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EVALUATION OF MAIZE HYBRIDS FOR MORPHO-QUANTITATIVE TRAITS UNDER PRAYAGRAJ AGRO-CLIMATIC CONDITIONS USING MAHALANOBIS D^2 ANALYSIS

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ABSTRACT

The development and cultivation of hybrids is the key to improving the productivity of Maize crop. The present study evaluated 26 maize (*Zea mays* L.) hybrids under the agro-climatic conditions of Prayagraj, Uttar Pradesh, during the Kharif season of 2024-2025 for genetic parameters and genetic variability in relation to yield and its morpho-quantitative traits. Analysis of variance (ANOVA) revealed significant differences among the hybrids, indicating substantial genetic variability. The traits field weight and biological weight recorded the high GCV (50.52 and 30.02) and PCV (50.96 and 30.25) values, respectively. The traits field weight, biological weight and plant height recorded the high heritability (>60%) along with high genetic advance expressed as a percentage of mean (>20%), suggesting predominant additive gene action and high potential for genetic improvement through selection.The assessment of genetic diversity grouped the 26 hybrids into 5 distinct clusters, with the majority (9 hybrids) falling into Cluster V. Among the clusters, the maximum intra-cluster distance was observed in Cluster V (3.6). The greatest inter-cluster distance (9.08) was observed between Cluster IV and Cluster I, suggesting that interbreeding among members in these two clusters could facilitate the production of highly desirable transgressive segregants. The pronounced inter-cluster distances, especially between Cluster IV and others, highlight its potential as a parent in heterotic cross combinations.Based on a genetic divergence study VH171310, ZH22698, ZH20379 and VH183007. These findings offer crucial direction for selecting diverse and high-performing hybrids to enhance maize productivity and adaptability in Eastern Uttar Pradesh.

Keywords: Cluster Analysis, Diversity, Genetic Variability, Heritability, Maize (*Zea mays* L.), Morpho-Quantitative Traits.

INTRODUCTION

Maize (*Zea mays* L.) occupies a significant position in global food, feed and industrial systems. In India, maize ranks third after rice and wheat in terms of area and production and plays a vital role in ensuring food security, economic development and agro-industrial advancement (Nadar *et al.,* 2024). The crop's productivity and adaptation are highly influenced by genetic makeup and

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Corresponding author e-mail i.d: kiranedla29@gmail.com prevailing agro-climatic conditions. Therefore, the identification and selection of superior hybrids suited to specific environments is essential to maximize yield and quality traits (Long, 2025). It is the most widely grown cereal crop in the world, cultivated for food, feed and industrial uses. Globally, the crop covers an estimated 193.7 million hectares, with a production of approximately 1,147.7 million metric tonnes as of 2023–2024, yielding an average of 5.83 tonnes per hectare (USDA, 2024). India ranks among the top ten maize producers globally. During the 2023–2024 agricultural year, India cultivated maize in 11.24 million hectares, producing about 37.67 million metric tonnes, with an average yield of 3.35 tonnes per hectare (Directorate of Economics and Statistics, 2024). Maize is grown extensively in states like Karnataka, Madhya Pradesh, Maharashtra, Rajasthan and Uttar Pradesh, both in the *kharif* and *rabi* seasons. In Uttar Pradesh, maize is a significant cereal crop due to its adaptability and rising demand in the poultry and starch industries. As per recent estimates, the state recorded an area of around 0.83 million hectares and production of 2.12 million tonnes in 2023–2024 (Mohanty *et al.,* 2025). The Prayagraj region, located in the eastern part of Uttar Pradesh, represents a unique agro-ecological zone with its own soil, climate and cropping system characteristics. Limited systematic studies have been conducted to assess the genetic variability of maize hybrids under local conditions (Singh *et al.,*2021). A survey of genetic variability determinants *viz.* genotypic and phenotypic coefficient of variations (GCV and PCV) indicates the degree of variation exists among sunflower genotypes with respect to particular character and also detail about role of the environment in expression of the character. Broad sense heritability (h^2) and genetic advance as percent of mean (GAM) defines selection effectiveness and also nature of gene action in inheritance of particular character. Evaluating this diversity under specific agro-climatic conditions allows breeders to exploit favorable traits through hybridization and selection (Kachapur *et al.,* 2023). Among the various multivariate techniques available, Mahalanobis' D^2 statistic is a powerful tool for assessing genetic divergence among genotypes. It allows for the classification of genotypes into distinct clusters based on multiple traits simultaneously, thus helping in the identification of genetically diverse parents for hybrid development. Hence, the present investigation was undertaken to evaluate the genetic diversity among maize hybrids for various morpho-qualitative traits under Prayagraj agro-climatic conditions using D^2 analysis. The key to future improvement lies in exploiting a wider range of inbred lines to create even better hybrids. Hence, this study was conducted to assess the variability and genetic diversity in newly developed maize hybrids in this specific agro-ecological zone.

