Plant Archives Vol. 25, No. 2, 2025 pp. 2189-2196 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.313

GENETIC DIVERSITY AND MORPHOLOGICAL VARIABILITY OF MAIZE (*ZEA MAYS* L.) INBREDS VIA DUS DESCRIPTORS AND CLUSTER ANALYSIS

Matta Revanth Kumar Reddy[1]*, Sunil Kumar[1], Manigopa Chakraborty[1], M.K. Barnwal[2], Shivam Mishra[3] and Nisha Bharti[1]
[1]Department of Genetics and Plant Breeding, Birsa Agricultural University,
Kanke, Ranchi – 834 006, India
[2]Department of Plant Pathology, Birsa Agricultural University, Kanke, Ranchi–834 006, India
[3]Department of Agricultural Statistics and Computer Application,
Birsa Agricultural University, Kanke, Ranchi – 834 006, India
*Corresponding author E-mail: mattarevanthkreddy@gmail.com

(Date of Receiving : 11-07-2025; Date of Acceptance : 10-10-2025)

ABSTRACT

The term *Zea mays* originates from the Spanish word *maiz*, meaning 'plant,' while the genus name *Zea* is derived from the Greek word for 'sustaining life,' signifying its fundamental role in human nutrition and agricultural systems. This study assessed genetic diversity and morphological variability among 60 maize genotypes (56 inbreds and 4 checks) at BAU, Kanke during *Kharif* 2024 using 24 DUS descriptors in a randomized block design with three replications. Frequency distributions indicating distinct variations: wide leaf blade in 85% of genotypes, straight leaf attitude in 68%, anthocyanin at tassel glume base in 80%, and long cob length in 63%, with uniform absence of pigmentation in leaf sheath and cob glumes, underscoring descriptor utility for genotype differentiation. Quantitative traits spanned informative ranges: days to 50% tasseling 41.6–52.3 days, silking 46.0–57.0 days, plant height 69.6–184.2 cm, cob length 9.5–31.2 cm, and yield per plant 34.6–81.1 g, with CM 139 earliest flowering, CM 213 highest yielding, and Suvan 2 tallest. Tocher's clustering organized genotypes into four groups: Cluster I (40%), Clusters II and III (26.7% each), and Cluster IV (6.7%), indicating a dominant pool alongside a distinct cluster containing check varieties. The combined DUS profiles, quantitative ranges, and cluster structure provide framework for germplasm categorization and parental selection planning

***Keywords* :** Maize inbreds; DUS descriptors; Morphological diversity; Genetic divergence; Cluster analysis.

Introduction

Maize (*Zea mays* L.) serves as a foundational cereal crop worldwide, prized for its efficient C_4 photosynthesis, adaptability to diverse climates, and multifunctional uses in food, feed, and industry. Its origins trace back to the wild grass teosinte (*Zea mexicana*), and although debates persist, it is widely agreed that modern maize was domesticated from this ancestral species (Galinat, 1988). Globally, maize plays a critical role in food security, especially in developing regions. It provides nearly 30% of the caloric intake for approximately 4.5 billion people across 94 developing countries where food insecurity and child malnutrition remain significant concerns (Von Braun *et al.*, 2010). Its kernels deliver a concentrated source of starch, protein, and oil that sustains household nutrition while supplying raw materials for starch, syrup, alcohol, and emerging nutraceutical markets, underpinning its reputation as the "Queen of Cereals" in both productivity and utility. Recent estimates place world maize production at approximately 1,219.82 million metric tons with an average yield of 6,050 kg ha^{-1}, reflecting its dominance alongside major producers such as the

United States, China, Brazil, and Argentina (USDA, 2024).

Within India, maize contributes nearly 9% to the national food basket and over 100 billion to agricultural GDP, supporting around 100 million person-days of employment annually (DAandFW, 2024). The national production of 38.09 million metric tons from 10.74 million hectares, at 3,545 kg ha^{-1}, underscores its strategic role in food and nutritional security. Karnataka, Bihar, Madhya Pradesh, Maharashtra, Andhra Pradesh, Tamil Nadu and Telangana account for over 95% of the output (Milind and Isha, 2013). In Jharkhand, however, maize productivity remains substantially below the national average at 1,910 kg ha^{-1} across 0.24 million hectares, constrained by fragmented holdings, input and varietal limitations, heterogenous environments, and biotic stresses. This productivity gap underscores the need for targeted improvement strategies tailored to local agro-ecologies and stress conditions.

