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GENETICS AND BREEDING | ORIGINAL ARTICLE

Assessment of Genetic Variability, Heritability and Genetic Advance for Yield Attributing Traits of Maize (*Zea mays*) Genotypes

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ABSTRACT

Maize ranks second after rice in terms of area and production in Nepal. Maize is a cross-pollinated, C_4 type crop that is highly responsive to fertilization, resulting in high daily productivity. Maize genetic diversity offers a better opportunity to plant breeders for improvement through selection. The aim of this study was to determine the genetic variability, heritability and genetic advance of several maize genotypes, along with correlation, and direct and indirect effects of various traits. The experimental site has a warm tropical climate. The experiment was conducted in a Randomized Complete Block Design with 3 replications and 9 treatments, respectively. All maize genotypes were obtained from the Prime Minister Agricultural Modernization Project, Dang, Nepal. Analysis of variance showed substantial differences for almost all traits under study. Grain yield (34.97%, 37.12%) and ear height (31.33%, 37.99%) had the highest genotypic coefficient of variation and phenotypic coefficient of variation. A high value of heritability was recorded for grain yield. Grain yield had the highest genetic advance as a percent of the mean (67.87%), followed by ear height (53.19%). Grain yield showed positive and significant phenotypic correlation with all traits except days to 50% tasseling, ear diameter and number of rows per ear. Path analysis revealed that traits like test weight, weight of kernel per ear and ear height had the most favorable impacts on yield, both directly and indirectly. The study showed that the selection of any of these traits would lead to an improvement in grain yield.

1. Introduction

Maize, scientifically known as *Zea mays* or often referred to as corn, is one of the important cereal crops. The local people of southern Mexico started cultivating maize approximately 10,000 years back. Maize belongs to the Poaceae/Gramineae family and is often called the "Queen of Cereals" due to its remarkable yield capacity and large-scale market applications as food, feed and for industrial uses (Saritha et al. 2020). It is the world's third most important cereal food source after wheat and rice (Bartaula et al. 2019). In Nepal, maize ranks second after rice in terms of both acreage and production (Kandel et al. 2019; MOALD 2023).

Maize, a cross pollinated and C4 crop, is highly responsive to fertilization and has high productivity per day. Despite its highly potential, global demand is still not being met. The global demand for maize has been increasing by an average annual growth rate of about 4-5% over the past decade (Thapa 2021). According to the yield gap research, as crop yield become closer to commercially achievable yield levels, non-technical factors such as limitations in knowledge system become increasingly significant (Idoje et al. 2021). The low productivity of maize is primarily caused by limitations like several abiotic (drought and low soil fertility) and biotic (parasitic weed Striga, illnesses, and insect pests) factors.

The improvement of food insecurity issues is facilitated by the development of maize varieties that exhibit desirable traits and produce high yields. The degree of genetic variability, and genetic advance in the population determines the extent of genetic improvement in maize yield. Knowledge of the variability of traits could be a

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critical factor in the successful planning of a maize improvement program (Mohammed et al. 2023). The genotypic coefficient of variation, phenotypic coefficient of variation, heritability, and genetic advance are valuable biometric instruments for quantifying genetic variability (Dey et al., 2021). It provides a better opportunity to plant breeders for genetic improvement through selection. The degree of genetic variability in the population and its heritability determines the maximum amount of advancement that can be made by selection, making them critical to the success of any crop improvement program.

The degree of heritability and trait variability are crucial factors to understand high-yielding crops like maize. The degree of variability in traits can be determined using parameters such as the genotypic and phenotypic coefficients of variation (GCV and PCV). Heritability indicates the extent to which a specific morphogenetic trait may be passed on to future generations (Bello et al. 2012). It also suggests that close relatives are more likely to share characteristics than distant relatives (Magar et al. 2021). Understanding a trait's heritability is pivotal for determining how much improvement can be achieved through selection (Robinson et al. 1949). Accurate heritability estimates are essential for efficient breeding programs for quantitative traits (Cobb et al. 2019). Correlation research can give reliable and useful insights about the nature, dimension, and direction of selection (Zeeshan et al. 2013). The correlation coefficient measures the relationship between two traits and the degree of mutual variability (Ye et al. 2024). Path analysis identifies the direct and indirect impacts of cause variables on effect variables. Path coefficient analysis is commonly used in crop breeding to understand the link between grain yield and its components. It identifies components with significant influence on yield, which may then be utilized as selection criterion (Aman et al. 2020). The efficiency of selection in exploiting genotypic variation depends on the heritability and genetic advance of the individual traits (Bilgin et al. 2010). Genetic variability (GA) indicates how well a trait evolves under certain selective pressures. Combining heritability and high GA can help predict the optimal genotypes for yield and related traits (Fonseca et al. 2021).