MATERIAL AND METHODS

The experiment was carried out at the Department of Genetics and Plant Breeding field experiment centre, Naini Agricultural Institute, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, during *Kharif* 2024-2025. The experiment material comprised 26 maize hybrids, which were obtained from the maize germplasm pool maintained at the CIMMYT Asia office, Hyderabad, Telangana. The details of the experimental materials are listed in Table 1. It included 22 CIMMYT hybrids along with 4 checks.

The gross field area of 178.2 m^2 was divided into two subplots. An irrigation channel of dimension 0.5 meters ran between adjacent subplots. These subplots were used to replicate the hybrids twice.A total of 26 maize hybrids have been sown in a Randomized block design. Each entry was sown in a double row of 1 metre in length in each replication. All of these hybrids were sown on one seed per hill. The spacing between the rows and between the plants is 60cm and 30cm, respectively. The crop was raised per the recommended package of practices.

The data were recorded for the following characters: Days to Maturity, Plant Height (cm), Ear Height (cm), Ear Length (cm), Number of Ears, Number of Kernel Rows, Number of Kernels per Row, Field Weight (gm), Ear Aspect, Grain Moisture %, Test Weight (gm), Biological Weight (gm), Grain Weight Per Plant (gm), Grain Weight Per Plot (gm) and Seed Yield Per Hectare (kg). To check the significance among genotypes, Analysis of variance was carried out as per methodology suggested by Panse and Sukhatme (1967). Phenotypic coefficient of variation and genotypic coefficient of variation were calculated by the formula given by Burton and Devane,1953. Heritability in broad sense (h^2) was worked out by using formula suggested by Burton and Devane,1953 and genetic advance i.e. the expected genetic advance was calculated by using the procedure given by Johnson *et al*.(1955).

RESULTS AND DISCUSSION

ANOVA Test for Different Quantitative Traits

The ANOVA results indicated that the mean sum of squares (MSS) due to genotypes was highly significant for all the traits studied, confirming the presence of substantial genetic differences among the hybrids. This significant variation reflects a broad range of diversity in the morpho-quantitative characteristics of the evaluated hybrids, which is crucial for effective selection in breeding programs. These findings align with previous studies that have also reported considerable genetic variability in maize for similar traits by Usman *et al.,* 2024. Such variability offers ample opportunities for identifying superior genotypes and advancing genetic gain through targeted selection and hybridization.

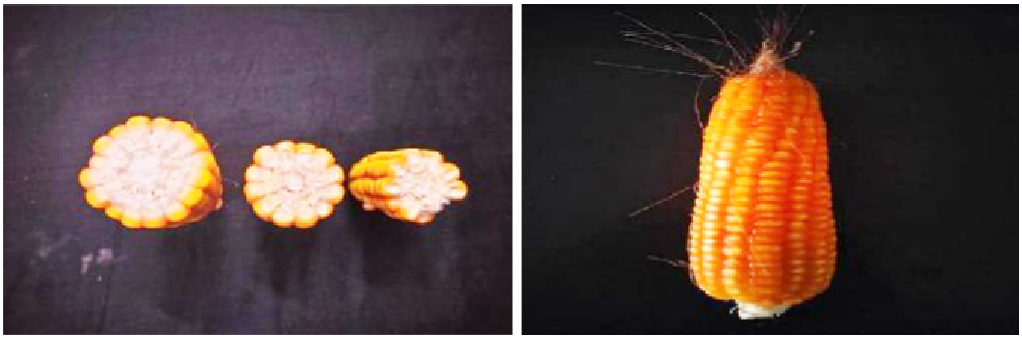
Coefficient of Variation (GCV and PCV), Heritability (h2), Genetic Advance (GA), and Genetic Advance as Percent of Mean (GAPM)

The objective of this study was to assess key genetic parameters, including heritability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and

