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RESEARCH PAPER

Phenotypic profiling of specialty corn through DUS descriptors for morphological distinctiveness

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Abstract: The present study aimed to perform phenotypic profiling of specialty corn genotypes for morphological distinctiveness using DUS (Distinctness, Uniformity and Stability) descriptors and to evaluate their yield performance. A total of 30 specialty corn genotypes comprising Popcorn and Sweet corn were evaluated under field conditions using a Randomized Block Design (RBD) with three replications. Morphological characterization was carried out using standard DUS descriptors, and quantitative traits including grain yield were recorded and subjected to statistical analysis to assess variability among genotypes. The analysis revealed considerable variation among the genotypes for several morphological traits, indicating clear phenotypic diversity. Grain yield in Popcorn genotypes ranged from 15.20 to 25.25 q ha^{-1}, with genotype BAUPP-23/24-9006 recording the highest yield of 25.00 q ha^{-1}. In Sweet corn, yield ranged from 8.26 to 10.73 q ha^{-1}, and genotype BAUSC-23/24-10102 produced the maximum yield of 10.73 q ha^{-1}. The wide range observed in yield and morphological traits confirms the presence of significant variability among the evaluated genotypes.

Keywords: Popcorn • Sweet corn • DUS descriptors • Genetic diversity • Phenotypic variation

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Introduction

Maize (*Zea mays* L.), a member of the Poaceae family and widely known as corn, ranks among the most important cereal crops globally. It originated in southern Mexico, where it was domesticated from its wild progenitor, teosinte, approximately 9,000–10,000 years ago. From its center of domestication, maize gradually dispersed throughout the Americas and was later introduced to Africa, Asia, and Europe following European exploration. Owing to its remarkable adaptability, maize can be cultivated across diverse agro-ecological zones ranging from temperate to tropical environments. Today, maize plays a central role as a staple food, an essential component of livestock feed, and an important raw material for several industrial applications, including starch, sweeteners, ethanol, and other bio-based products (Matsuoka *et al*., 2002; Ranum *et al*., 2014; Shiferaw *et al*., 2011).

In India, maize is the third most widely cultivated cereal after rice and wheat, with production occurring across a wide range of agro-climatic regions. According to the Government of India's advance estimates, during the 2023-24 cropping season maize was cultivated on approximately 10.74 million hectares with a production of about 37.66 million tonnes. In 2024–25, the area under maize remained nearly unchanged at around 10.73 million hectares; however, production increased significantly to approximately 42.28 million tonnes. This increase in output reflects improvements in productivity driven by the adoption of improved hybrids, better crop management practices, and increasing cultivation of specialty maize types (Government of India, 2024; Agricultural Statistics at a Glance, 2023).

Despite the expansion in cultivation, the national average yield of maize in India remains relatively low, around 3.5 tonnes per hectare, compared with the global average of approximately 6.0 t/ha. Nevertheless, some states such as West Bengal, Telangana, and Bihar have achieved yields close to or exceeding the global average (Livemint, 2024; FAS-USDA, 2024). Maize is cultivated across three seasons–*Kharif*, *Rabi*, and Summer–with the majority of production occurring during the *Kharif* season in states such as Karnataka, Madhya Pradesh, Maharashtra, Bihar, and Telangana (Livemint, 2024; Maize Outlook Report, 2024). These trends highlight the increasing importance of maize not only for food and feed but also as a crucial raw material for India's expanding poultry, starch, and biofuel industries.

In recent years, specialty maize types such as Popcorn and Sweet corn have gained increasing commercial and consumer interest due to their unique quality attributes, nutritional value, and value-added market potential. Effective utilization and conservation of such germplasm require systematic characterization and identification of distinct genetic resources. One of the most widely accepted approaches for varietal characterization is the application of Distinctness, Uniformity, and Stability (DUS) descriptors, which provide a standardized framework for evaluating morphological and agronomic traits. DUS testing is essential for varietal identification, protection of plant breeders' rights, and maintenance of genetic purity in breeding programs (UPOV, 2002; PPV&FRA, 2007; Prasanna *et al*., 2021).

