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RESEARCH ARTICLE

Dissecting genetic interrelationships of morphological and yield traits in maize using heritability, correlation and path analysis

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Abstract

Maize (*Zea mays* L.) is a globally important cereal crop valued for food, feed and industrial applications. Enhancing grain yield requires a clear understanding of genetic variability and the interrelationships among yield-contributing traits. The present study was conducted to assess genetic variability, heritability and trait associations in fifteen maize hybrids grown under normal field conditions during the spring season of 2024 at the University of Agriculture, Faisalabad. The experiment was laid out in a randomized complete block design with three replications. Analysis of variance revealed highly significant differences among genotypes for all studied morphological and yield-related traits, indicating the presence of considerable genetic variation. High broad-sense heritability was observed for plant height, tassel length, number of tassel branches and 100-seed weight, suggesting that these traits are predominantly governed by genetic factors and can be effectively improved through selection. In addition, high heritability coupled with moderate to high genetic advance for these traits indicates the predominance of additive gene action, making them reliable selection criteria in breeding programs. Correlation analysis indicated strong positive associations among key yield components, particularly between seeds per row, seeds per cob and rows per cob, highlighting their collective contribution to grain yield. Path coefficient analysis further demonstrated that number of tassel branches, seeds per row and rows per cob exerted substantial direct effects on grain yield, emphasizing their importance as primary selection indices. Furthermore, the presence of substantial phenotypic and genotypic coefficients of variation for several traits suggests ample scope for genetic improvement through hybridization and selection. The study also underscores the importance of indirect selection strategies, where improvement in highly correlated traits can lead to enhanced grain yield and the traits can be effectively utilized under normal agro-climatic conditions for the development of high-yielding maize hybrid .

Keywords: Maize, hybrid, correlation , yield, heritability

Introduction

Maize (*Zea mays* L.) is the third most.important cereal crop in the poaceae family (Mohammedali *et al.*, 2021). Maize is a C4 plant with substantial genetic potential that is utilized as a crop to study photosynthesis (Zhi *et al.*, 2024). Maize is also called "queen of cereals" due to its maximum genetic potential for high yield among the cereal crops. About 10% of the nation's total food grain production comes from maize and ranks third after rice and wheat (Singh, 2023). In addition to being a basic food and human fuel, maize is utilized as animal and poultry feed (Islam *et al.*, 2020). 72% of maize is made up of starch, which is extensively utilized in industries (Huma *et al.*, 2019). Its grain is a rich source of starch (72%), vitamins A and B (3%- 5%), proteins (1.6 %), oil (4.9 %), fiber (5.8%), sugar (3.0%) and ash (1.7%) (Rehman *et al.*, 2023). Maize is additionally significant impacted by various diseases and insects that for the most part show up during later phase of harvest (Fadhli *et al.*, 2023). Major issues with optimal maize productivity throughout the growing season have been recognized as biotic and abiotic aspects (Abegunde, 2023). The information on the relationship between yield and yield contributing traits is important for planning yield improvement program (Ferdous *et al.*, 2023). The United States, Mexico, Brazil, India, and China are among the top maize-producing nations (Dragomir *et al.*, 2022). The U.S. alone contributes nearly 35% of global maize output, playing a major role in its agricultural economy (Erenstein *et al.*, 2022). In Pakistan, maize production remains comparatively low (Muhammad *et al.*, 2023). About 98% of the crop is cultivated in Punjab and Khyber Pakhtunkhwa, making them the leading producing regions (Akhtar *et al.*, 2023). During the 2024-2025 season, maize was cultivated on 1.4 million hectares in Pakistan, with production dropped to 8.2 million tones due to reduced sowing area. This marks a 15.4% decline from the previous year's 9.7 million tones. Maize remains vital to the agriculture sector but is sensitive to input costs and climate changes (GOP, 2024-25). In maize breeding, improving economically valuable traits while maintaining genetic diversity is crucial. Genotypic and phenotypic coefficients of variation help quantify trait variability and guide selection strategies (Muhammad *et al.*, 2023). Heritability plays a key role by estimating the genetic contribution to phenotypic traits, enabling breeders to distinguish genetic effects from environmental influence (Dudhe et al., 2024). Correlation analysis identifies traits closely linked with grain yield, facilitating indirect selection for improvement (Wang *et al.*, 2023). Yield is influenced by multiple traits, understanding their interrelationships supports more efficient breeding decisions (Magar *et al.*, 2021). Traits with strong positive correlations to yield are prioritized to develop high-yielding genotypes (Shikha *et al.*, 2020).Path coefficient analysis serves as a valuable tool for plant breeders to identify superior genotypes by partitioning the direct and indirect contributions of yield components to overall productivity. This approach begins with the evaluation of diverse genotypes, followed by the estimation of variance and covariance among different traits and their combinations. Earlier Rawi *et al.*, (2018), Ahmed *et al.*, (2020), Taiwo *et al.*, (2020), Islam *et al.*, (2020), Kumawat *et al.*, (2020), and Hamdi and Al-Rawi (2021), have applied this method in maize improvement programs. Their findings highlighted that while some traits exert a direct influence on grain yield, others contribute indirectly through interrelationships with key yield attributes. Since hybrid development relies heavily on the careful selection of elite parental lines, path analysis provides a scientific basis for this selection (Mohammed *et al.*, 2024; Sangare *et al.*, 2019).