The aim of this study was to determine the genetic variability, heritability and genetic advance of several maize genotypes, along with correlation, and direct and indirect effects of various traits

2. Materials and Methods

2.1. Experimental location

The study was carried out in the research field of Prithu Technical College, located in Lamahi Municipality of the Dang district. The experimental site lies approximately 410 km west from the Nepal's capital, Kathmandu. Geographically, it is situated at 27°42'09''N latitude and 82°30'49''E longitude, at the elevation of 257 meters above sea level. The location falls within Inner Terai region of Mid-Western Region of Nepal. The site experiences a warm tropical climate with an average temperature of 27.5°C, ranging from 11° to 43°C. May is the warmest month, with average temperatures in April-May reaching around 33 °C, while December and January have average temperatures of 18°C. The area receives an average annual rainfall of 600 mm. The cropping history of the experimental field followed a maize-mustard-fallow sequence.

2.2. Experimental Design and Layout

Experiment was conducted using a Randomized Complete Block Design (RCBD) with 3 replications and 9 treatments. Each individual plot measured $6m^2$ (2.4m*2.5m) and contained 4 rows. The total area of research field was $205.2m^2$(21.6m×9.5m). Plant-to-plant spacing was maintained at 25 cm, while row-to-row spacing was 60 cm. A spacing of 1 meter was maintained between replications.

2.3. Plant Materials

Nine maize genotypes namely Rampur Hybrid-14 (RH-14), Rampur Hybrid-16 (RH-16), Rampur Hybrid-12 (RH-12), SA2181-4, Rampur Hybrid-10 (RH-10), Suwarna, Chand 905, GTWY, and 10V10 were used in the experiment. All genotypes were obtained from the Prime Minister Agricultural Modernization Project (PMAMP), Dang, Nepal.

2.4. Land Preparation and Crop Management

The experimental field was prepared by ploughing with a tractor two weeks before seeding. The soil was then refined using spades and leveled. During field preparation, stubble of the previous crop and weeds were manually removed. Well-decomposed farm-yard manure at the rate of 6 tons per hectare was incorporated into the soil one-week prior sowing. Chemical fertilizer at the rate of 120:60:40 kg NPK/ha were applied through Urea, DAP, and MOP. During the final land preparation, half of the nitrogen (N) was applied as a split dose, while the entire phosphorus (P) and potassium (K) were applied as a basal dose. The remaining dose of the nitrogen was top-dressed at 45 days after planting.

Maize seeds were sowed on December 17, 2022, at a rate of two seeds per hill. Thinning was carried out at 30 days after sowing to maintain one plant per hill. Manual weeding was done twice: once at 35 days after sowing (DAS), and another at tasseling at 75 DAS. Irrigation is carried out at three critical growth stages: the knee-high stage, tasseling stage and milking stage. Harvesting was done after 150 days, on May 17, 2023, when signs of maturity were observed.

2.5. Data Collection

Observation was recorded from five randomly selected plants per plot for all the traits under consideration. Data on the various traits were collected from these selected plants. The traits evaluated in the study included (i) days to 50% tasseling, (ii) plant height, (iii) ear height, (iv) ear weight,(v) ear length, (vi) ear diameter, (vii) number of rows per ear, (viii) number of kernels per row, (ix) number of kernels per ear, (x) weight of kernels per ear, (xi) test weight, and (xii) grain yield. Test weight and grain yield were determined from the following equations:

$$\text{Test weight} = \frac{100 - \text{Moisture\%}}{100 - \text{Required moisture \% (i.e., 15\%)}} \times 1000 \text{ kernel weight}$$

$$\text{Grain yield}\left(\frac{\text{ton}}{\text{ha}}\right) = \frac{\text{Grain yield per plot at 15\% moisture}}{\text{Plot size in m}^2} \times 1000$$