Table 1. List of 22 CIMMYT hybrids along with 4 checks

S.No.	Hybrids	S.No.	Hybrids	S.No.	Hybrids	S.No.	Hybrids	S.No.	Hybrids
1	Internal Check: 1	7	KH151871	13	VH181219	19	ZH22741	25	VH19601
2	Commercial Check: 2	8	VH171310	14	VH19227	20	ZH22742	26	VH18614
3	VH182239	9	ZH221149	15	VH19490	21	ZH20265		
4	ZH22698	10	VH183007	16	ZH22744	22	VH152761		
5	Commercial Check: 1	11	ZH20379	17	ZH22740	23	VH18580		
6	ZH221145	12	Commercial Check: 3	18	ZH22731	24	ZH20154		

Emergence of Silk and Tassel **Plant Height** **Ear Height**



Number of Kernels per row Number of Kernel rows

Quantitative traits in Maize

genetic advance as a percentage of the mean (GAPM). This comprehensive evaluation aimed to understand the extent of genetic variability and the potential for genetic improvement in the studied maize hybrids.The detailed findings for each trait, including estimates of genetic variability and potential for improvement,are presented in Table 2.

Genotypic (GCV) and Phenotypic (PCV) Coefficients of Variation

The summary statistics such as mean, range, GCV, PCV, GAM and heritability values of the studied traits were shown in Table 2. Field weight trait ranges from 272.86 to 1878.72 with mean value of 842.25. Whereas, the trait biological weight ranges from 103.6 to 311.58 with mean value of 208.34. The findings showed that the PCV estimates exceeded the GCV estimates for all traits, suggesting a significant environmental influence on their expression. Notably, field weight and biological weight traits recorded the higher estimates of PCV and GCV values. The high GCV values enable the rewarding of direct selection for these traits. Moderate PCV and GCV values observed for plant height (cm), ear length (cm) and number of ears traits. The lower estimates of PCV and GCV was observed for the trait number of days to maturity and ear height (cm). Further, the low GCV value implies that the direct selection is not rewarding for such traits. Similar results were observed by Antony *et al.,* 2024.

Heritability (h^2) and Genetic Advance as Percent of Mean (GAPM)

A wide range of heritability was observed across the fifteen traits evaluated (Table 3). Traits such as plant height (97.67%), number of kernels per row (93.97%), field weight (98.28%), biological weight (98.46%), grain

Table 2. Analysis of variance for different characters in maize hybrids

	Summary of ANOVA			
	Source of variance	**Mean sum of squares (MSS)**		
S.No.	**Degrees of freedom**	**Genotype**	**Replication**	**Error**
		25	**1**	**25**
1	Days to Maturity	15.259*	290.942	6.742
2	Plant Height(cm)	2314.142**	7.948	27.239
3	Ear Height(cm)	93.459**	1.062	18.196
4	Ear Length(cm)	8.394**	0.156	1.707
5	Number of Ears	0.240**	0.396	0.025
6	Number of Kernel Rows	2.677**	3.481	0.550
7	Number of Kernels per Row	34.313**	0.073	1.066
8	Field Weight (gm)	365406.294**	1369.094	3166.429
9	Ear Aspect	1.139**	0.019	0.107
10	Grain Moisture %	3.688**	0.103	0.243
11	Test Weight(gm)	29.862**	1.167	1.906
12	Biological Weight (gm)	7885.209**	271.275	61.041
13	Grain Weight Per Plant (gm)	810.200**	27.857	9.347
14	Grain Weight Per Plot (gm)	182294.893**	6267.823	2103.016
15	Seed Yield Per Hectare (kg)	506374.703**	17410.620	5841.710

Significant at 1% level of significance (**) Significant at 5% level of significance (*)

weight per plant (97.71%), grain weight per plot (97.71%) and seed yield per hectare (97.71%) exhibited very high heritability, indicating that these are largely governed by genetic factors and can be effectively improved through selection. Correspondingly, these traits also showed high GAPM values field weight (103.19%), seed yield per hectare (78.23%), grain weight per plant and plot (78.23%), and Test weight (38.48%) further supporting their strong genetic control and potential responsiveness to selection.

According to GAPM classifications, values below 10% are considered low, 10–20% as moderate and above 20% as high. Traits such as days to maturity (2.93%) showed low GAPM along with low heritability (38.71%), suggesting limited genetic gain and greater environmental influence. Ear height (10.02%) and number of kernel rows (12.93%) showed moderate GAPM, while ear length (22.70%), grain moisture (24.44%) and ear aspect (68.78%) demonstrated high genetic advance as percent of the mean. The combination of high heritability and high GAPM for key traits such as seed yield, grain and biological weight, field weight and kernel number per row suggests that these characters are primarily controlled by additive gene action and can be efficiently improved through simple selection.

