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REVIEW ARTICLE

ASSESSMENT OF GENETIC VARIABILITY AND TRAIT INTERRELATIONSHIPS IN MAIZE HYBRIDS (ZEA MAYS L.)

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ABSTRACT

Maize is a globally important cereal crop that plays a crucial role in food security and agricultural sustainability. Understanding the genetic and phenotypic variability of maize genotypes is essential for improving yield potential and adaptability through breeding programs. This study aimed to evaluate the genetic and phenotypic variability of 24 maize genotypes, including local and commercial checks, under winter growing conditions in Chitwan, Nepal. The experiment was conducted at the National Maize Research Program (NMRP) in Rampur, Chitwan, during the winter of 2023 using a Randomized Complete Block Design (RCBD) with three replications. Key agronomic traits, including days to 50% anthesis and silking, plant height, ear height, cob characteristics, kernel traits, and grain yield, were recorded. Statistical analyses included the estimation of phenotypic and genotypic coefficients of variation (PCV and GCV), heritability, genetic advance as a percentage of the mean (GAM), correlation analysis, and path analysis. Results revealed high genetic variability for ear height, plant and ear aspect, and grain yield, indicating their potential for genetic improvement. High heritability estimates (>60%) were observed for flowering traits, plant and ear height, cob characteristics, and grain yield, suggesting minimal environmental influence. Correlation analysis showed significant positive associations between grain yield and traits such as plant height, ear height, cob length, cob diameter, and kernel-related traits. Path analysis identified the number of ears per hectare as key contributors to grain yield. These findings highlight the importance of optimizing ear traits for yield improvement. The identified high-yielding genotypes with favorable agronomic traits can be further evaluated in multi-location trials to assess their stability and adaptability for broader cultivation.

KEYWORDS

Maize genotypes, Genetic variability, Grain yield, Heritability, Genetic advance

1. INTRODUCTION

Maize (Zea mays L.) is one of the most widely cultivated crop globally, valued as a key food, feed, and industrial grain due to its versatile applications and broad adaptability to diverse environmental conditions. It is second most important grain crop after rice in Nepal, serves as food, feed, fodder, and an industrial raw material (Tripathi et al., 2022). Maize serves as a crucial staple crop in Nepal, playing a significant role in ensuring food security due to its high productivity and commercial versatility. It is both produced and consumed as a primary food source in regions where food and nutrition insecurity remain major challenges (Dhakal et al., 2018). In Nepal, it is cultivated on 940,256 hectares of land, producing 2,976,490 metric tons (mt) with an average yield of 3.16 metric tons per hectare (MoALD, 2023).

Maize is a dual-purpose crop, extensively utilized as both human food and livestock feed. The current demand for maize grains has significantly increased due to their growing use in poultry and livestock feed. However, local maize production falls short of meeting the national feed requirements, primarily driven by the rapid expansion of poultry and dairy farming (Osti, 2020). Despite the availability of 45 registered commercial maize hybrids, 83% of Nepalese farmers continue to grow open-pollinated varieties (OPVs), while only 17% for hybrid varieties (Gairhe et al., 2021). The hybrids grown in large numbers in Nepal come from the formulation provided by several international companies. The main factor for low yield among the hybrids has been due to a lack of location-specific hybrids suitable for the area (Tripathi et al., 2016). A majority of the maize varieties grown in Nepal are sourced from the Indian market due to the lack of dependable and commercially viable hybrid maize seeds produced locally. The production of national hybrid seeds is inadequate because of insufficient research on seed production and poor collaboration between the private and public sectors in hybrid maize seed production (Kandel, 2021). Moreover, the genetic variations for various economic traits have not been explored using these high-performing maize hybrids that can assure the success of maize breeding programs. A great genetic resource could be utilized from these genetic materials (Prasanna, 2012).