Morphological characterization using DUS (Distinctness, Uniformity, and Stability) descriptors remains a practical entry point for assessing genetic variability, guiding parental selection, and avoiding redundancy in germplasm curation, especially where multi-environment testing and molecular assays face resource constraints (PPV&FRA, 2007; Selvi *et al.*, 2013; Naseer *et al.*, 2018). Complementary divergence analyses, such as Mahalanobis D^2, cluster analysis, and factor analysis, enable the quantification of inter-genotypic distances and the rational identification of diverse parents to exploit heterosis, thereby widening the breeding base and enhancing selection efficiency (Mahalanobis, 1928). Together, these approaches offer a cost-effective pipeline for translating phenotypic diversity into breeding gains under variable Indian conditions.

The present study evaluated 60 maize genotypes against 24 DUS descriptors to: (i) quantify morphological variability across leaf, root, tassel, ear, plant and kernel traits; (ii) frequency distribution and mean performance for key phenological and yield components; (iii) assess genetic divergence and clustering patterns to identify complementary parents; and (iv) prioritize inbreds for hybrid development tailored to regional production constraints in Jharkhand and similar environments.

Materials and Methods

The study was conducted during *Kharif* 2024 at the western research farm of Birsa Agricultural University (BAU), Kanke (23°25′47.3″ N, 85°18′48.3″ E, 625 m AMSL), located in a humid subtropical plateau region with monsoon-driven rainfall, well-suited for maize cultivation. The experiment evaluated 60 maize genotypes, including 56 inbred lines sourced from ICAR-Indian Institute of Maize Research (IIMR), Hyderabad, and four widely grown hybrids—Suvan 1, Suvan 2, DHM 117, and DHM 121 which served as checks for comparative assessment.

A randomized block design (RBD) with three replications was implemented to control field variability and improve the precision of genotype evaluation (Gomez and Gomez, 1984). Each plot comprised two rows, each 2 meters in length, with 60 cm row spacing and 20 cm plant spacing, and one seed per hill to ensure uniform competition. Three guard rows were maintained around the experiment to reduce border effects. Uniform agronomic practices, including fertilization, weed control, and pest management, were consistently applied to minimize non-genetic variation. Data were collected from five randomly selected competitive plants per genotype in every replication to capture representative within-plot variation (PPV & FRA, 2007).

Morphological characterization followed 24 DUS descriptors (PPV&FRA, 2007), presented in Table 1, with observations made at defined growth stages on a per-plant basis. Phenological traits such as days to 50% tasseling, silking, and the tassel–silking interval were recorded at plot level, while plant and ear height were measured at the dry silk stage. Ear and kernel traits, including 1000-kernel weight, were recorded at harvest to stabilize moisture-related variation. Qualitative traits were summarized through frequency distributions to reveal population structure, while quantitative traits were averaged per plot and replication to compute genotype means, ranges, and grand means. This approach highlighted key traits like maturity, plant stature, cob dimensions, and yield potential. Additionally, the dataset was designed to support advanced analyses such as Mahalanobis D^2 and hierarchical clustering, helping to identify genetically diverse parents for future heterosis breeding (Mahalanobis, 1928), with all computations aligned to standard biometric procedures.

Table 1 : DUS Descriptors and Scoring Criteria for Morphological Characterization of Maize Inbred Lines and Checks