2.6. Statistical Analysis

Analyses of variance (ANOVA) of the recorded parameters were performed using a Randomized Complete Block Design (RCBD), with each considered as a replication. Means separation was carried out using the Least Significant Difference (LSD) test at 0.05 level of significance to identify significant differences among treatment means. Data were entered in Microsoft Excel 2019 and analyzed using R software (version 4.2.2). Correlation coefficient among various traits was calculated using SPSS version 22.0. Direct and indirect effects were assessed through path coefficient analysis as suggested by (Dewey & Lu 1959), using the "Variability" package in R studio. Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were computed using following formula,

$$\text{GCV} = \frac{\text{genotypic standard deviation } (\sigma_g)}{\text{general mean (X)}} \times 100\%$$

$$\text{PCV} = \frac{\text{phenotypic standard deviation } (\sigma_p)}{\text{general mean (X)}} \times 100\%$$

And categorized as low (0-10%), moderate (10-20%), or high (>20%) according to Sivasubramanian and Menon (1973).

Broad-sense heritability was calculated using the formula provided by Falconer (1981),

$$\text{Heritability in Broad Sense } (H^2_{bs}) = \frac{\text{genotypic variance } (\sigma^2_g)}{\text{phenotypic variance } (\sigma^2_p)} \times 100\%$$

Heritability is categorized as low (0-30%), moderate (30-60%), or high (>60%) based on the classification by Robinson et al. (1949).

Genetic advances (GA) for each trait at 5% selection intensity was estimated using the formula described by Johnson et al. (1955).

$$GA = k * \sigma_p * H^2_{bs}$$

Where, k is a constant (selection differential, where k= 2.056 at 5% selection intensity).

Genetic advances as percent of mean (GAM) were calculated to compare the extent of predicted improvement among different traits under selection, using the following formula,

$$\text{GAM} = \frac{\text{Genetic advances (GA)}}{\text{Mean of population in which selection will be employed (x)}} \times 100\%$$

And GAM is categorized as low (0-10%), moderate (10-20%), or high (>20%) according to Johnson et al. (1955).

3. Results

3.1. Analysis of Variance

The analysis of variance (ANOVA) results revealed significant differences among the genotypes for almost all traits (Table 1), indicating a high degree of genetic variability. This wide range of variation across traits provides an opportunity for the effective selection of superior genotypes for use in breeding programs. Similar findings of notable heterogeneity among maize genotypes for multiple traits have been reported by Bartaula et al. (2019) and Rani et al. (2023). However, the differences were non-significant for the traits days of 50% tasseling and ear diameter. This aligns with the finding of Rai et al. (2021), who also reported non-significant variation in ear diameter.

3.2. Mean Performance

The average performance of the nine maize genotypes and their different agronomic traits is summarized in **Table 2.** Days to 50% tasseling range from 123 days for Chand 905 to 135.67 days for GTWY, indicating variation in maturity among different genotypes. The highest values for plant height (230.73 cm), ear height (81.40 cm), ear weight (206.20 gm), fresh yield (11,305.77 kg/ha), and almost all other traits like ear diameter (ED), number of kernels per row (NKPR), number of kernels per ear (NKPE), weight of kernels per ear (WKPE), and test weight (TW) were recorded in Suwarna, making it the best performing genotype. Furthermore, 10V10 and Chand 905 also produced strong yield of 9,183.23 kg/ha and 8,456.92 kg/ha, respectively, along with favorable test weights. On the other hand, GTWY and SA2181-4 had the lowest yields of 3,750.86 kg/ha and 3,923.55 kg/ha, respectively. The coefficient of variation (CV) was moderate across the traits, suggesting a reasonable level of experimental accuracy and reliability.

3.3. Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV)

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged from 4.43% to 37.99%, and 2.29% to 34.97%, respectively (**Table 3**). In all traits, GCV values were lower than PCV values, indicating traits were more influenced by environmental factors for their expression. The highest GCV and PCV were observed for grain yield (34.97%, 37.12%) and ear height (31.33%, 37.99%). Traits such as ear weight (21.27%, 34.32%) and weight of kernel per ear (20.58%, 34.45%) also showed high variability. Moderate value of GCV and PCV were recorded for plant height (15.51%, 19.68%) and test weight (16.51%, 18.63%). The number of kernels per row (18.41%, 24.23%) and number of kernels per ear (14.77%, 22.87%) showed moderate GCV and high PCV. Ear length had low GCV (9.64%) but moderate PCV (15.29%). Traits such as days to 50% tasseling (2.29%, 4.43%), ear diameter (4.29%, 7.72%), and number of rows per ear (8%, 9.89%) showed low variation.