Selection is a crucial step in the breeding process. Its effectiveness is enhanced by estimating genetic parameters, which provide insights into the gene actions governing qualitative traits help determine the suitability of various breeding methods for achieving genetic improvement (Bartaula et al., 2019). Thus, the estimation of genetic parameters, including variances, coefficients of variation, heritability, and genotypic, phenotypic, and environmental correlations, provides insight into the magnitude of genetic diversity in the population and also that expected from selection gain (Bartaula et al., 2019). Estimation of coefficients of variation offer insights into the genetic variability present in different quantitative traits. However, they do not indicate the proportion of variation that is heritable. Thus, combining the coefficient of variation with heritability estimates provides a clearer understanding of the potential progress or improvement that could be achieved through selection (Bhadru et al., 2020). Heritability combined with genetic advance offers a more accurate evaluation of the trait of interest in a population following selection compared to heritability estimates alone (Rafiq et al., 2010). Correlation, determined by specific coefficients, measures the degree of genetic and

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non-genetic associations between traits, enabling indirect selection for correlated traits (Rai et al., 2015). However, it does not provide a clear understanding of the relative significance of direct and indirect contributions of individual component traits to yield (Olawamide and Fayeun, 2020). It examines the underlying cause of the relationship between two variables by analyzing simple correlations among the traits, as well as their linearity and additive effects (Faysal et al., 2022). Hence, this study was conducted to assess the performance and analyze the genetic parameters, including genetic variability, heritability, genetic advance, and trait associations among maize genotypes, with a focus on yield and yield-related traits.

2. MATERIALS AND METHODS

2.1 Location and planting materials

The research was carried out at the National Maize Research Program (NMRP) Rampur, Nepal, located at 27°40'N latitude, 84°21'E longitude, and an elevation of 228 meters above sea level, during the winter of 2023/24. A total of 24 maize genotypes were evaluated in the experiment. Two national hybrids, Rampur Hybrid-10 and Rampur Hybrid-16, were used as local checks, while SULTAN was included as a commercial check. The experimental materials were obtained from Multi-National Company and the National Maize Research Program, Rampur, Chitwan, Nepal. The selection of the various genotypes was done on the basis of the importance and suggestion from NARC for the trial to be conducted in NMRP for various traits analysis and for release of new genotypes.

Table 1: List of genotypes used for experiment

SN	Genotypes	Source	SN	Genotypes	Source
1	SULTAN(Commercial Check)	MNCH	13	RML147/CML430	NMRP
2	RH10 (National Check)	NMRP	14	RML150/RL111	NMRP
3	RH16 (National Check)	NMRP	15	RML152/RML96	NMRP
4	RL143/RML96	NMRP	16	RML187/RML96	NMRP
5	RL240/RML96	NMRP	17	RML2137/RL2118	NMRP
6	RL252/RML98	NMRP	18	RML32/CML613	NMRP
7	RL284/RML146	NMRP	19	RML36/RML2244	NMRP
8	RL35-1/RML2001	NMRP	20	RML5/RML17	NMRP
9	RML108/RL2118	NMRP	21	RML62/RML2	NMRP
10	RML14/RML76	NMRP	22	RML76/TZEIOR157	NMRP
11	RML142/RML17	NMRP	23	RML98/RML145	NMRP
12	RML145/TZEIO157	NMRP	24	CML161/RML96	NMRP

2.2 Experimental details

A field experiment was conducted using a Randomized Complete Block Design (RCBD) with three replications. Each experimental plot measured two rows of 4 meters in length and 0.75 meters in width. Maize plants were arranged in two rows per plot with a row spacing of 20 cm, while a 0.5-meter gap was maintained between the blocks to ensure proper separation. The recommended fertilizer application rate of 180:60:40 kg ha^{-1} ($N:P_2O_5:K_2O$). Nitrogen was applied using urea, di-ammonium phosphate (DAP), and muriate of potash (MOP). Phosphorus and potassium fertilizers, along with farmyard manure (15 t ha^{-1}), were incorporated as a basal dose at the time of land preparation. Nitrogen was applied in three split doses to optimize nutrient availability throughout the growing period. Pre-emergence weed control was achieved by applying a combination of Atrazine (2.0 g) and Pendimethalin (4.5 ml per liter) immediately after planting. Additionally, manual weeding was performed twice during the crop cycle to manage weed infestation, supplemented by routine intercultural operations. Irrigation was provided as required, with six to eight irrigations applied throughout the crop growth period, ensuring optimal soil moisture conditions for plant development.