Most studies on heritability and trait associations in maize have been conducted under stress conditions, such as drought, salinity, or nutrient supplementation (Ilyas *et al.,* 2019). These stress treatments often modify the expression of yield related traits, which makes it difficult to accurately assess the true genetic potential of genotypes (Dogar *et al.,* 2023). There is still limited research on evaluating genetic variability, heritability, and trait associations under normal, untreated field conditions, which is crucial for selecting stable and high yielding maize varieties that perform well without relying on heavy external inputs (Singamsetti *et al.,* 2023). Evaluating maize genotypes under untreated, normal field environments can reveal their actual genetic potential without confounding effects from stress treatments or inputs (Dogar *et al.,* 2023). Such an approach helps identify stable, high-yielding genotypes better suited to low-input farming systems, which are common in developing countries like Pakistan. Moreover, combining heritability estimates with correlation analyses under representative field conditions facilitates more efficient and reliable indirect selection of desirable traits, ensuring long-term genetic gains (Amegbor *et al.,* 2022). It is hypothesized that specific morphological and yield-associated traits in maize are largely governed by genetic factors and exhibit strong positive associations with grain yield. This would support their use in indirect selection to enhance breeding efficiency. The aims of this study is to evaluate the heritability and inter-trait correlations among morphological and yield-related characteristics of diverse maize genotypes under normal field conditions, in order to identify traits with high genetic control and their potential contribution to grain yield improvement.

Materials and methods

The experiment was conducted during the spring season of 2024 at the research area of the University of Agriculture, Faisalabad. The location falls under the arid to semi-arid agro-climatic zone of central Punjab, ideal for maize cultivation. All genotypes were grown under uniform agronomic practices without the application of any external treatments or stress conditions. The experimental material consisted of 15 hybrids that were collected from Maize Laboratory, University of Agriculture Faisalabad. The seeds were seeded in the field. These hybrids sown along their standard for the analysis of heritability and correlation. The plant protection measures and other agronomic techniques were constant throughout the season. The intervals between plants and rows were 15 and 75 cm, respectively. Observation was made by randomly selected three plants from each genotype for all the traits under consideration both morphological and yield contributing traits such as include plant height, number of leaves, leaf length, leaf width, tassel length, number of tassel branches, stem diameter, number of rows per cob, number of seeds per row, and yield contributing traits such

Table 1: List of 15 maize hybrids used in this study

Treatment	Genotypes	Treatment	Genotypes	Treatment	Genotypes
1	PBG-01	6	PBG-06	11	PBG-11
2	PBG-02	7	PBG-07	12	PBG-12
3	PBG-03	8	PBG-08	13	PBG-13
4	PBG-04	9	PBG-09	14	PBG-14
5	PBG-05	10	PBG-10	15	PBG-15

such as include plant height, number of leaves, leaf length, leaf width, tassel length, number of tassel branches, stem diameter, number of rows per cob, number of seeds per row, number of seeds per cob, 100 seed weight and pith diameter. The experiment was laid out using a Randomized Complete Block Design (RCBD) with three replications. Data recorded for all studied traits were analyzed through ANOVA (steel *et al.*, 1997) by using the statistical software Statisticx 8.1. Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.*, (1995). Variance components, including error variance (σ^2e), genotypic variance (σ^2g) and phenotypic variance (σ^2p), were estimated from the expected mean squares obtained through analysis of variance (ANOVA) to assess the extent of genetic variability among the varieties. The calculation of phenotypic and genotypic coefficie/nts of variation was carried out according to the method proposed by Sing and Chaudhary (1985). GCV is genotypic coefficient of variation, Vg is genotypic variance, GCV and PCV values were categorized as low (0-10%), moderate (10-20%), and high (20% and above). The estimate was obtained by computing the ratio of genotypic variance to phenotypic variance according to Falconer (1995) and Johnson *et al.*, (1995). Values were classified as low (0-30%), moderate (30-60%) and high (≥60%) described by Johnson et al. (1995). Correlation was calculated using Pearson's method as described by Kwon and Torrie (1964) with the help of R software. The significance of the correlation values was tested at 5% ($p < 0.05$) and 1% ($p < 0.01$) probability levels. Correlation coefficient was further partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Wright (1921) and later described by Dewey and Lu (1959).