S. No.	Part	Characteristics	State
1	Leaf	Angle between blade and stem (just above ear)	Small (<45°) / Wide (>45°)
2		Altitude of blade (above upper ear)	Droopy / Straight
3		Anthocyanin coloration of sheath	Absent / Present
4		Width of leaf blade (cm, above ear)	Narrow (<8 cm) / Wide (>8 cm)
5	Roots	Anthocyanin coloration of brace roots	Absent / Present
6	Tassel	Anthocyanin at base of glume	Present / Absent
7		Anthocyanin of glumes excluding base (middle third)	Present / Absent
8		Anthocyanin coloration of anthers	Absent / Present
9		Density of tassel (middle third of main axis)	Dense / Sparse
10		Length of main axis (lowest side branch to tip)	Short (<20 cm) / Medium (20–30 cm) / Long (>30 cm)
11		Angle of lateral branches (lower third of tassel)	Narrow (<45°) / Wide (>45°)
12		Attitude of lateral branches	Straight / Curved / Droopy
13		Days to 50% tasseling (from sowing)	<45 (Very Early) / 45–50 (Early) / 50–55 (Late) / >55 (Very Late)
14	Ear	Anthocyanin coloration of silks (at emergence)	Present / Absent
15		Days to 50% silking	Very Early (<48) / Early (48–53) / Medium (53–58) / Late (>58)
16		Ear Placement (base to top ear insertion)	Low / Medium / High
17		Cob length (cm)	Short (<10 cm) / Medium (10–15 cm) / Long (>15 cm)
18		Cob diameter (cm)	Small (<4 cm) / Medium (4–5 cm) / Large (>5 cm)
19		Cob shape	Conical / Conico-cylindrical / Cylindrical
20		Number of rows per cob (middle of ear)	Few (8) / Medium (10–12) / Many (14)
21		Anthocyanin coloration of glumes of cob	White / Light purple / Dark purple
22	Plant	Plant Height (dry silk stage, cm)	Inbreds: Short (<120 cm) / Medium (120–150 cm) / Long (>150 cm) Hybrids: Short (<150 cm) / Medium (150–180 cm) / Long (181–210 cm) / Very Long (>210 cm)
23	Kernel	Arrangement (middle of ear)	Straight / Spiral / Irregular
24		Test weight (1000 kernel weight, g)	Very Small (<100 g) / Small (100–200 g) / Medium (200–300 g) / Large (>300 g)

Result and Discussion

Leaf traits showed clear majority of genotypes with wide leaf blade in 51 genotypes (85%), straight leaf attitude in 41 (68%), and a near-balanced split for leaf angle (wide 31, 52%; small 29, 48%) indicating ample morphological contrast for distinctness showing proximity with kumar *et al.* (2024). Anthocyanin pigmentation was uniformly absent in leaf sheath and cob glumes (0%), yet frequently present in tassel glume base (48, 80%), anthers (37, 62%), and brace roots (33, 55%), These pigmentation patterns are essential for genotype identification and breeding programs, as noted by Selvi *et al.*, (2013) who found that UMI 551 had noticeable tassel anthocyanin coloration at the glume base among 17 maize inbred lines studied. Tassel attributes concentrated in breeder-preferred mid-classes dense tassel (34, 57%), medium length (33, 55%), wide angle (32, 53%) and drooping attitude (34, 57%) These variations in tassel morphology are important for pollen production and hybrid seed production efficiency, as reported by Madhukeshwara and Sajjan (2015) who found significant variation in tassel characteristics among maize hybrids. These readings are given grapically as the frequency in table 1 along with number of genotypes in the parenthesis and visual diffrences are shown in fig. 2a, 2b, 2c and 2d. Reproductive timing skewed early with tasseling: 55% early, 37% very early; silking: 60% early, 22% very early aligning with breeding emphasis of timely crop completion and stress escape, Blum (2011) stated Early flowering reduces the anthesis–silking interval, enabling drought escape and sustaining grain yield, with early‑maturing hybrids yielding 20–30% more under terminal drought. Ear and kernel traits showed structured variation: ear placement was mainly medium (33, 55%); cob length was predominantly long (38, 63%) while small-to-medium diameters dominated (47 small, 78%; 7 medium, 12%); cob shape favored conical and conico-cylindrical states (32, 53%; 21, 35%); rows per cob were medium primarily to many (35, 58%; 22, 37%); kernel arrangement was primarily straight (31, 52%); and test weight classes fell in small and medium (39, 65%; 21, 35%) are similar to Saha *et al.* (2024) who used DUS descriptors for characterizing thirty-two maize inbred lines and found that fourteen traits were dimorphic and six characters were trimorphic indicating that all traits were informative with respect to trait expression and characterization.