Several studies have employed DUS descriptors for morphological characterization and identification of maize varieties and inbred lines. These studies have demonstrated that DUS traits are effective in distinguishing genotypes and documenting phenotypic variation within germplasm collections. However, many earlier investigations have primarily focused on conventional field maize or hybrid breeding lines, with relatively limited attention given to specialty maize types such as Popcorn and Sweet corn. Furthermore, variability in environmental conditions and the limited number of evaluated germplasm lines in some studies have constrained the comprehensive assessment of phenotypic diversity using DUS descriptors.

Given the growing demand for specialty maize and the need for efficient germplasm characterization, a detailed evaluation of phenotypic diversity using standardized descriptors becomes particularly important. Assessing the genetic variability present in specialty maize collections not only facilitates the identification of distinct and stable genotypes but also provides valuable information for parent selection in breeding programs aimed at improving yield, quality traits, and adaptability.

Therefore, the present study was undertaken to characterize and evaluate specialty maize germplasm using DUS descriptors in order to assess phenotypic diversity, establish distinct morphological traits, and identify promising genotypes that may serve as potential genetic resources for maize improvement and breeding programs.

Materials and methods

The present investigation was carried out during the *Kharif* season of 2024 at the Western Research Farm of Birsa Agricultural University (BAU), Kanke (23°252 47.33 N, 85°182 48.33 E; 625 m AMSL). The site, located in a humid subtropical plateau region with monsoon-driven rainfall, offers optimal agro-climatic conditions for maize cultivation.

A total of 30 specialty corn genotypes–including 15 popcorn and 15 sweet corn lines. A total of 24 morphological descriptors were recorded at different growth stages of the crop.These included traits related to plant morphology, leaf characteristics, tassel traits, ear morphology, and kernel attributes defined under Distinctness, Uniformity, and Stability (DUS) guidelines. The experiment was laid out in a randomized block design (RBD) with three replications to minimize environmental variability and enhance the precision of genotype comparisons, following the approach described by Balakrishna *et al*. (2016). Each genotype was grown in two rows of 2 m length, with a spacing of 60 cm between rows and 20 cm between plants. Standard agronomic practices recommended for maize cultivation in the region were followed to ensure optimal crop growth. Fertilizer application, irrigation, weed management, and plant protection measures were carried out as per recommended agronomic guidelines. Phenotypic characterization of the maize genotypes was carried out using the Distinctness, Uniformity, and Stability (DUS) descriptors as described in the guidelines of the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA, 2007) and the International Union for the Protection of New Varieties of Plants (UPOV, 2002) for maize.

Observations were recorded from five randomly selected competitive plants per genotype in each replication, and the average value was used for further analysis. Quantitative traits such as plant height, ear length, and number of kernel rows per ear were measured using standard field measurement techniques.Qualitative traits were recorded using the standardized scoring scales provided in the DUS guidelines. Each state of expression was assigned a numerical code corresponding to the descriptor states defined by PPV&FRA and UPOV. For example, traits such as anthocyanin coloration of leaf sheath, tassel branch density, ear shape, and kernel color were scored according to the predefined categorical scales.

To facilitate statistical analysis, qualitative trait states were converted into numerical codes based on the descriptor scale. The frequency distribution of each trait state across genotypes was calculated to assess phenotypic variability.

To examine the genetic relationships and grouping patterns among the maize genotypes, hierarchical cluster analysis was performed using the morphological descriptor data. Prior to clustering, both qualitative (coded) and quantitative traits were standardized to minimize the influence of scale differences among variables. A Euclidean distance matrix was computed to estimate the dissimilarity among genotypes. The resulting clusters were represented through a dendrogram, which illustrated the degree of similarity and divergence among the evaluated genotypes. The data obtained from the genotypes mentioned in the above Table no. 1 were subjected to comprehensive statistical analysis using R software (version 4.5.1) with the R-Studio integrated development environment (R Core Team, 2024).

Result

Leaf architecture and blade characteristics

Leaf morphological traits showed considerable variability between Popcorn and Sweet corn genotypes. In Popcorn (T1–T15), 70% of genotypes had narrow leaf angles (<45°), whereas in Sweet corn (T31–T45), a slightly higher proportion exhibited narrow angles. Most genotypes in both groups had drooping leaf blades (Popcorn 87%, Sweet corn 80%), with leaf blade width mostly narrow (<8 cm) in Popcorn and moderate in Sweet corn.