These findings are by earlier studies conducted by Hasan *et al.*(2025), who also reported moderate GA values for traits like days to 50% silking and tasseling. Similarly,

Table 3. Estimation of genetic parameters for 26 maize hybrids.

	Range			Coefficient of Variation		Herita-bility (%)	Genetic Advance	GA% Mean
Traits	**Mean**	**Min**	**Max**	**PCV (%)**	**GCV(%)**			
Days to Maturity	89.98	86	95.5	3.68	2.29	38.71	2.64	2.93
Plant Height(cm)	224.51	162.64	261.17	15.24	15.06	97.67	68.84	30.66
Ear Height(cm)	103.47	87.24	113.66	7.22	5.92	67.40	10.37	10.02
Ear Length(cm)	13.43	9.06	17.01	16.68	13.56	66.04	3.05	22.70
Number of Ears	1.77	1.2	2.33	20.47	18.42	80.98	0.60	34.16
Number of Kernel Rows	13.33	11.07	14.9	9.52	7.73	65.89	1.72	12.93
Number of Kernels Per Row	26.76	19.88	34.01	15.712	15.23	93.97	8.14	30.41
Field Weight (gm)	842.25	272.86	1878.72	50.96	50.52	98.28	869.13	103.19
Ear Aspect	1.95	1	3.7	40.33	36.69	82.79	1.34	68.78
Grain Moisture %	10.35	7.5	12.37	13.53	12.67	87.64	2.53	24.44
Test Weight (gm)	18.77	13.17	29.77	21.23	19.91	88.00	7.22	38.48
Biological Weight (gm)	208.34	103.6	311.58	30.25	30.02	98.46	127.85	61.36
Grain Weight Per Plant (gm)	52.06	16.85	88.74	38.86	38.41	97.71	40.74	78.23
Grain Weight Per Plot (gm)	781.27	252.75	1331.1	38.86	38.41	97.71	611.23	78.23
Seed Yield Per Hectare(kg)	1302.12	421.25	2218.5	38.86	38.41	97.71	1018.72	78.23

high GAPM values for traits such as grain yield per plant, Test weight and number of kernels per row were also supported by the findings of Hasan *et al.,* 2025. Moreover, reports by Banjara *et al.,* 2025, reinforce the conclusion that traits under high heritable influence and high genetic advance offer the best prospects for genetic improvement through direct selection in maize breeding programs.

Genetic Divergence

Genetic divergence analysis is a powerful tool in plant breeding for identifying genetically diverse genotypes, which can be effectively used in hybridization programs to obtain maximum heterosis. In the present study, Mahalanobis' D^2 statistics was employed to evaluate the extent of genetic variability among 26 maize hybrids based on multiple morpho-quantitative traits under Prayagraj agro-climatic conditions, which were grouped into five distinct clusters (Table 4). This clustering also included four check varieties: Internal Check:1, Commercial Check:1, Commercial Check:2 and Commercial Check:3. The distribution of check varieties across clusters allowed for direct comparisons with test hybrids and provided a benchmark to assess their relative performance.

The intra and inter-cluster distances (Table 5,Fig.1) provide important information regarding the degree of genetic similarity or dissimilarity among genotypes. The intra-cluster distances ranged from 0 (Cluster IV) to 3.604 (Cluster V), suggesting that the hybrids within Cluster IV were highly similar, while moderate variability existed within Cluster V. The inter-cluster distances were highest between Cluster I and Cluster IV (9.08), followed by Cluster III and Cluster IV (8.32), and Cluster II and Cluster IV (6.10). These wide genetic distances indicate that the genotypes grouped in these clusters are highly divergent and could serve as ideal candidates for hybridization to exploit maximum heterosis. Conversely, the lowest inter-cluster distance was observed between Cluster I and Cluster III (4.62), implying relatively lower genetic divergence between these groups.

Internal Check : 1 and Commercial Check:1 was both grouped in Cluster I along with genotypes VH171310, VH182239, and ZH22698. Commercial Check : 2 also fell under Cluster I, indicating genetic similarity among these entries. Commercial Check : 3, on the other hand, was placed in Cluster II, alongside ZH221149, ZH20379 and VH183007.