Table 1. Mean sum of squares for different traits of nine maize genotypes

Traits	Mean Square	
	Between genotypes (df=8)	Error (df=16)
Days to 50% tasseling	49.26	23.57
Plant Height	2397.5**	406
Ear Weight	3474*	1210
Ear Length	9.645*	3.241
Ear Height	655.9***	89.1
Ear Diameter	0.16334	0.06955
Number of rows per ear	4.946***	0.74
Number of kernels per row	1946.1**	381.7
Number of kernels per ear	11673*	3708
Weight of kernel per ear	2075.6*	779.1
Test weight	7293***	612
Grain yield	18581377***	751298

*** = Significant at 0.1% level of significance, ** = Significant at 1% level of significance, * = Significant at 5% level of significance.

Table 2. Mean Performance for different traits of nine maize genotypes

Treatments	DT(50%)	PH	EH	EL	EW	ED
Rampur Hybrid-14	131ab	140.13c	33.35b	13.82bc	111.53bc	3.85b
Rampur Hybrid-16	125.67b	143.03bc	34.89b	13.29c	104.07bc	4.08b
Rampur Hybrid-12	128.67ab	176.53b	40.28b	15.65bc	114.97bc	4.03b
SA2181-4	124b	167.87bc	38.20b	14.36bc	128.80bc	4.29ab
Rampur Hybrid-10	124.33b	168.87bc	35.42b	15.33bc	121.80bc	3.94b
Suwarna	129.27ab	230.73a	81.40a	18.92a	206.20a	4.65a
Chand 905	123b	173.63bc	47.91b	16.78ab	160.60ab	4.10b
GTWY	135.67a	155.47bc	39.82b	14.73bc	97.67c	4.01b
10V10	129.33 ab	139.27c	43.66b	13.56c	116.87bc	4.10b
Mean	127.83	164.25	42.26	15.07	125.8	4.11
SEM(±)	2.803	11.633	5.45	1.039	20.083	0.152
LSD(α=0.05)	8.403	34.877	16.338	3.116	60.209	0.456
CV	3.796	12.126	21.511	11.875	26.93	6.406

Treatments	NRPE	NKPR	NKPE	WKPE	TW	FY
Rampur Hybrid-14	14.87bcd	119bcd	340.20bcd	85.80bc	287.95bc	6841.95cd
Rampur Hybrid-16	15.07bc	101.60cd	295.60cd	82.27bc	271.84cd	5669.93d
Rampur Hybrid-12	13.60cd	146.33ab	379.53abc	99.80bc	262.62cd	5747.27d
SA2181-4	17.60a	106.53cd	343.80bcd	97.67bc	238.84de	3923.55e
Rampur Hybrid-10	13.47d	111.33cd	296.13bcd	95.67bc	303.59bc	7862.66bc
Suwarna	13.57d	163.03a	450.97a	158.77a	364.51a	11305.77a
Chand 905	14.60bcd	148.47ab	401.47ab	125.80ab	318.99b	8456.92b
GTWY	15.50b	85.67d	248.33d	71.33c	200.12e	3750.86e
10V10	14.87bcd	134.33abc	383.07abc	92.07bc	325.18ab	9183.23b
Mean	14.75	122.02	332.23	98.38	282.01	6564.99
SEM(±)	0.497	11.28	35.157	16.115	14.283	500.432
LSD(α=0.05)	1.489	33.817	105.4	48.313	42.82	1500.296
CV	5.815	15.752	17.459	27.631	8.651	12.433

DT (50%) = Days to 50% tasseling, PH = Plant height, EH = Ear height, EL = Ear length, EW = Ear weight, ED = Ear diameter, NRPE = Number of rows per ear, NKPR = Number of kernels per row, NKPE = Number of kernels per ear, WKPE = Weight of kernel per ear, TW = Test weight, FY = Final yield