Anthocyanin pigmentation

Anthocyanin expression varied by tissue and genotype group. In Popcorn, brace root pigmentation was present in 60% of genotypes, tassel base pigmentation in 33%, and anther pigmentation in 53.33%. Sweet corn showed similar trends, but silk pigmentation was slightly less frequent (40%), reflecting varietal differences. Leaf sheath pigmentation was absent in both groups. These patterns are consistent with allelic control by ZmR1 and homologous regulatory genes (Styles & Ceska, 1977; Grotewold, 2006) and can be used as DUS-based markers to differentiate Popcorn from Sweet corn in breeding programs.

Table 1. List of thirty maize genotypes used in present investigation procurred from department of Genetics and Plant Breeding, BAU, Kanke, Ranchi

S. No.	Name of genotype	Sources/ pedigree	Nomencla-ture
1.	BAUPP-23/24-9004	BPCH6 -1	T1
2.	BAUPP-23/24-9005	MPC 23-40-1	T2
3.	BAUPP-23/24-9007	IPH2-23R-1-1	T3
4.	BAUPP-23/24-9054	DMRHP 1402-2	T4
5.	BAUPP-23/24-9101	DMRHP 1402-3	T5
6.	BAUPP-23/24-9107	BPCH 6- 9107-3	T6
7.	BAUPP-23/24-9106	LPCH 3- 2	T7
8.	BAUPP-23/249052	IPH2-23R-1-2	T8
9.	BAUPP-23/24-9002	DMRHP 1402-1	T9
10.	BAUPP-23/24-9051	BPCH 6- 9107-2	T10
11.	BAUPP-23/24-9102	PP-11-3	T11
12.	BAUPP-23/24-9057	LPCH-3-2	T12
13.	BAUPP-23/24-9105	IPH2-23R-1-3	T13
14.	BAUPP-23/24-9055	PP-11-2	T14
15.	BAUPP-23/24-9006	PP-09-1	T15
16.	BAUSC-23/2-10054	PUSA SWEET CORN -1-4	T31
17.	BAUSC-23/24-10052	GDH 23 GS 11-2	T32
18.	BAUSC-23/24-10004	MISTHI-1	T33
19.	BAUSC-23/24-10155	MISHTI-4	T34
20.	BAUSC-23/24-10102	MISTHI-3	T35
21.	BAUSC-23/24-10001	GDH 23 GS 11-1	T36
22.	BAUSC-23/24-10104	PUSA SWEET CORN -1-3	T37
23.	BAUSC-23/24-10101	MSC 23-61-3	T38
24.	BAUSC-23/24-10154	PUSA SWEET CORN -1-4	T39
25.	BAUSC-23/24-10053	CMVL SWEET CORN 1-2	T40
26.	BAUSC-23/24-10051	MSC 23-61-2	T41
27.	BAUSC-23/24-10003	PUSA SWEET CORN -1-1	T42
28.	BAUSC-23/24-10153	MSC 23-61-4	T43
29.	BAUSC-23/24-10002	MSC 23-61-1	T44
30.	BAUSC-23/24-10005	CMVL SWEETCORN 1-1	T45

Tassel and spikelet traits

Spikelet density differed slightly between groups: Popcorn genotypes had dense spikelets in 73%, while Sweet corn showed dense arrangements in 67%. Tassel length in Popcorn ranged from 11.8–16.04 cm, whereas Sweet corn ranged from 15.94–18.17 cm, indicating longer tassels in Sweet corn. Lateral branch attitude was predominantly straight in both groups (Popcorn 77%, Sweet corn 80%). These traits are critical for pollen production, outcrossing efficiency, and varietal identification, with Sweet corn lines showing slightly more open tassels, potentially facilitating hybrid seed production.