Table 4. Distribution of 26 maize hybrids in different clusters using D^2 statistics

Cluster Group	No. of hybrids	Name of hybrid
1	6	VH171310, VH182239, Internal Check:1, Commercial Check:2, ZH22698, Commercial Check:1
2	4	ZH221149, ZH20379, VH183007, Commercial Check:3
3	6	ZH22731, ZH22741, ZH221145, ZH22740, KH151871, VH181219
4	1	VH19227
5	9	ZH22742, VH19490, ZH22744, VH18614, ZH20265, ZH20154, VH18580, VH152761, VH19601

The intra and inter-cluster distances

Table 5. Average Intra and Inter cluster distances of 26 maize hybrids

Cluster	CI	CII	CIII	CIV	C V
C I	2.947346				
C II	4.920047	3.034597			
C III	4.623814	5.055006	3.442944		
C IV	9.083386	6.105321	8.321435	0	
C V	7.14766	4.628081	6.447671	4.892003	3.604004

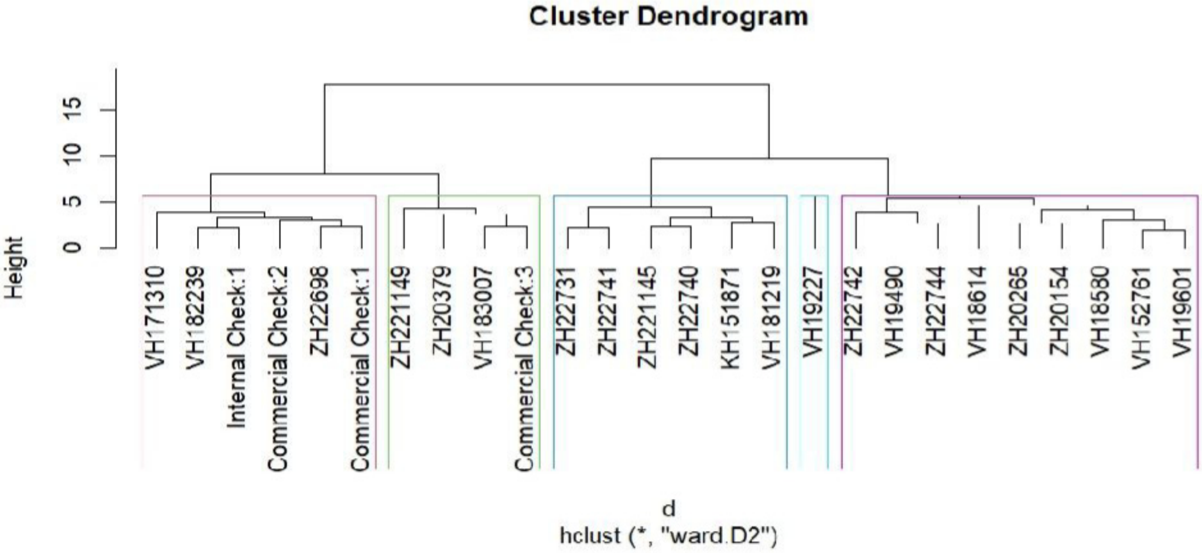


Fig. 1. Cluster Dendogram Showing Grouping of Hybrids

Intra and Inter-Cluster Distances

This grouping suggests that Cluster I contains genotypes genetically similar to the commonly used checks, while genotypes in Clusters III, IV, and V may represent more divergent material.

Cluster Means

The cluster mean values for 15 morpho-quantitative traits (Table 6.) further emphasized the genetic variability across clusters. Cluster IV showed superiority in several traits including plant height (256.42 cm), ear length (16.58 cm), number of ears (2.31), kernels per row (33.37), grain weight per plant (88.74 g) and seed yield per hectare (2218.5 kg). These results suggest that the genotype VH19227, which forms a single-entry cluster (Cluster IV), is a highly promising hybrid possessing multiple desirable traits. This indicates that VH19227 is a significantly superior genotype over all check varieties for most yield-related traits.