Table 3. Estimation of PCV, GCV, Heritability, Genetic Advance and GAM for different traits of nine genotypes of maize

Parameter	Mean	GCV (%)	PCV (%)	H^2_{bs} (%)	GA	GAM (%)
Days of 50 % tasseling	127.88	2.29	4.43	26.65	3.11	2.43
Plant Height	166.17	15.51	19.68	62.05	41.81	25.16
Ear Weight	129.17	21.27	34.32	38.42	35.07	27.15
Ear Length	15.16	9.64	15.29	39.71	1.9	12.51
Ear Height	43.88	31.33	37.99	67.95	23.34	53.19
Ear Diameter	4.12	4.29	7.72	31.01	0.2	4.93
Number of rows per ear	14.79	8	9.89	65.45	1.97	13.34
Number of kernels per row	124.03	18.41	24.23	57.72	35.7	28.82
Number of kernels per ear	348.79	14.77	22.87	41.73	68.6	19.66
Weight of kernel per ear	101.02	20.58	34.45	35.68	25.6	25.32
Test weight	285.96	16.51	18.63	78.44	86.1	30.11
Grain yield	6971.35	34.97	37.12	88.78	4731.9	67.87

GCV= Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, H^2_{bs}=Heritability broad sense, GA= Genetic Advance, GAM=Genetic Advance as percent of mean

Bartaula et al. (2019), Rai et al. (2021), Rani et al. (2023), Kumar et al. (2024) and Zewdu et al. (2024) have all reported high GCV and PCV estimates for grain yield, indicating high genetic variability and potential for selection. Similarly, Jatto et al. (2024) observed similar results for cob weight and kernels per row. Also, Jatto et al. (2024), Kandel et al. (2018), Kumar et al. (2024), and Lal et al. (2020) reported moderate GCV and PCV for plant height and test weights. In addition, Lal et al. (2020) recorded a similar result for ear length. Similar to this finding, Rai et al. (2021) also reported low GCV and PCV values for almost all the same traits, particularly for traits such as days to 50% tasseling and ear diameter. Tesfaye et al. (2021) also found similar results for ear length, ear diameter, and number of rows per ear. Furthermore, Jatto et al. (2024) reported low estimations of GCV and PCV for days to 50% tasseling and ear diameter.

3.4. Heritability and Genetic Advance (GA)

Among the twelve traits studied, high heritability was recorded for plant height (62.05%), ear height (67.95%), number of rows per ear (65.45%), test weight (78.44%), and grain yield (88.78%) (Table 3). A high heritability value indicates that these traits are less influenced by environmental factors, and that phenotypic values are more likely to reflect the underlying genotypic values. Moderate heritability was observed for ear weight (38.42%), ear length (39.71%), ear diameter (31.01%), number of kernels per row (57.72%), number of kernels per ear (41.73%), and weight of kernel per ear (35.68%). In contrast, days to 50% tasseling exhibited low heritability (26.65%).

Similarly, high genetic advance as a percent of mean was observed for grain yield (67.87%) followed by ear height (53.19%), test weight (30.11%), number of kernels per row (28.82%), ear weight (27.15%), weight of kernel per ear (25.32%), and plant height (25.16%). Moderate genetic advance as a percent of mean was recorded for number of kernels per ear (19.66%), number of rows per ear (13.34%), and ear length (12.51%). And remaining other traits shows low genetic advance as a percent of mean.

Kandel et al. (2019) and Meena et al. (2016) also observed high heritability and GAM for grain yield, plant height and test weight. Similarly, Magar et al. (2021) observed moderate heritability for ear weight, ear length, and ear diameter, which is in agreement with the results of our study. Furthermore, our current finding is supported by the observation of Rani et al. (2023) for grain yield, test weight, number of kernels per row and ear length.

Heritability is the most crucial factor in breeding for many quantitative traits. However, the heritability estimate by itself does not provide enough information about the extent of genetic advancement. More accurate information is provided by heritability estimates combined with estimations of genetic advancement. When additive gene effects govern a trait, the outcome is higher heritability and genetic advance, whereas when non-additive gene effects govern a trait, the outcome may be higher heritability but lower genetic advancement (Magar et al. 2021).