Flowering time

Days to 50% tasseling (TAS) and silking (SIL) exhibited moderate variation. In Popcorn, TAS ranged from 44–48 days and SIL from 46.3–50.66 days, while in Sweet corn, TAS ranged from 43–45.3 days and SIL from 47–49.66 days. The anthesis-silking interval (ASI) was slightly narrower in Sweet corn (2.0–3.0 days) than in Popcorn (2.33–3.0 days), indicating more synchronized flowering, which is favorable for seed set. Sweet corn genotypes flowered slightly earlier than Popcorn, which is important for hybridization timing in breeding programs.

Ear morphology and placement

Ear traits also differentiated the two groups. In Popcorn, medium ear placement was predominant, with cob length mainly medium (12.0-16.04) and diameter mostly small. Sweet corn showed slightly higher ear placement and larger cob diameters (3.11–4.33 cm), with longer ears (16.07–18.17 cm), reflecting market-preferred ear size. Cob shape in Popcorn was primarily cylindrical, whereas Sweet corn had a similar distribution but with slightly more conico-cylindrical forms, making ear morphology a reliable marker for varietal distinction.

Plant height and kernel traits

The kernel arrangement among the genotypes was predominantly irregular (43%), followed by straight (33%) and spiral (23%) patterns. Kernel count per cob (KC) ranged from 25.97 (T10) to 40.63 (T35), with Popcorn generally showing lower kernel counts and test weight (TW), while Sweet corn had slightly higher values. Test weight ranged from 10.6 g (T13) to 39.12 g (T7), reflecting genetic differences and agronomic significance.

Table 2. Standardized Morphological Profiling of Specialty Maize Using DUS Parameters (PPV&FRA, 2007; UPOV, 2002)

S. No.	Part of Plant	Character	State of Expression	No. of genotypes	Frequency
1	Leaf	Angle of Leaf	Small (< 45 °)	21	70.00
			Wide (>45°)	9	30.00
2		Altitude of Leaf blade (above upper ear)	Straight	4	13.33
			Drooping	26	86.67
3		Anthocyanin Coloration of Leaf Sheath	Present	0	0.00
			Absent	30	100.00
4		Width Leaf Blade (cm)	Narrow (<8 cm)	17	56.67
			Wide (>8 cm)	13	43.33
5	Roots	Anthocyanin Coloration of Brace Roots	Present	18	60.00
			Absent	12	40.00
6	Tassel	Anthocyanin Coloration at Base of Glumes	Present	10	33.33
			Absent	20	66.67
7		Anthocyanin Coloration of Glumes Excluding Base (middle third)	Present	12	40.00
			Absent	18	60.00
8		Anthocyanin Coloration Of Anthers	Present	16	53.33
			Absent	14	46.67
9		Density of Tassel (middle third of main axis)	Sparse	8	26.67
			Dense	22	73.33

Table 2 contd...

S. No.	Part of Plant	Character	State of Expression	No. of genotypes	Frequency
10		Length of main axis (lowest side branch to tip,cm)	Small (<20 cm)	3	10.00
			Medium (20–30 cm)	18	60.00
			Large (>30 cm)	9	30.00
11		Angle of lateral branches (lower third of tassel)	Small (<45°)	19	63.33
			Wide (>45°)	11	36.67
12		Attitude of Tassel	Staright	23	76.67
			Drooping	7	23.33
13		Days To 50% Tasseling	Very Early (<45)	6	20.00
			Early (45–50)	19	63.33
			Medium (50–55)	5	16.67
			Late (>55)	0	0.00
14	Ear	Anthocyanin Coloration Of Silks	Present	13	43.33
			Absent	17	56.67
15		Days To 50% Silking	Very Early (<48)	9	30.00
			Early (45–50)	17	56.67
			Late (50–55)	4	13.33
			Very Late (>55)	0	0.00
16		Ear Placement (base to top ear insertion, cm)	Low	3	10.00
			Medium	24	80.00
			High	3	10.00
17		Cob Length (cm)	Short (<10 cm)	0	0.00
			Medium (10–15 cm)	13	43.33
			Long (>15cm)	17	56.67
18		Cob Diameter (cm)	Small (<4 cm)	21	70.00
			Medium (4–5 cm)	6	20.00
			Large (>5 cm)	3	10.00
19		Cob Shape	Conical	3	10.00
			Conico-Cylindrical	13	43.33
			Cylindrical	14	46.67
20		Number Of Rows Per Cob	Few (8)	0	0.00
			Medium (10-12)	10	33.33
			Many (14)	20	66.67
21		Anthocyanin Coloration Of Cob Glumes	Absent	30	100.00
			Present	0	0.00
22	Plant	Plant Height (cm)	Short (<120 cm)	12	40.00
			Medium (120–150 cm)	18	60.00
			Long (150-180 cm)	0	0.00
			Very Long (>180 cm)	01	3.33
23	Kernel	Kernel Arrangement (Middle of ear)	Straight	10	33.33
			Spiral	7	23.33
			Irregular	13	43.33
24		Test Weight (1000 kernel weight, g)	Very Small (<100 g)	15	50.00
			Small (100–200 g)	15	50.00
			Medium (200–300 g)	0	0.00
			Large (>300 g)	0	0.00