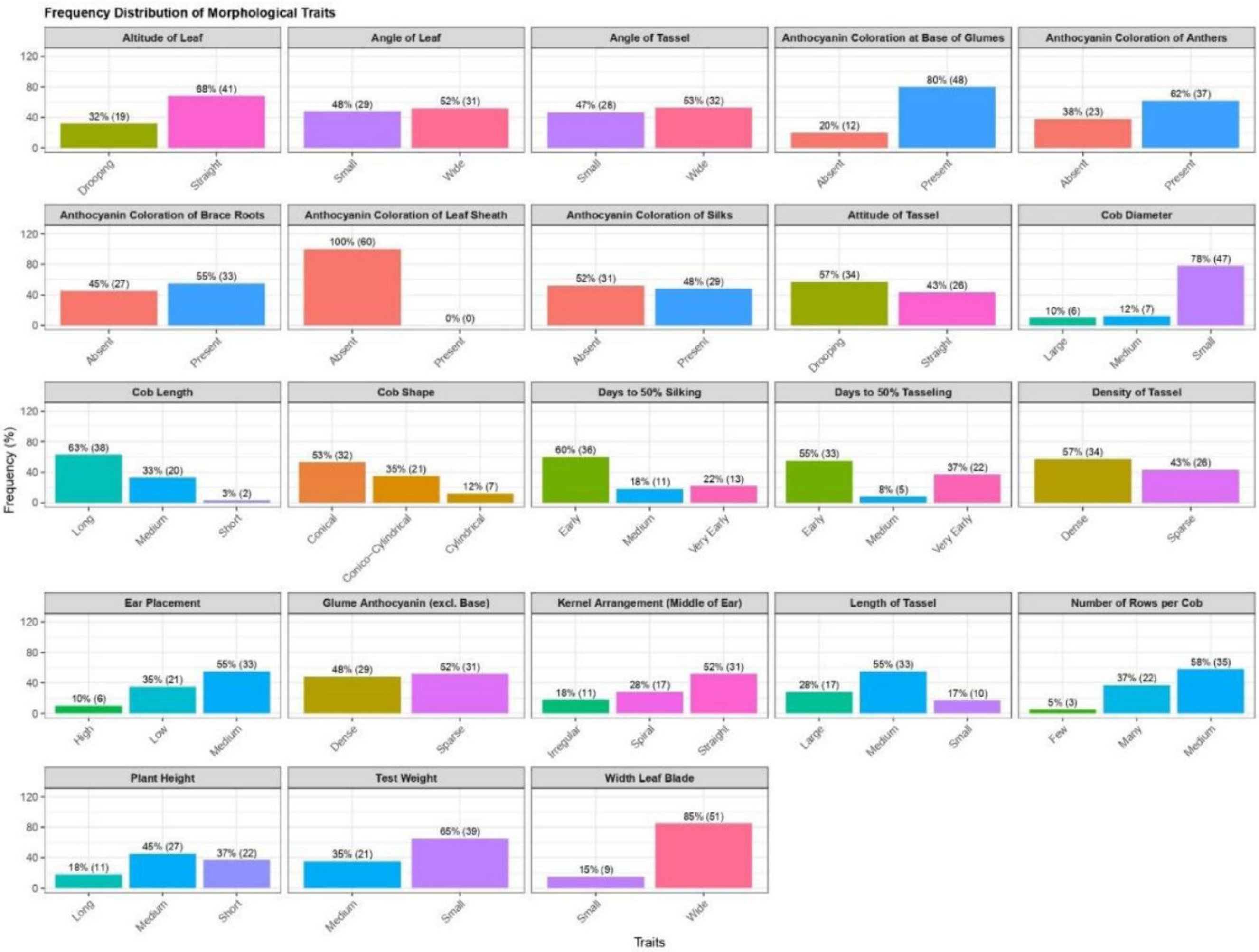

Fig.1: Frequency distributions histogram for the maize DUS traits

Fig 2a. Variation in Brace Root Colouration

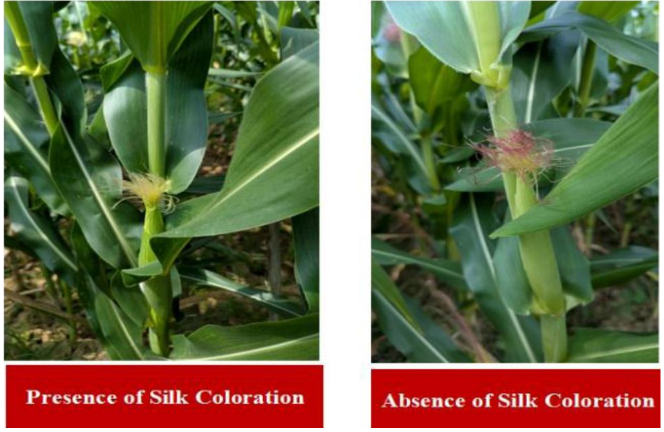

Fig 2b. Variations in Silk Colouration


Presence of Coloration on Tassel Glumes
Absence of Coloration on Tassel Glumes
Droopy Tassel
Straight Tassel
Presence of Coloration Base of Glumes
Presence of Coloration Base of Glumes
Sparse Tassel
Dense Tassel