2.3 Climatic condition of study location

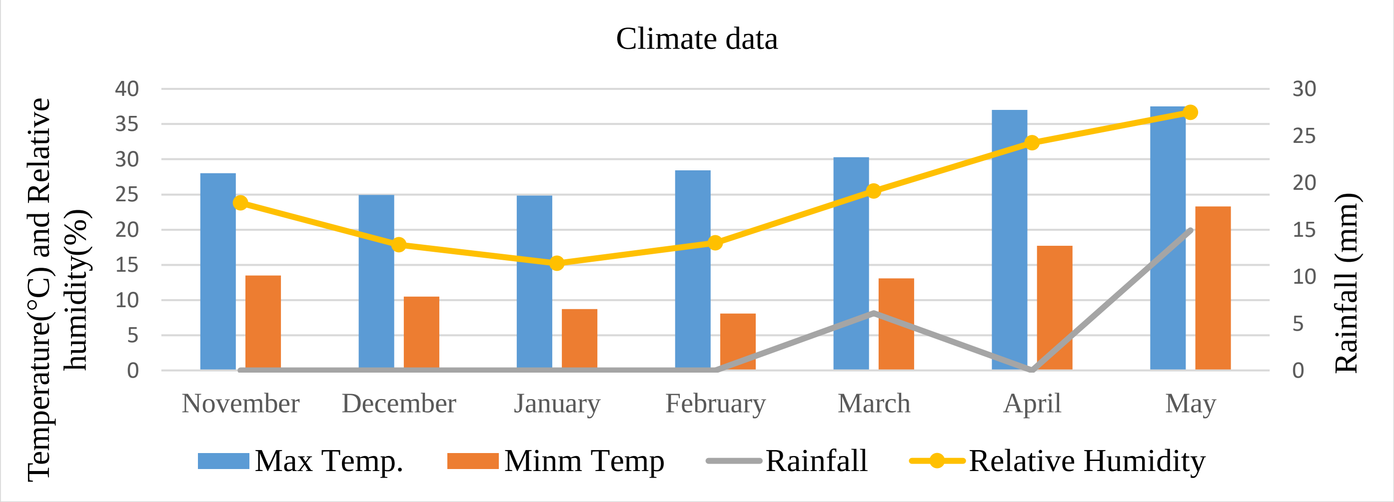

Figure 1: Average Climatic Conditions of the Study Site throughout the Research Period at NMRP, Chitwan (Nov 2023- April 2024).

3. DATA RECORDING AND ANALYSIS

Data on the number of days for 50% of the plants to attain anthesis, silking, and the anthesis-silking interval (ASI) were recorded at the plot level. On the other hand, parameters such as plant height (cm), ear height (cm), plant aspect, ear aspect, cob length (cm), cob diameter (cm), number of kernel rows, kernels per row, thousand-kernel weight (g), and moisture content (%) were measured from five representative plants within each plot. The field weight (kg) recorded per plot was transformed into grain yield (t ha-1) using formula adopted by a researcher and multiplying it with a conversion factor of 0.8, and adjusting for 12.5 percent moisture content (Kafle et al., 2020).

Grain yield ($kgha^{-1}$)

$$\text{Grain yield}\left(\frac{\text{kg}}{\text{ha}}\right) = \frac{\text{E.W}\left(\frac{\text{kg}}{\text{plot}}\right) \times (100 - \text{GMH}) \times \text{C.S} \times 10000}{(100 - \text{GMD}) \times \text{PHA}}$$

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Where,

E.W. = Ear fresh mass (kg) per plot at harvest

GMH = Grain moisture level (%) at the time of harvest

GMD = Desired grain moisture level, i.e., 12.5%

PHA = Effective harvested plot area (m^2)

C.S. = Cob-shelling ratio, set to 0.8

4. STATISTICAL ANALYSIS

IBM SPSS software was utilized to conduct correlation and path coefficient analysis, as well as to estimate various genetic parameters such as genotypic and phenotypic variance, GCV and PCV, heritability, genetic advance, and genetic advance as a percentage of the mean using the following formulas.

4.1 Genotypic and Phenotypic Co-Efficient Of Variation:

The genotypic and phenotypic coefficient of variation was computed according to (Ali et al., 2013) and expressed as percentage.

Genotypic coefficient of variation (GCV) = $(\sigma g/X) \times 100$

Phenotypic coefficient of variation (PCV) = $(\sigma p/ X) \times 100$

Where,

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

X = General mean of the trait in the above case,

PCV and GCV values were categorized as low, moderate and high indicated by researchers as follows:

0 – 10 %	: Low
10 – 20 %	: Moderate
>20 %	: High

4.2 Heritability

Broad sense heritability (h^2bs) = Vg/Vp,

Where, Vg = genetic variance and Vp = phenotypic variance (Demelie and Aragaw, 2016).