Cluster III also recorded high performance in key yield attributes such as ear length (15.8 cm), number of ears (2.139), kernels per row (31.1) and grain weight per plant (73.62 g). In contrast, Cluster V recorded the lowest values for most traits including plant height (188.58 cm), grain weight per plant

Table 6. Cluster Means of different characters in maize hybrids

Trait	C I	C II	C III	C IV	C V
Days to Maturity	86.375	91.5	93.1	89	89.05
Plant Height(cm)	244.24	241.901	253.319	256.42	188.589
Ear Height(cm)	106.498	107.758	108.653	100.59	97.407
Ear Length(cm)	14.808	12.469	15.8	16.58	11.97
Number of Ears	1.5075	1.8033	2.139	2.31	1.6375
Number of Kernel Rows	13.291	13.645	14.112	14.035	12.71
Number of Kernels Per Row	27.149	26.177	31.1	33.37	24.145
Field Weight (gm)	1165.118	743.459	1233.459	1878.725	473.137
Ear Aspect	1.1125	1.875	1.43	1.3	2.675
Grain Moisture %	11.19	11.325	10.894	10.94	9.1135
Test Weight (gm)	25.3425	16.5508	19.468	22.495	16.7565
Biological Weight (gm)	246.989	215.765	278.029	311.58	143.269
Grain Weight Per Plant (gm)	55.23	44.1	73.62	88.74	35.083
Grain Weight Per Plot (gm)	1057.275	661.5	1104.3	1331.1	526.245
Seed Yield Per Hectare(kg)	1762.125	1102.5	1840.5	2218.5	877.075

(35.08 g) and seed yield (877.075 kg/ha), indicating the presence of lower-yielding genotypes in this group. Cluster I and Cluster II exhibited moderate values across traits, with Cluster I performing well in Test weight (25.34 g) and field weight (1165.12 g).

Contribution of Traits to Genetic Divergence

The relative contribution of individual traits to total genetic divergence was estimated using D² analysis and is presented in Table 7. Among the 15 traits studied, field weight (34.1%) contributed the most to total divergence, followed by biological weight (14.6%), grain weight per plant (12.6%) and grain weight per plot (13.1%). These yield-related traits collectively accounted for more than 70% of the observed genetic variability. In contrast, traits like ear height (0.1%), grain moisture (0.9%) and ear length (1.1%) made minimal contributions.

This suggests that selection based on yield components such as field weight,

Ear Length (cm)

Grain Weight (gm)

Table 7. Percent contribution of 15 characters towards genetic divergence

Characters	Percent contribution
Days to Maturity	1.5%
Plant Height(cm)	8.7%
Ear Height(cm)	0.1%
Ear Length(cm)	1.1%
Number of Ears	3.2%
Number of Kernel Rows	2.1%
Number of Kernels Per Row	2.7%
Field Weight (gm)	34.1%
Ear Aspect	1.3%
Grain Moisture %	0.9%
Test Weight (gm)	1.3%
Biological Weight (gm)	14.6%
Grain Weight Per Plant (gm)	12.6%
Grain Weight Per Plot (gm)	13.1%
Seed Yield Per Hectare(kg)	2.8%

biological weight and grain weight per plant is likely to be more effective in identifying diverse and high-performing genotypes. The greater divergence contributed by yield-related traits also aligns with the primary breeding objective of enhancing productivity under the specific agro-climatic conditions of Prayagraj.

The presence of check varieties in Clusters I and II serves as a benchmark for genetic and agronomic performance. The fact that genotypes in Clusters III and IV outperformed checks across multiple traits indicates the availability of superior genetic material in the experimental hybrids. Notably, VH19227 (Cluster IV) and several Cluster III entries (e.g., ZH22731, ZH22741, ZH221145) can be utilized for future hybrid development due to their high divergence and favorable performance. Similar findings were noted by Singh *et al.*2021.

These findings suggest that crossing genetically divergent and agronomically superior genotypes from Cluster IV or III with stable check-type entries from Cluster I may result in heterotic hybrids with enhanced yield potential and adaptability under Prayagraj agro-climatic conditions.

CONCLUSION

To conclude, the present study established notable genetic variability and divergence among maize hybrids evaluated under the agro-climatic conditions of Prayagraj.

Hybrids like VH19227, VH171310, ZH22698, ZH20379, and VH183007 stood out for their superior performance in multiple morpho - quantitative traits, highlighting their potential for both direct release and use as diverse parental lines in hybrid development.

Special focus should be directed towards traits exhibiting high heritability and genetic advance - most notably field weight, biological weight, and grain weight per plant as they significantly contribute to genetic divergence and hold promise for effective selection. The wide genetic diversity identified in this study offers a strong foundation for improving maize yield, resilience and adaptability, supporting the development of high-performing, region-specific hybrids for eastern Uttar Pradesh.

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