Fig 2c. Variations in Different Tassel

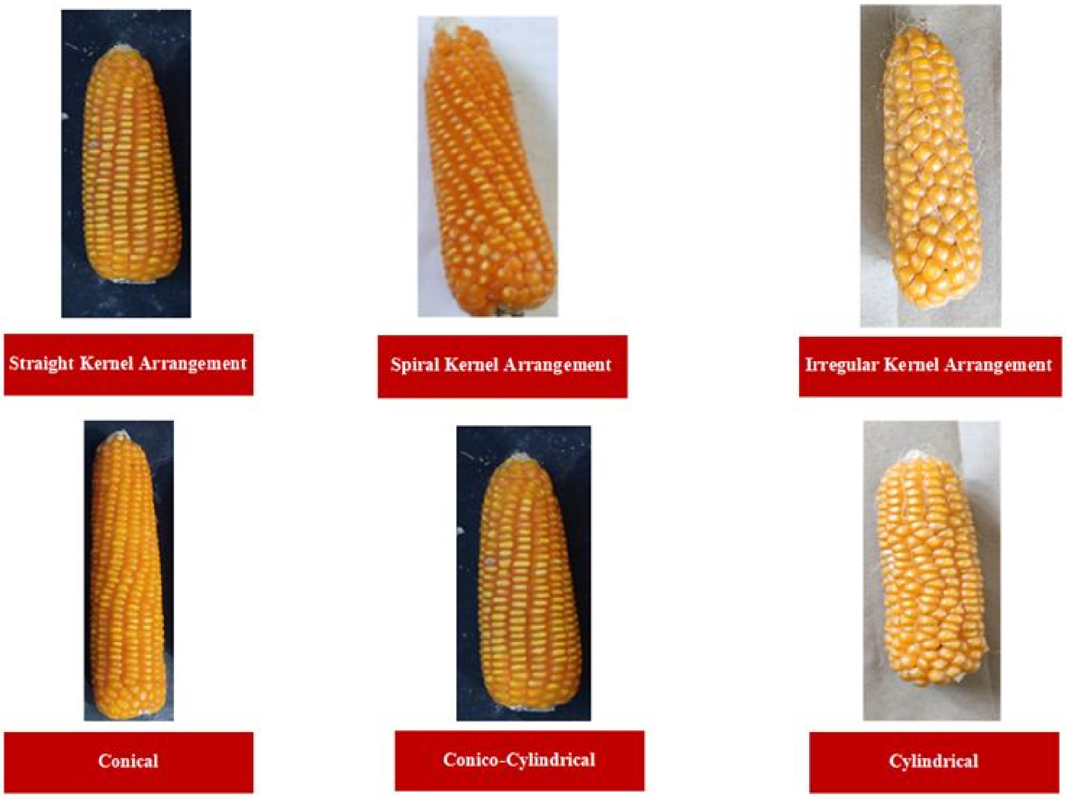
Straight Kernel Arrangement
Spiral Kernel Arrangement
Irregular Kernel Arrangement
Conical
Conico-Cylindrical
Cylindrical

Fig 2d. : Variations in Different Cob Traits

As summarized in Table 2, Mean performance for quantitative traits, Days to 50% tasseling ranged 41.6–52.3 days (mean 46.6), with CM 139 earliest (41.6) and CML 394 latest (52.3); 32 genotypes were earlier than the mean. Days to 50% silking ranged 46.0–57.0 days (mean 51.2), with CM 139 earliest (46.0) and CML 394 latest (57.0); 30 genotypes were earlier than the mean. Tassel–silking interval spanned 3.3–5.3 days (mean 4.5), with IML 307-1 at 3.3 (lowest) and CM 119 at 5.3 (highest); 29 genotypes were below the mean. Bolaños and Edmeades, (1996) stated narrow Anthesis-Silking Interval ranges have been reported yield stability under stress conditions.