The heritability percentage was categorized as low, moderate and high as described by researchers as follows:

0-30%	: Low
30-60%	: Moderate
>60%	: High

If heritability of traits is very high (>0.8), selection for such a traits should be fairly easy (O. B. et al., 2012). This is because there would be close correspondence between the genotype and phenotype. In case of lower heritability estimates (<0.3), selection may be considerably difficult or virtually impractical due to the masking effect of environment on genotypic effects.

4.3 Genetic Advance and Genetic Advance as Percentage Of Mean (GAM)

The extent of genetic advance to be expected by selecting about five percent of the genotypes was calculated by using the following formula given by (Wani et al., 2022).

GA = I. σp. H^2bs

Where,

i = Efficacy of selection which is 2.06 at 5% selection intensity

σp = Phenotypic standard deviation

Hbs ^{2}= Broad sense heritability

The genetic advance was classified as low, moderate and high as following by (Bucio Alanis, 1966).

0-10%	: low
10-20%	: moderate
>20%	: high

Genetic advance shows the degree of gain obtained in a character under a particular selection pressure. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection.

GAM= $(GA/ X) \times 100$

Where,

GA = genetic advance

X= general mean of character

The GA as percent of mean was categorized as low, moderate and high as following by

0-10 %	: Low
10-20%	: Moderate
20 and above	: High

5. RESULTS AND DISCUSSION

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

The phenotypic and genotypic coefficients of variation (PCV and GCV) of traits in the current study exhibited low (<10%), moderate (10–20%), and high (>20%) values. The variability in PCV and GCV across different traits is presented in Table 2. Among the studied quantitative traits, high GCV values were recorded for ear height (24.5), and grain yield (31.69), indicating strong genetic influence and potential for selection (Neupane et al., 2020; Kharel et al., 2017). Similarly, high PCV values were observed for ear height (26.35), number of kernels per row (21.01), and grain yield (35.37) (Regmi et al., 2022; Raj et al., 2023). Conversely, traits such as days to 50% anthesis and days to 50% silking recorded low GCV and PCV, indicating limited genetic variability (Shrestha et al., 2023). In all cases, PCV values were higher than their corresponding GCV values, suggesting the influence of environmental factors on trait expression (Kumar et al., 2024). Traits such as days to 50% anthesis, days to 50% silking, plant height, and cob diameter displayed minimal differences between GCV and PCV, indicating that genetic improvement through selection would be effective as environmental effects on these traits are limited. However, substantial differences between GCV and PCV for plant aspect, the number of kernel rows, and grain yield suggest that phenotypic selection would be less effective for genetic improvement (Rai et al., 2021). These findings highlight the importance of understanding PCV and GCV values in designing effective breeding strategies for maize improvement.

5.2 Heritability (H^2)

The current study observed considerable differences in heritability values across various traits (Table 2). Among the phenological traits, high heritability estimates (>0.60) were recorded for days to 50% silking (88%), days to 50% anthesis (87%), plant height (87%), ear height (86%), and shoot lodging (73%), indicating minimal environmental influence on their expression (Regmi et al., 2022).

Yield-attributing traits, such as cob diameter (93%), cob length (75%), number of rows per ear (83%), thousand-kernel weight (67%), and grain yield (80%), also demonstrated high heritability, suggesting limited environmental impact on these traits (Maruthi and Rani, 2015). Moderate heritability (30 to 60%) was observed for anthesis and silking interval (44%) and root lodging (49%). The phenotypic nature of these traits is more susceptible to environmental influence, as also noted by (Ullah et al., 2017). High heritability for grain yield supports findings by (Rai et al., 2022). These findings underscore the potential for effective selection in breeding programs targeting traits with high heritability, as genetic improvement is less constrained by environmental variability.

5.3 Genetic Advance (GA) and Genetic Advance as Percentage of Mean (GAM)

Heritability alone does not necessarily indicate the potential for genetic improvement through selection. Therefore, examining genetic advance in conjunction with heritability offers a more comprehensive perspective. High heritability does not always correspond to substantial genetic advancement, as noted by Wani et al. (2022); traits with high heritability should also exhibit high genetic advance for more reliable conclusions. Genetic advance as a percentage of the mean (GAM) is classified into low (<10%), moderate (10–20%), and high (>20%). In the present study, high heritability accompanied by high genetic advance was observed for traits such as plant height, ear height, and thousand-kernel weight, indicating that these traits are controlled by non-additive gene action and are suitable for genetic improvement through selection (Shrestha et al., 2023).