Figure 1. Straight and droopy leaves

Figure 2. Dense and sparse Tassel

Figure 3. Anthocyanin absent and present

Figure 4. Narrow and wide leaves

Figure 5. Long and short tassel

Figure 6. Anthocyanin in brace roots

Figure 7. Anthocyanin in tassel

Figure 8. Kernel arrangement

These quantitative measures align with qualitative DUS descriptors, confirming that kernel size, arrangement, and weight are reliable indicators for varietal differentiation and breeding selection (Hallauer *et al*., 2010; Akinwale *et al*., 2011).

Diversity analysis

Hierarchical cluster analysis using Ward's variance method grouped the 30 maize genotypes into two distinct clusters based on their phenological traits. The dendrogram shows a clear separation at a higher fusion distance, indicating substantial divergence among the genotypes for the measured phenological parameters.

Discussion

The morphological characterization of 30 specialty maize genotypes using DUS descriptors (Table 2) revealed

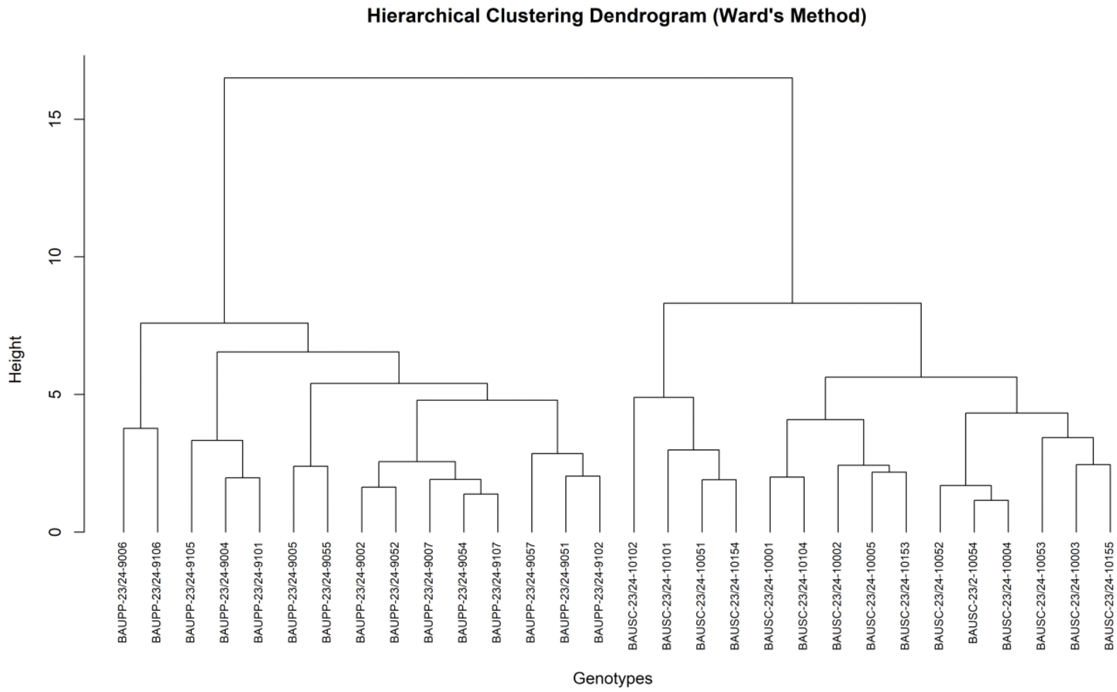

Figure 9. Dendrogram of 30 Specialty corn

substantial variation in vegetative, reproductive, and kernel traits, highlighting their usefulness for differentiating Popcorn and Sweet corn germplasm. Leaf morphology showed considerable diversity, with most genotypes exhibiting narrow leaf angles (<45°) and drooping leaf blades, which together contribute to a relatively compact canopy architecture that may enhance light interception and photosynthetic efficiency. Variation in leaf blade width was also observed, where Popcorn genotypes generally possessed narrower leaves compared with Sweet corn. Differences in anthocyanin pigmentation were evident across several plant organs, particularly in brace roots, tassel structures (glumes and anthers), and silks, while pigmentation was absent in the leaf sheath and cob glumes across all genotypes (Table 2). Such tissue-specific pigmentation patterns are regulated by genes involved in the anthocyanin biosynthetic pathway and serve as stable morphological markers for maize characterization and varietal identification (Styles & Ceska, 1977; Grotewold, 2006). Tassel architecture also varied among the genotypes, with a predominance of dense spikelet distribution, medium to large main axis length, and mostly straight lateral branches, traits that are important for efficient pollen production and hybrid seed production (UPOV, 2002; PPV&FRA, 2007).