High heritability with high GAM was reported for grain yield, plant height, cob height, and test weight, which indicates the control of additive gene action and a greater opportunity for selecting these traits. Low heritability combined with low GAM was recorded for days to 50% tasseling, which indicates greater influence of non-additive gene actions and environment, thereby it limits the opportunity to improve the trait through selection. For such traits, enhanced agronomic and management practices may be more effective than genetic selection (Beksisa & Ayano 2016).

3.5. Phenotypic correlation coefficient

The correlation coefficients demonstrate how intense and directional a trait relationship is, by revealing positive values for direct relations and negative values for inverse relations (Redhu et al. 2023). Table 4 shows the phenotypic correlation coefficients that exist between different traits of nine maize genotypes.

Days to 50% tasseling showed a negative correlation with all other traits, indicating that delay in tasseling leads to decreased values in agronomic and yield-related traits. Strong and statistically significant correlation was observed between plant height and ear height (0.876**), ear length (0.748**), ear weight (0.698**) as well as weight of kernel per ear (0.700**). The measurements of ear height showed important positive relationships with ear length, ear weight, ear diameter, number of kernels per row, number of kernels per ear, weight of kernel per ear, and grain yield. This suggests, elevation in ear heights leads to improved ears and yield traits.

The weight of kernel per ear (WKPE) showed the strongest positive relationship with ear weight (0.972**) followed closely by ear length (0.912**). The test weight (TW) showed significant positive relationships with number of kernels per row (0.624**), number of kernels per ear (0.533**) and weight of kernel per ear (0.480*). These variables significantly influence the test weight.

Grain yield (FY) exhibited positive correlations with all traits except days to 50% tasseling (-0.119) and number of rows per ear (-0.436*). Grain yield showed positive and significant correlation with plant height (0.446*), ear height (0.661**), ear length (0.460**), ear weight (0.549**), number of kernels per row (0.646**), number kernel per ear (0.584**), weigh of kernel per ear (0.574**) and test weight (0.917**) respectively. Grain yield displayed the most significant relationship with test weight, followed by ear height and number of kernels per row. This demonstrates critical role of these traits in yield improvement.

However, number of rows per ear (NRPE) demonstrated weak or negative correlations with most traits and with significantly negatively associated with final yield (-0.436*), implying that kernel row number along may not contribute to higher yields.

Rai et al. (2021), Jatto et al. (2024), Kinfe and Tsehaye (2015), and Bartaula et al. (2019) supported these finding. Borkhatariya et al. (2022) revealed strong associations between yield and various yield factores which suggests these traits are influenced by several linked genes. The results underline the significance of these traits while choosing or enhancing superior genetic variants for breeding programs.

Table 4. Phenotypic correlation coefficient among different traits of nine genotypes of maize

Traits	DT(50%)	PH	EH	EL	EW	ED	NRPE	NKPR	NKPE	WKPE	TW
DT(50%)											
PH	-0.23										
EH	-0.085	.876**									
EL	-0.266	.748**	.749**								
EW	-0.346	.698**	.780**	.879**							
ED	-0.201	.618**	.723**	.720**	.825**						
NRPE	-0.07	-0.265	-0.207	-0.237	-0.057	0.199					
NKPR	-0.25	.525**	.640**	.767**	.766**	.549**	-0.359				
NKPE	-0.241	.498**	.658**	.741**	.811**	.674**	-0.099	.948**			
WKPE	-.388*	.700**	.775**	.912**	.972**	.827**	-0.115	.836**	.859**		
TW	-0.213	0.299	.479*	0.355	.445*	0.208	-.508**	.624**	.533**	.480*	
FY	-0.119	.446*	.661**	.460*	.549**	0.33	-.436*	.646**	.584**	.574**	.917**

** = Significant at 1% level of significance, * = Significant at 5% level of significance, DT (50%) = Days to 50% tasseling, PH = Plant height, EH = Ear height, EL = Ear length, EW = Ear weight, ED = Ear diameter, NRPE = Number of rows per ear, NKPR = Number of kernels per row, NKPE = Number of kernels per ear, WKPE = Weight of kernel per ear, TW = Test weight, FY = Final yield

Table 5. Direct effect (values in diagonal) and indirect effect (values in off-diagonal) of the different traits on grain yield