Likewise, moderate genetic values were recorded for days to 50% anthesis and days to 50% silking, indicating some scope for genetic gain. The high GAM observed for plant height (32.90%), ear height (46.93%), and grain yield (58.48%) suggests significant potential for genetic improvement (Neupane et al., 2020; Shrestha et al., 2023). Traits such as cob length (23.72%), number of kernel rows (22.38%), number of kernels per row (24.75%), and thousand-kernel weight (22.52%) also showed high GAM. Cob diameter (15.71%) and days to 50% silking (10.04%) exhibited moderate GAM (Martin et al., 2017). Conversely, days to 50% anthesis (9.87%) showed low GAM, indicating that non-additive gene effects predominantly govern this trait, making direct selection less effective due to high environmental influence (Acharya et al., 2020; Regmi et al., 2022; Kharel et al., 2017). Traits with low GAM suggest that indirect breeding methods might be more appropriate for genetic improvement, as environmental factors account for much of the observed variation (Neupane et al., 2020).

Table 2: Estimation of genetic parameters (PCV, GCV, heritability, GA and GAM)

Traits	GCV	PCV	H^2(%)	GA	GAM
AD	5.14	5.52	87	10.76	9.87
SD	5.21	5.57	88	11.05	10.04
PH	17.12	18.34	87	67.44	32.90
EH	24.50	26.35	86	50.22	46.93
CL	13.28	15.32	75	3.73	23.72
CD	7.90	8.18	93	0.74	15.71
NOKR	11.90	13.03	83	3.06	22.38
NOKPR	15.89	21.01	57	7.62	24.75
TKW	13.34	16.27	67	80.16	22.52
GY	31.69	35.37	80	4.71	58.48

Note: GCV = genotypic coefficient of variation, PCV = phenotypic coefficient of variation, h^2= heritability, GA = genetic advance, GAM =

genetic advance as percentage of mean, AD= days to 50% anthesis, SD= days to 50% silking, PH= Plant Height, EH= Ear Height, PA= Plant Aspects, EA= Ear Aspects, CL= Cob Length, CD= Cob Diameter, NOKR = Number of Kernel row, NOKPR= Number of Kernel per Rows, TKW= Thousand Kernel Weight and GY= Grain yield

5.4 Estimation of phenotypic correlation co-efficient among the traits

The results of the study indicated that grain yield exhibited a positive and significant correlation with several key agronomic traits, including days to 50% anthesis, days to 50% silking, plant height, ear height, number of ears harvested, cob length, cob diameter, number of kernel rows, and number of kernels per row. This suggests that an increase in the values of these traits can effectively contribute to higher grain yield in maize hybrids (Rai et al., 2022). Anthesis and silking intervals demonstrated a positive but non-significant correlation with grain yield, while cob length and cob diameter also showed non-significant yet positive relationships with yield. On the contrary, thousand-kernel weight exhibited a non-significant but negative correlation with grain yield, aligning with the results reported by (Kinfe et al., 2015). The negative association between thousand-kernel weight and grain yield suggests that these traits may be influenced by trade-offs in biomass allocation (Munawar et al., 2013). Furthermore, traits such as anthesis days, silking days, plant height, ear height, number of ears harvested, number of kernel rows, and number of kernels per row demonstrated positive correlations with grain yield. These relationships highlight the importance of these traits in maize breeding programs aimed at enhancing grain production (Adhikari et al., 2018). Correspondingly, a positive correlation between days to 50% anthesis and days to 50% silking was also found, while similar relationships for cob length and cob diameter were observed (Thapa et al., 2025; Gautam et al., 2022; Thapa et al., 2022). Positive correlations of plant height, ear height, number of kernel rows, and number of kernels per row with grain yield were also highlighted (Hamidou et al., 2018). The significant and positive associations between grain yield and kernel-related traits underscore their critical role in enhancing hybrid maize productivity. These traits can be effectively leveraged to boost grain production in maize, thereby providing valuable insights for maize improvement strategies (Kandel and Shrestha, 2020).