Results and discussion

The ANOVA revealed highly significant differences ($p \leq 0.01$) among the 15 maize genotypes for all measured traits, indicating the existence of considerable genetic variability (Table 2) and mean values presented in table 3. The mean squares for genotypes were much higher than error variances for most traits, confirming that genetic factors predominantly contributed to variation. For plant height (PH), the genotype mean square was 683.5 with an F-value of 80.5, while error variance was only 8.5. This large difference demonstrates strong genetic control and stability. The mean plant height ranged from 110.8 cm (PBG-09) to 162.4 cm (PBG-15), with a low CV% (2.3%) indicating precision of measurement. Similar results were reported by Gautam *et al.,* (2022), who highlighted PH as a reliable selection trait due to high heritability and low environmental influence. In case of number of leaves (NOL), the genotype mean square was 2.9 with an F-value of 2.6, which was significant but relatively lower compared to other traits, reflecting moderate genetic variability. The number of leaves ranged from 10.7 (PBG-15) to 14 (PBG-03 and PBG-14), with a coefficient of variation (CV) of 8.6%, indicating acceptable experimental precision. Leaf length (LL) recorded a high genotype mean square of 200.1 and an F-value of 23.2, suggesting substantial genetic variability. Leaf length ranged from 35.6 cm (PBG-14) to 59.3 cm (PBG-04) and the CV was 6.4% also confirmed its relative stability. Leaf width (LW) showed moderate variation (MS = 0.9, F = 3.7). The leaf width ranged from 6.4 cm (PBG-15) to 8.9 cm (PBG-13) and the CV value was 7.0%, indicating reasonable data accuracy indicating both genetic and environmental influence. These were supported by earlier findings (Magar *et al.*, 2021) .

Table 2: Analysis of variance for traits under study in maize hybrids

Source of variation and degree of freedom	Plant height	Number of leaves	Leaf length	Leaf width	Tassel length (cm)	Stem diameter (cm)	Number of				Pith diameter (cm)	Seed weight (g)
							tassel branches (cm)	seeds / cob	seeds / row	rows / cob		
Replication (2)	0.5	4.4	3.8	0.2	2.5	0.1	1.0	3.8	6.9	201.5	0.1	5.7
Genotype (14)	683.5	2.9	200.1	0.9	84.3	0.1	38.4	8.4	44.6	17896.8	0.2	61.3
Error (28)	8.5	1.1	8.6	0.3	3.2	0.0	2.9	2.5	10.9	4752.2	0.0	3.2
F Value	80.5**	2.6**	23.2**	3.7**	26.1**	2.7**	13.0**	3.4**	4.1**	3.8**	6.5**	19.2**
CV(%)	2.3	8.6	6.4	7	5.7	12.7	16.1	11.1	11.5	16.9	7	8.4