	DT(50%)	PH	EH	EL	EW	ED	NRPE	NKPR	NKPE	WKPE	TW
DT(50%)	**0.132**	0.024	-0.012	0.049	0.060	0.042	-0.001	-0.018	0.045	-0.234	-0.130
PH	-0.027	**-0.119**	0.425	-0.154	-0.135	-0.149	-0.019	0.043	-0.117	0.471	0.212
EH	-0.003	-0.104	**0.484**	-0.155	-0.150	-0.176	-0.016	0.052	-0.154	0.518	0.344
EL	-0.032	-0.090	0.369	**-0.203**	-0.168	-0.171	-0.018	0.064	-0.174	0.617	0.251
EW	-0.041	-0.083	0.380	-0.177	**-0.192**	-0.198	-0.007	0.063	-0.190	0.655	0.316
ED	-0.023	-0.074	0.353	-0.144	-0.157	**-0.242**	0.011	0.045	-0.157	0.555	0.137
NRPE	-0.003	0.035	-0.125	0.057	0.020	-0.041	**0.063**	-0.034	0.038	-0.115	-0.421
NKPR	-0.029	-0.061	0.306	-0.155	-0.146	-0.130	-0.025	**0.083**	-0.226	0.560	0.457
NKPE	-0.025	-0.058	0.315	-0.148	-0.153	-0.160	-0.010	0.079	**-0.238**	0.573	0.382
WKPE	-0.046	-0.083	0.373	-0.186	-0.186	-0.199	-0.011	0.069	-0.202	**0.673**	0.341
TW	-0.023	-0.034	0.224	-0.068	-0.081	-0.044	-0.035	0.051	-0.122	0.308	**0.746**
Residue	=0.0719										

DT (50%) = Days to 50% tasseling, PH = Plant height, EH = Ear height, EL = Ear length, EW = Ear weight, ED = Ear diameter, NRPE = Number of rows per ear, NKPR = Number of kernels per row, NKPE = Number of kernels per ear, WKPE = Weight of kernel per ear, TW = Test weight.

3.6. Phenotypic path analysis

Correlation coefficients simply showed the relationship between yield and yield attributing characters but do not show the direct and indirect effects of individual traits on yield. Therefore, path coefficient analysis was used to measure direct as well as indirect effects of independent variables on dependent variable i.e. Final yield (FY) (K. C. et al. 2025).

Path coefficient analysis showed a positive direct effect on FY by different traits like DT (50%), NRPE, NKPR, EH, WKPE, TW among which TW (0.74583) had the highest effect followed by WKPE (0.67334) (Table 5). This implies that higher TW leads to increased grain yield. Other traits including PH (-0.11874), EL (-0.20261), EW (-0.19158), ED (-0.24156), and NKPE (-0.2377) showed a negative direct effect on FY.

Among the indirect effects on FY, the strongest positive indirect effect was recorded by WKPE via EW (0.655). This show that the positive effect of WKPE on FY is partially mediated through EW which make it critical path for improving yield. The highest negative indirect impact on FY was observed by TW via NRPE (-0.421) followed by WKPE via DT(50%) (-0.234). The residue value of 0.0719 indicates the portion of the final yield that cannot be explained by the direct and indirect effects of the traits possibly due to unmeasured factors.

Borkhatariya et al. (2022, 2025) revealed a positive direct effect of days to tasseling which matches our result. Also, other traits including plant height, ear height, number of rows per ear and test weight were found similar with the results reported by Aman et al. (2020). However, the finding of plant height contradicts with the finding of Borkhatariya et al. (2022).

4. Conclusion

Every attribute under study were significant, indicating there is presence of genetic variability that can be exploited in crop improvement initiatives. For each trait examined, phenotypic coefficient of variation (PCV) exceeded genotypic coefficient of variation (GCV), suggesting environmental influences. Traits such as grain yield, test weight, plant height and ear height having high GCV, PCV, heritability along with high genetic advance as percentage of mean were used in selection process of crop improvement program. Correlation studies showed that most of the traits under study such as ear length, ear weight, number of kernels per row, number kernel per ear and weight of kernel per ear had showed significant positive correlation with grain yield. Path analysis revealed that traits like test weight, weight of kernel per ear and ear height had the most favorable impacts on yield, both directly and indirectly. This showed that the selection of any of these traits would lead to improvement in grain yield.

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Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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