Table 3: Estimation of phenotypic correlation co-efficient among quantitative and qualitative traits of maize hybrids

	AD	SD	ASI	PH	EH	NOEha	PA	EA	CL	CD	NOKR	NPKPR	TKW	GY
AD	1**													
SD	0.903**	1**												
ASI	-0.189	0.249*	1**											
PH	0.496**	0.457**	-0.07	1**										
EH	0.480**	0.495**	0.049	0.883**	1 **									
NOEha	0.110	0.135	0.061	0.316**	0.430**	1**								
PA	0.061	0.143	0.191	0.350**	0.368**	0.170	1**							
EA	-0.31**	-0.334**	-0.06	-0.134	-0.197	0.119	0.431**	1**						
CL	0.366**	0.362**	0.003	0.411**	0.333**	-0.055	-0.034	-0.36**	1**					
CD	0.053	-0.025	-0.18	-0.052	-0.050	-0.095	-0.277*	-0.39**	0.070	1**				
NOKR	0.078	0.171	0.215	0.160	0.276*	0.158	0.087	-0.37**	0.043	0.428**	1**			
NOKPR	0.338**	0.326**	-0.01	0.256*	0.246*	0.113	0.015	-0.33**	0.610**	0.022	0.073	1**		
TKW	0.068	-0.0145	-0.18	-0.082	-0.217	-0.273*	-0.234*	0.056	0.105	0.206	-0.292*	-0.142	1**	
GY	0.363**	0.3758**	0.039	0.457**	0.558**	0.736**	-0.009	-0.288*	0.259*	0.226	0.394**	0.355**	-0.08	1**

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Note: AD= days to 50% anthesis, SD= days to 50% silking, PH= Plant Height, EH= Ear Height, PA= Plant Aspects, EA= Ear Aspects, CL= Cob Length, , NOEha= Number of Ears harvested, CD= Cob Diameter, NOKR = Number of Kernel row, NOKPR= Number of Kernel per Rows, TKW= Thousand Kernel Weight and GY= Grain yield

* and ** indicate significant at 5% and 1% level of probability, respectively.

5.5 Estimation of phenotypic path co-efficient analysis among the traits

High correlation coefficients do not always provide an accurate representation and may lead to misleading conclusions, as the relationship between two variables could be influenced by a third factor. Therefore, it is essential to analyze the cause-and-effect relationships between dependent and independent variables to better understand their interactions. Path coefficient analysis enables the separation of direct effects from indirect influences through other traits by decomposing the correlation (Alam et al., 2024). The present study reveals that among the evaluated traits, the number of ears harvested exerts the highest positive direct effect on grain yield, emphasizing that increasing ear count per unit area significantly enhances productivity. This finding aligns with previous research that highlighted the importance of ear number in yield improvement (Crevelari et al., 2018). Traits such as ear height and plant height also contribute positively to grain yield, indicating that taller plants with elevated ears tend to perform better in terms of productivity. Cob-related characteristics, including cob length and cob diameter, show moderate positive effects, underscoring their role in kernel development and yield formation (Long et al., 2024; Yahaya et al., 2021). Moreover, the number of kernel rows per cob and the number of kernels per row positively influence grain yield, highlighting the critical role of kernel count in overall productivity (Aman et al., 2020; Prakash et al., 2019). Interestingly, ear aspect exhibits a negative effect on grain yield, indicating that poor ear characteristics can reduce productivity. A notable finding is the weak negative direct effect of thousand-kernel weight, suggesting a potential trade-off between kernel size and kernel number. This observation agrees with previous results (Matin et al., 2017). Selecting for an optimal kernel size, rather than focusing solely on maximizing kernel weight, may be more effective for yield improvement (Gogoi et al., 2025). The residual value of the model (0.1765) indicates that 82.35% of the total variation in grain yield is explained by the included traits. This underscores the significance of key agronomic parameters such as plant density, ear characteristics, and plant architecture for maximizing maize yield. These findings provide valuable insights for guiding breeding programs and agronomic practices aimed at enhancing maize productivity.

