH:** Plant Height, **EH:** Ear height, **EL:** Ear Length, **EG:** Eargirth, **NGPE:** Number of grains/ ear, **100 GW:** 100 grain wt., **NCPP:** Number of Ear /Plant, **SH%:** Shelling percent, **GYPP:** grain yield per plant

Table 10: Average intra and inter cluster D² values for grain yield and its attributing characters in maize inbreds

| Clusters | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII |
|-------------|--------------|--------------|-------------|-------------|-------------|-------------|-------------|
| Cluster I | 20.24 | 33.46 | 27.78 | 34.65 | 60.22 | 56.90 | 168.49 |
| Cluster II | | 23.49 | 32.97 | 39.88 | 37.95 | 34.29 | 151.21 |
| Cluster III | | | 0.00 | 52.05 | 59.11 | 57.21 | 164.29 |
| Cluster IV | | | | 0.00 | 61.44 | 49.72 | 176.24 |
| Cluster V | | | | | 0.00 | 33.55 | 120.32 |
| Cluster VI | | | | | | 0.00 | 149.11 |
| Cluster VII | | | | | | | 0.00 |

Table 11: Percentage contribution of grain yield and its attributing characters to genetic divergence in Maize inbred

| Sr. no | Source | Times Ranked | Contribution% |
|--------|--------|--------------|---------------|
| 1 | DT | 3 | 0.22% |
| 2 | DS | 2 | 0.15% |
| 3 | STI | 0 | 0.00% |
| 4 | PH | 214 | 15.53% |
| 5 | EH | 89 | 6.46% |
| 6 | EL | 7 | 0.51% |
| 7 | EG | 4 | 0.29% |
| 8 | NGPE | 665 | 48.26% |
| 9 | 100 GW | 200 | 14.51% |
| 0 | GYPP | 194 | 14.08% |

References

- Ambika R, Dharampaul C, Singh N. Prospecting high oil in corn (*Zea mays L.*) germplasm for better quality breeding. Maydica. 2018;63(1):1-5.
- Azam MG, Sarker U, Banik BR. Genetic variability of yield and its contributing characters on CIMMYT maize inbreds under drought stress. Bangladesh J Agric Res. 2014;39(3):419-426.
- Bisen N, Rahangdale CP, Sahu RP. Genetic variability and correlation studies of yield and yield component in maize hybrids (*Zea mays L.*) under Kymore Plateau and Satpura hill region of Madhya Pradesh. Int J Agric Environ Biotechnol. 2018;11(1):71-77.
- Biswas A, Sarker U, Banik BR, Rohman MM, Mian MK. Genetic divergence study in salinity stress tolerant maize (*Zea mays L.*). Bangladesh J Agric Res. 2014;39(4):621-30.
- Dewey DR, Lu KH. A correlation and path co-efficient analysis of components of crested wheat grass seed production. Agron J. 1959;51:515-518.
- Dowswell CR, Paliwal RL, Cantrell RP. Maize in the third world. Westview Press; 1996. p.1-37.
- Grace B, Marker S, Rajasekhar D. Assessment of quantitative genetic variability and character association in maize (*Zea mays L.*). J Pharmacogn Phytochem. 2018;7(1):2813-2816.
- Jagadev PN, Kanungo P, Lenka D. Genetic variability, association and path coefficient studies in quality protein maize inbreds. Pharma Innov J. 2021;10(12):776-779.
- Jawaharlal J, Reddy GL, Kumar RS. Genetic variability and character association studies in maize. Agric Sci Digest. 2011;31(3):173-177.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron J. 1955;47:314-8.
- Lad DB, Borle UM, Dhumal NU. Studies on genetic variability, association of characters and path analysis in maize (*Zea mays L.*) inbreds. Int J Pure Appl Biosci. 2018;6(4):241-245.
- Mahalanobis PC. On the generalized distance in statistics. Proc Natl Inst Sci India. 1936;2:49-55.
- Mani BR, Deshpande SK. Genetic divergence studies in maize (*Zea mays L.*). 2016.
- Munawar M, Shahbaz M, Hammad G, Yasir M. Correlation and path analysis of grain yield components in exotic maize (*Zea mays L.*) hybrids. Int J Sci Basic Appl Res. 2013;12(1):22-27.
- Niharika S. Genetic variation and association study for grain yield in germplasm accessions of maize (*Zea mays L.*). Indian J Agric Res. 2017;51(2):120-127.
- Pandey Y, Vyas RP, Kumar J, Singh L, Singh HC, Yadav PC. Heritability, correlation and path coefficient analysis for determining interrelationships among grain yield and related characters in maize (*Zea mays L.*). Int J Pure Appl Biosci. 2017;5(2):595-603.

17. Panse VG, Sukhatme PV. Statistical method for agricultural workers. New Delhi: ICAR; 1967.
18. Premalatha M, Kalamani A. Correlation studies in maize (*Zea mays L.*). Int J Plant Sci (Muzaffarnagar). 2010;5(1):376-380.
19. Rajitha A, Babu DR, Lal A, Rao VS. Heterosis and combining ability for grain yield and yield component traits in maize (*Zea mays L.*). Electron J Plant Breed. 2015;5(3):378-84.
20. Rajwade JK, Jagadev PN, Lenka D, Gupta S. Correlation and path coefficient studies on elite genotypes of maize inbred lines. J Pharmacogn Phytochem. 2018;7(2):2765-71.
21. Rao CR. Advanced statistical methods in biometrical research. New York: John Wiley & Sons; 1952.
22. Reddy VR, Jabeen F, Sudarshan MR, Rao AS. Studies on genetic variability, heritability, correlation and path analysis in maize (*Zea mays L.*). Crop Res. 2012;44(3):391-393.
23. Singh G, Ravindra K, Jasmine. Genetic parameters and character association study for yield traits in maize (*Zea mays L.*). J Pharmacogn Phytochem. 2017;6(5):808-13.
24. Sukumar K, Hemalatha V, Reddy VN, Reddy SN. Character association and path analysis for yield and quality traits in quality protein maize (*Zea mays L.*). Int J Curr Microbiol Appl Sci. 2019;8(8):3097-111.
25. Sumalini K, Manjulatha G. Heritability, correlation and path coefficient analysis in maize. Maize J. 2012;1(2):97-101.
26. Wright S. Correlation and causation. J Agric Res. 1921;20:557-587.