Highly significant at $P \leq 0.01$

Table 3: Mean value for the traits

Genotypes	Plant height (cm)	Number of leaves	Leaf length (cm)	Leaf width (cm)	Tassel length (cm)	Number of tassel branches (cm)	Stem diameter (cm)	Number of seeds per cob	Number of seeds per row	Number of rows per cob	Pith diameter (cm)	Seed weight (g)
Pbg-01	111.3	11	53.6	7.5	31.2	6.7	1.8	14.7	26.7	390	2.6	25.5
PBG-02	117.6	12	52.7	7.5	34	13	1.8	16.7	28	468	3.4	22.8
PBG-03	115.7	14	59.2	7	36.2	8.7	1.9	17	29	490	2.9	19.4
PBG-04	150.3	13	59.3	7.3	40.1	5.7	1.4	16.3	28	454	2.7	14.7
PBG-05	124.9	13.7	38.1	6.7	23.6	9	1.7	14.7	29.3	430	2.4	22.3
PBG-06	121.2	11.7	41.2	7.3	40.7	5.3	1.6	11.7	23.7	275	2.54	28.5
PBG-07	132.1	12.3	51.5	7	29.6	12	1.7	14	35.7	501	2.4	20.5
PBG-08	117.2	12	44.6	7.1	34.1	9	2.3	12	23.7	283	2.6	17.6
PBG-09	110.8	12.7	47.6	6.9	26.0	16.3	1.9	13.3	32.3	430	3.05	22.5
PBG-10	120.5	12.3	35.7	6.8	29.2	10	1.7	12.3	24.3	301	2.5	13.6
PBG-11	125.4	12	38.4	7	26.5	11.3	1.9	15	32.3	483	2.4	25.7
PBG-12	115.6	12	40.0	7.6	35.9	13.3	2	13.3	26	346	2.4	27.0
PBG-13	130.7	12	47.7	8.9	30.7	12.3	2.1	12.7	35	446	2.6	17.6
PBG-14	145.1	14	35.6	7.2	25.8	9.7	2.1	13	26.3	352	2.6	18.4
PBG-15	162.4	10.7	38.7	6.4	27.2	17.7	1.6	14.7	31	457	2.60	25.3

The mean squares for genotypes were much higher than error variances for most traits, confirming that genetic factors predominantly contributed to variation. For plant height (PH), the genotype mean These were supported by earlier findings (*et al.*, 2021) For tassel-related traits, tassel length (TL) displayed significant variation (MS = 84.3, F = 26.0) with mean values ranging from 23.6 cm (PBG-05) to 40.7 cm (PBG-06). The trait had a low CV (5.7%) while number of tassel branches (NTB) had MS = 38.4 with F = 13.0, demonstrating meaningful variability. Mean values ranged from 5.3 (PBG-06) to 17.7 (PBG-15) while CV was 16.1%, suggesting some variation due to environment. This agrees with Ishaq *et al.*, (2015), who also found tassel traits highly variable across maize genotypes. Stem diameter (SD) showed relatively low genotype mean square (0.1, F = 2.7) Mean values ranged from 1.4 cm (PBG-04) to 2.3 cm (PBG-08) and the trait exhibited a relatively high CV 12.7%). Similarly, pith diameter (PD) had MS = 0.22 with F = 6.5, indicating it as a stable trait with clear genetic influence. Pith diameter values ranged from 2.4 (PBG-05) to 3.4 (PBG-02) across genotypes, with low CV (7%). Yield-contributing traits were also highly variable. Number of rows per cob (NRC) exhibited MS = 8.4 with F = 3.4 and the mean number of rows per cob ranged roughly between 11.7 (PBG-06) and 17(PBG-3) across genotypes, with a CV of 11.2%, while number of seeds per row (NSR-1) had a remarkably high mean square of 44.6 and F = 4.1, but with the highest CV (11.5%), indicating strong environmental interaction. Mean values ranged from around 23.6 (PBG-6 and PBG-8) to 35.6 (PBG-7) seeds per row. Number of seeds per cob (NSC-1) followed a similar pattern (MS = 17896.8, F = 3.7). The mean value ranged from 275 (PBG-06) to 501(PBG-07) number of seeds among genotypes, and experimental error was low with CV = 16.9%. These results are consistent with findings by Mohammed *et al.*, (2024), who observed high variability in seed set traits but emphasized their environmental sensitivity. For seed weight (SW), the genotype mean square was 61.3 with an F-value of 19.2. Mean weights ranged from 13.6 (PBG-10) to 28.5 (PBG-06) among genotypes, CV was relatively low at 8.4%. This indicates that SW is a stable and genetically controlled trait, in agreement with Chaudhary *et al.*, (2022), who also reported its importance as a selection criterion for yield improvement. Overall, traits such as plant height, leaf length, tassel length, and seed weight showed high genotypic mean squares, strong F-values, and lower CV%, confirming them as reliable indicators for selection. On the other hand, traits like NTB, SD, and NSR-1 exhibited higher environmental sensitivity, suggesting the need for multi-environment testing. These findings collectively confirm the presence of substantial genetic variability, which can be effectively utilized in maize breeding programs to improve yield and related traits.