Phenological and ear-related characters also exhibited moderate variability among the evaluated genotypes (Table 2). Most lines were categorized as early to very early for days to 50% tasseling and silking, indicating relatively synchronized flowering and favorable anthesis–silking intervals for effective fertilization. Sweet corn genotypes tended to flower slightly earlier than Popcorn, suggesting potential advantages in hybridization timing. Ear placement was predominantly medium, while cob length ranged from medium to long, with small to medium cob diameters and shapes varying from conical to cylindrical. The majority of genotypes produced many kernel rows per cob, although kernel arrangement varied among straight, spiral, and irregular patterns, reflecting substantial genetic diversity in ear architecture. Plant height mainly ranged from short to medium classes, which is desirable for improved lodging resistance and crop management. Kernel traits also varied, particularly in test weight, where most genotypes fell within very small to small categories, consistent with the typical grain characteristics of specialty maize types. Among the Popcorn, BAUPP-23/24-9006 genotype has performed the best and in Sweetcorn, BAUSC-23/24-10102 was the outperformer in terms of yield and other yield attributing characters. The hierarchical cluster analysis using Ward's variance method (Figure 9) grouped the 30 genotypes into two major clusters, indicating significant phenotypic divergence among the evaluated germplasm. Similar patterns of morphological variability and clustering in maize germplasm have been reported by Hallauer *et al*. (2010) and Akinwale *et al*. (2011), emphasizing the importance of such diversity for selecting genetically distinct parental lines in maize breeding programs.

Conclusion

The investigation showed that specialty corn genotypes differ widely in many visible and agronomic traits. Differences in leaf shape, angle, and pigmentation were clear, while tassel size and branching pattern also varied between genotypes. Ear traits such as cob length, diameter, and shape, as well as kernel arrangement and seed weight, showed large variation, making them very useful for identifying and selecting varieties.Group-wise differences were also evident. Popcorn was characterized by smaller ears and moderate yield, reflecting its inherent trade-off between popping quality and productivity whereas Sweet corn, despite desirable ear traits and early maturity showed lower test weight because of low starch and high sugar content hence lower yield making it highly suitable for markets. Overall BAUPP-23/24-9006 genotype was the outperformer in Popcorn, recording the highest yield of 25.00 q ha^{-1}. In Sweet corn, yield ranged from 8.26 to 10.73 q ha^{-1}, and genotype BAUSC-23/24-10102 produced the maximum yield of 10.73 q ha^{-1}. The marked separation between the two clusters suggests significant variability in phenological behavior among the evaluated genotypes, providing useful differentiation for selection and breeding programmes targeting maturity traits.

Declarations

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Consent for publication: Not applicable.

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