Days to 75% maturity ranged 76.6–94.6 days (mean 86.1), with IML 418-1 earliest (76.6) and IMLSB 1294-1 latest (94.6); 30 genotypes matured earlier than the mean. Plant height spanned 69.6–184.2 cm (mean 127.3), with CM 153 shortest (69.56 cm) and Suvan 2 tallest (184.2 cm); 31 genotypes were shorter than the mean. Ear placement ranged 41.0–108.7 cm (mean 76.7), with CM 153 lowest ear (41.0 cm) and Suvan 2 highest ear (108.7 cm); approximately half of genotypes were below the mean, Zhao *et al.* (2022) emphasized that optimizing ear-plant height ratio improves kernel number and lodging resistance in maize. Cob length ranged 9.5–31.2 cm (mean 16.7), with CM 139 maximum (31.2) and DQL 100 minimum (9.5); 33 genotypes exceeded the mean. Cob diameter ranged 2.8–5.9 cm (mean 3.9), with DHM 121 maximum (5.9) and DI 217 minimum (2.8); 24 genotypes exceeded the mean. Rows per cob ranged 8.0–16.0 (mean 12.2), with CML 278 highest (16.0) and IMLSB 114-1 lowest (8.0); 28 genotypes were below the mean. Kernels per row ranged 12.3–33.9 (mean 23.7), with CM 213 highest (33.9) and CML 342dv lowest (12.3); 31 genotypes were above the mean, Kangarasu *et al.* (2013) stated both number of kernel rows per cob and number of kernels per row exhibit strong positive direct effects on grain yield and highlighted them as key traits for yield improvement in Indian maize germplasm.. Yield per plant ranged 34.6–81.1 g (mean 53.7 g), with CM 213 maximum (81.1 g) and CM 153 minimum (34.6 g); 23 genotypes exceeded the mean These findings corroborate earlier reports that grain yield in maize is strongly influenced by kernel number per ear and cob dimensions (Sofi *et al.*, 2007).

Table 2 : Mean performance, ranges and notable genotype for quantitative traits

Trait (Units)	**Mean**	**Minimum/Earliest**		**Maximum/Late**	
		Value	**Genotype**	**Value**	**Genotype**
Days to 50% Tasseling (days)	46.6	41.6	CM 139	52.3	CML 394
Days to 50% Silking (days)	51.2	46.0	CM 139	57.0	CML 394
Tassel–Silking Interval (days)	4.5	3.3	IML 307-1	5.3	CM 119
Days to 75% Maturity (days)	86.1	76.6	IML 418-1	94.6	IMLSB 1294-1
Plant Height (cm)	127.3	69.6	CM 153	184.2	Suvan 2
Ear Placement (cm)	76.7	41.0	CM 153	108.7	Suvan 2
Cob Length (cm)	16.7	9.5	DQL 100	31.2	CM 139
Cob Diameter (cm)	3.9	2.8	DI 217	5.9	DHM 121
Rows per Cob	12.2	8.0	IMLSB 114-1	16.0	CML 278
Kernels per Row	23.7	12.3	CML 342dv	33.9	CM 213
Yield per Plant (g)	53.7	34.6	CM 153	81.1	CM 213

Tocher's clustering grouped 60 maize genotypes into four clusters based on quantitative traits, revealing significant genetic diversity. Cluster I with 24 genotypes (40%) including VQL 1, DI 219 and IMLSB lines formed a major gene pool has distint characters, consistent with Anusha *et al.* (2022). Clusters II and III had 16 genotypes each (26.7%), while Cluster IV, with only Suvan 1, Suvan 2, DHM 117, and DHM 121 (6.7%), was distinct, showing superior plant height, ear placement, and yield, as noted by Kumar *et al.* (2020) and distribution pattern illustrated in Fig. 3.