Estimation of variance components and heritability

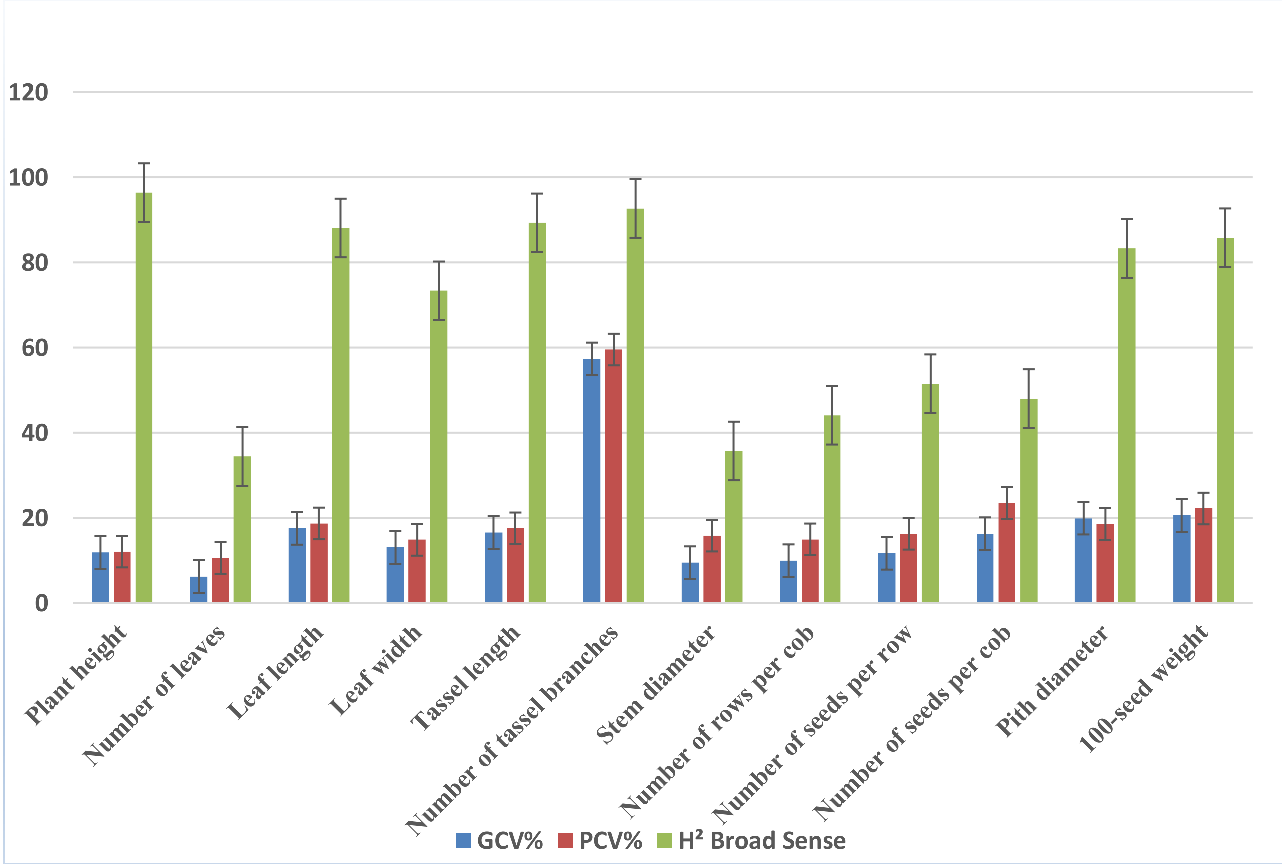
Plant height showed the Genotypic coefficient of variance GCV ($\sigma^2 g = 11.8$) was nearly equal to phenotypic coefficient of variance PCV ($\sigma^2 p = 12.6$) and the trait recorded very high broad-sense heritability ($H^2 = 0.9$), suggesting that variation is mainly genetic. The high heritability estimate for plant height indicates that selection would be highly effective for this trait, as supported by earlier findings (Ishaq et al., 2015). Number of leaves recorded low GCV (6.2%) and PCV (10.5%), coupled with low heritability (0.3). Such results demonstrate that environmental factors play a significant role, and selection for leaf

Table 4: Genotypic and phenotypic coefficient of variance and heritability estimate for various traits of maize