Table 4: Estimation of phenotypic path co-efficient analysis among quantitative and qualitative traits of maize hybrids

	AD	SD	ASI	PH	EH	NOEha	PA	EA	CL	CD	NOKR	NOKPR	TKW	GY
AD	**0.294**	-0.206	-0.025	-0.057	0.166	0.069	-0.008	0.017	0.018	0.006	0.014	0.057	0.012	0.363 **
SD	0.265	**-0.228**	0.034	-0.052	0.171	0.085	-0.019	0.018	0.018	-0.003	0.030	0.055	-0.003	0.3758 **
ASI	-0.056	-0.057	**0.134**	0.008	0.017	0.039	-0.025	0.003	0.000	-0.020	0.038	-0.003	-0.033	0.0393
PH	0.146	-0.104	-0.010	**-0.114**	0.305	0.199	-0.046	0.007	0.020	-0.006	0.028	0.043	-0.014	0.4574 **
EH	0.141	-0.113	0.007	-0.101	**0.346**	0.271	-0.048	0.011	0.016	-0.006	0.049	0.042	-0.038	0.5589 **
NOEha	0.032	-0.031	0.008	-0.036	0.149	**0.630**	-0.022	-0.006	-0.003	-0.011	0.028	0.019	-0.048	0.7368 **
PA	0.018	-0.033	0.026	-0.040	0.127	0.107	**-0.130**	-0.023	-0.002	-0.031	0.015	0.003	-0.041	-0.0095
EA	-0.092	0.076	-0.008	0.015	-0.068	0.075	-0.056	**-0.054**	-0.018	-0.044	-0.066	-0.057	0.010	-0.2884 *
CL	0.107	-0.083	0.001	-0.047	0.115	-0.035	0.004	0.020	**0.049**	0.008	0.008	0.103	0.019	0.2592 *
CD	0.016	0.006	-0.024	0.006	-0.017	-0.060	0.036	0.021	0.003	**0.112**	0.075	0.004	0.036	0.226
NOKR	0.023	-0.039	0.029	-0.018	0.095	0.100	-0.011	0.020	0.002	0.048	**0.176**	0.013	-0.051	0.3948 **
NOKPR	0.099	-0.075	-0.002	-0.029	0.085	0.071	-0.002	0.018	0.030	0.003	0.013	**0.169**	-0.025	0.3558 **
TKW	0.020	0.003	-0.025	0.009	-0.075	-0.172	0.030	-0.003	0.005	0.023	-0.051	-0.024	**0.176**	-0.0886

Residual effect = 0.1765

Note: AD= days to 50% anthesis, SD= days to 50% silking, PH= Plant Height, EH= Ear Height, PA= Plant Aspects, EA= Ear Aspects, CL= Cob Length, NOPha= Number of Plants per Hectare, NOEha= Number of Ears per Hectare, CD= Cob Diameter, NOKR = Number of Kernel row, NOKPR= Number of Kernel per Rows, TKW= Thousand Kernel Weight and GY= Grain yield

* and ** indicate significant at 5% and 1% level of probability, respectively.

6. CONCLUSION

This study provides valuable insights into the genetic and phenotypic variability among maize hybrids and their relationship with grain yield. Traits such as plant height, ear height, and grain yield exhibited high heritability and genetic advance, indicating strong potential for genetic improvement through selection. Positive and significant correlations of grain yield with key agronomic traits, such as the number of kernel rows, number of kernels per row, and ear count underscore their critical role in enhancing productivity.

Path analysis revealed that traits like the number of ears per hectare had the most substantial positive direct effects on grain yield, emphasizing their importance in breeding strategies and agronomic practices. Cob characteristics, including cob length and diameter, also contributed positively to yield. However, negative effects from ear aspect and thousand-kernel weight suggest that selecting for optimal ear and kernel traits, rather than solely focusing on kernel size, may yield better results. The findings highlight the influence of both genetic and environmental factors on trait expression, suggesting the need for breeding strategies that enhance traits with stable heritability while mitigating the environmental impact on yield-constraining characteristics. The study underscores the importance of optimizing plant density and ear traits to develop high-yielding, resilient maize cultivars, providing a valuable framework for future maize improvement programs.

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AUTHORS' CONTRIBUTIONS

Conceptualization and methodology: Mahendra Parshad Tripathi and Bijay Mahato

Software and validation: Mahendra Parshad Tripathi and Bijay Mahato

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Writing the original draft: Bijay Mahato and Mahendra Parshad Tripathi

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Supervision: Mahendra Parshad Tripathi

DATA AVAILABILITY

The datasets used or analyzed during this study can be obtained from the corresponding author upon request.

CONFLICT OF INTEREST

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The authors declare that there are no conflicts of interest. All contributors have reviewed and approved the final version of the manuscript.

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