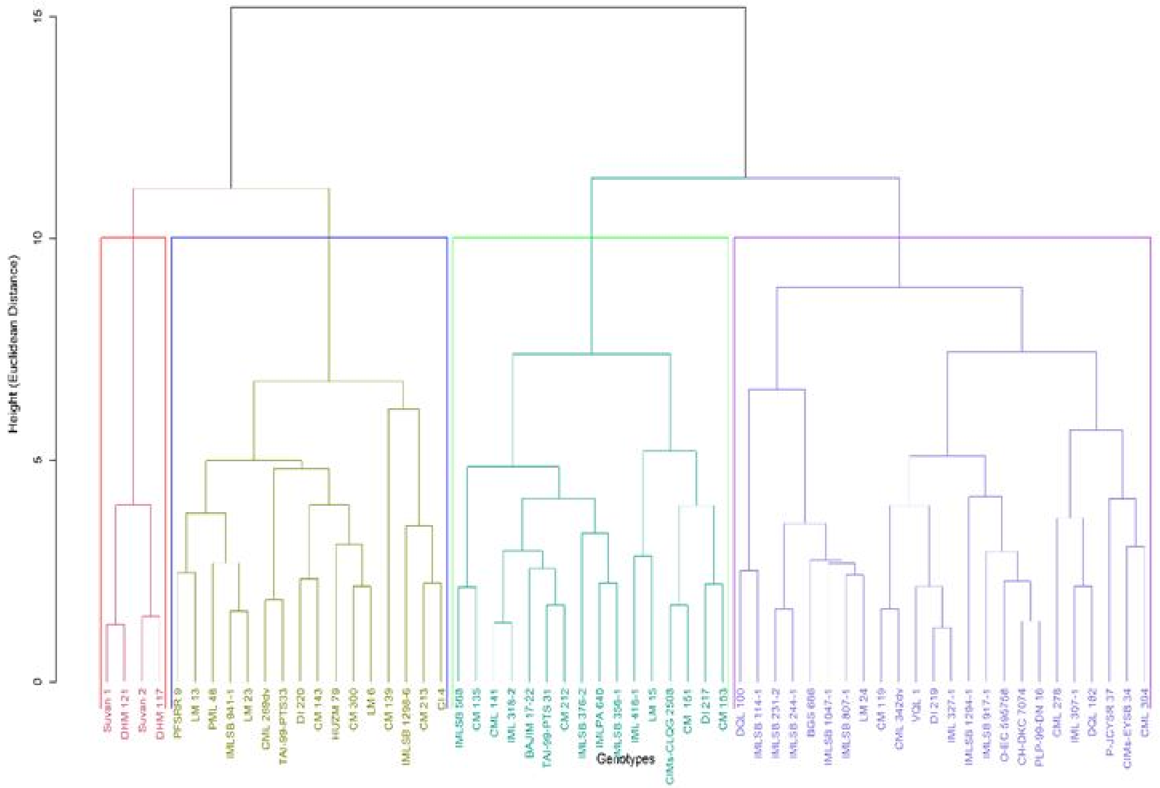

Fig. 3 : Hierarchical clustering dendrogram of 60 Maize genotypes

Conclusion

The morphological assessment of 60 maize genotypes through 24 DUS descriptors demonstrated substantial genetic variability essential for germplasm classification and breeding applications. Frequency analysis revealed predominant traits including wide leaf blades (85%), straight leaf attitude (68%), anthocyanin presence at tassel glume base (80%) and long cob configuration (63%) establishing clear morphological signatures for genotype identification. Quantitative evaluation spanning days to 50% tasseling (41.6-52.3 days), plant height (69.6-184.2 cm), cob dimensions (9.5-31.2 cm length; 2.8-5.9 cm diameter), and yield per plant (34.6-81.1 g) confirmed wide phenotypic ranges suitable for diverse selection objectives. Notable performers emerged across traits: CM 139 for early maturity and extended cob length, CM 213 for superior kernel number and yield expression, DHM 121 for enhanced cob diameter and Suvan 2 for plant stature characteristics.

Hierarchical clustering organized genotypes into four distinct groups, with Cluster I representing the diverse gene pool (40%) and Cluster IV containing commercially established hybrids (6.7%), indicating meaningful genetic structure. The integrated DUS profiling and clustering framework provides practical tools for germplasm curation, parent selection and breeding program optimization tailored to regional production systems. These findings establish a comprehensive characterization baseline supporting future genetic improvement initiatives in maize.

Acknowledgments

Grateful acknowledgment is extended to Department of GPB, Birsa Agricultural University (BAU), Kanke, for providing experimental fields, facilities and logistical support.

Conflicts of Interest/Competing Interests: The authors declare no conflicts of interest.

Authors' Contributions:

Matta Revanth Kumar Reddy (Corresponding Author) - Conceptualization, Data curation, Data collection, Formal analysis, Investigation, Methodology, Visualization, Writing Original Draft, Writing – Review and Editing.

Dr. Sunil Kumar, Dr. Manigopa Chakraborty, Dr. M.K. Barnawal (Co Author) - Supervision, Validation.

Dr. Shivam Mishra (Co Author) - Resources, Software.

Nisha Bhrati (Co Author) - Writing – Review and Editing.

References

Anonymous (2007). Guidelines for the conduct of tests for distinctness, uniformity and stability on maize (*Zea mays*). The Protection of Plant Varieties and Farmers'Rights authority, New Delhi. *Plant Variety J. India*, **1**(1), 1-13.

Anonymous 2024. United Portal for Agricultural Statistics., Department of Agriculture and Farmers Welfare. Ministry of Agriculture and Farmers welfare, New Delhi.

Anusha, B. K., Lohithaswa, H. C., and Anilkumar, C. (2022). Genetic diversity analysis in maize (*Zea mays* L.) using D² statistics. *Journal of Crop and Weed*, ***18***(2), 123–130.

Bolaños, J. and Edmeades, G. O. (1996). The importance of the anthesis-silking interval in breeding for drought tolerance in tropical maize. *Field Crops Research*, **48**(1), 65–80.

Blum, A. (2011). Drought resistance – is it really a complex trait? *Functional Plant Biology*, **38**(10), 753–757.

Galinat WC (1977) The origin of corn. In: Sprague GF (ed) Corn and corn improvement. *American Society of Agronomy*, Madison, pp 1–47

Willey, R. W. (1979). Intercropping - its importance and research needs. 1. Competition and yield advantages. *Field Crop Abstract*, **32**, 1–10.

Jadhav, S. S., Mote, M. S., Karad, S. R., Salunke, A. J. and Ghosale, R. R. (2024). Evaluation of divergence for drought condition in maize (*Zea mays* L.). *International Journal of Advanced Biochemistry Research*, ***8***(12), 659–675.

Kanagarasu, S., Nallathambi, G., and Ganesan, K. N. (2013). Correlation and path analysis in maize (*Zea mays* L.). Electronic Journal of Plant Breeding, **4**(2), 478–484

Kumar S., Singh M. and Rani K.J. 2024. DUS descriptors-based characterization of maize cultivars for varietal protection. Indian J. Agric. Sci., **94**: 243–249.

Kumar, A., Singh, B. and Sharma, S. (2020). Heterotic hybrid frequency in relation to combining ability and parental genetic divergence in maize. *Indian Journal of Agricultural Sciences*, ***90***(4), 712–718.

Li, Z., Li, C., Zhang, R., Duan, M., Tian, H., Yi, H., Xu, L., Wang, F., Shi, Z., Wang, X., Wang, J., Su, A., Wang, S., Sun, X., Zhao, Y., Wang, S., Zhang, Y., Wang, Y., Song, W. and Zhao, J. (2023). Genomic analysis of a new heterotic maize group reveals key loci for pedigree breeding. *Frontiers in Plant Science*, ***14***, 1213675.

Madhukeshwara, B. P. and Sajjan, A. S. (2015). Morphometric characterization of maize hybrids and their parents using DUS guidelines. *Advance Research Journal of Crop Improvement*, **6**(2), 178-182.

Mahalanobis, P. C. (1928). A statistical study at the University of Calcutta: On the generalized distance in statistics. Proceedings of the National Institute of Sciences of India, **2**(1), 49–55.

Milind, P. and Isha, B. (2013). Maize: Nutrition and health benefits. International Research *Journal of Pharmacy*, **4**(7), 1–7.

Naseer, S., Malik, T. A., Raza, Q., and Farooq, A. (2018). Distinctness, uniformity and stability (DUS) characterization in crops: A review. International Journal of Development and Sustainability, **7**(3), 1034–1043.

Prasanna, B. M., Cairns, J. E., Zaidi, P. H. and Beyene, Y. (2020). Maize breeding for climate resilience: Advances and future perspectives. *Field Crops Research*, ***245***, 107628.

Saha, S., Rana, V. B., Sanghavi, B., Pawan, V. and Mahadevu, P. (2024). Morphological characterization and dendrogram analysis of DUS (Distinctiveness, Uniformity, Stability) traits in maize inbred lines (*Zea mays* L.). Plant Archives **24**(1), 431-438.

Sofi, P. A., Rather, A. G., Wani, S. A. and Dar, S. A. (2007). Correlation and path coefficient analysis in maize (*Zea mays* L.). *Asian Journal of Plant Sciences*, **6**(4), 705–708.

Von B. J., Swaminathan, M. S. and Rosegrant, M. W. (2010). Agriculture, food security nutrition and the millennium development goals, Intenational Food Policy Research Institute. Washington D. C., United States.

Wen, W., Guo, T., Chavez Tovar, V. H., Li, H., Yan, J. and Taba, S. (2016). The strategy for the utilization of maize genetic diversity in breeding. *Theoretical and Applied Genetics*, ***129***(8), 1465–1476.

Zhao, Y., Zhang, S., Lv, Y., Ning, F., Cao, Y., Liao, S., ... and Huang, S. (2022). Optimizing ear-plant height ratio to improve kernel number and lodging resistance in Maize (*Zea mays* L.). *Field Crops Research*, **276**, 108376.