Traits	Vg (σ^2g)	Vp (σ^2p)	Mean (X)	GCV (%)	PCV (%)	H^2 broad sense	H^2 (%)
Plant height	224.9	233.4	126.7	11.8	12.1	0.9	96.4
Number of leaves	0.6	1.7	12.4	6.2	10.6	0.3	34.4
Leaf length	63.8	72.4	45.6	17.5	18.	0.9	88.1
Leaf width	0.9	1.1	7.2	13.0	14.8	0.8	73.3
Tassel length	27.0	30.2	31.4	16.6	17.5	0.9	89.3
Number of tassel branches	37.4	40.3	10.7	57.3	59.5	0.9	92.7
Stem diameter	0.0	0.1	1.8	9.5	15.8	0.4	35.7
Number of rows per cob	1.9	4.4	14.1	9.9	14.9	0.4	44.1
Number of seeds per row	11.2	21.8	28.8	11.7	16.3	0.5	51.5
Number of seeds per cob	4381.6	9133.6	407	16.3	23.5	0.5	48
Pith diameter	0.2	0.2	2.6	19.9	18.5	0.8	83.3
100-seed weight	19.4	22.5	21.4	20.6	22.2	0.9	85.8

number would be ineffective in early generations (Ishaq *et al.*, 2015). Leaf length exhibited high GCV (17.5%) and PCV (18.7%) values. The high heritability (0.9) indicates that the trait is largely genetically controlled, making selection effective for improvement, as supported by Syahruddin and Suwardi (2023). Leaf Width (cm) exhibited moderate GCV (13.0%) and PCV (14.8%) values. The high heritability (0.8) suggests that genetic factors play a dominant role, making selection for wider leaves feasible as noted by Syahruddin & Suwardi (2023). Tassel Length (cm) showed high GCV (16.5%) and PCV (17.5%) values, along with high heritability (0.9). This indicates that tassel length is largely governed by genetic factors, and direct selection would be effective for improvement. (Ishaq *et al.*, 2015). Number of Tassel Branches Extremely high GCV (57.3%) and PCV (59.5%) were observed, reflecting the presence of substantial genetic variability. The high heritability (0.9) further emphasizes that this character is strongly heritable and can be improved effectively through selection as confirmed by Ishaq *et al.*, (2015). Stem Diameter (cm) showed Low GCV (9.5%) and relatively higher PCV (15.8%) were observed, indicating strong environmental modulation. The low heritability (0.4) implies that genetic progress for this trait through selection would be limited, unless environmental variation is controlled (Syahruddin and Suwardi, 2023). Number of Rows per Cob showed low GCV (9.9%) compared to PCV (14.9%), with moderate heritability (0.4). The results indicate that environmental factors significantly influence this trait, and selection would be less effective (Shakarchy *et al.*, 2023). Number of Seeds per Row the GCV (11.7%) was lower than the PCV (16.25%), showing moderate environmental influence. With moderate heritability (0.5), genetic improvement through selection is possible but may require careful management of environmental effects (Hosseini *et al.*, 2025). Number of Seeds per Cob the genotypic coefficient of variation (16.3%) was lower than the phenotypic coefficient of variation (23.5%), indicating that environmental factors considerably influenced this trait. The moderate heritability value (0.5) suggests that both genetic and environmental effects contributed to the observed variability, and selection may be moderately effective (sarviya and petal, 2024). Pith Diameter (cm) high GCV (19.9%) along with PCV (18.5%) and high heritability (0.8) suggested that this character is mainly governed by additive genetic effects and that improvement through direct selection would be reliable (Gautam et al., 2022). 100 Seed Weight exhibited high GCV (20.6%) and PCV (22.2%) values, accompanied by a high heritability estimate (0.9). Such results reflect strong genetic determination and suggest that simple phenotypic selection can bring about considerable improvement in this character (Dogar *et al.*, 2023).

Fig 1: Graphical representation of coefficient of variation and broad sense heritability



Correlation analysis

Correlation analysis among the studied traits in maize revealed important inter-relationships that are highly relevant for selection and yield improvement. Seed number per row (NSR) exhibited the strongest positive association with number of seeds per cob (NOS) (r = 0.8), suggesting that row productivity is a major determinant of overall kernel set (Fig.2). This strong linkage highlights that selecting for improved NSR would directly translate into greater cob filling, consistent with earlier findings that cob architecture significantly contributes to yield potential (Magar *et al.,* 2021). Similarly, NOS showed a high correlation with number of rows per cob (NR) (r = 0.8), reflecting that genotypes producing more rows also tend to achieve better seed arrangement and higher kernel counts, in agreement with reports by Gautam *et al.,* (2022). Leaf length (LL) showed a moderate positive correlation with pith diameter (PD) (r = 0.5) and tassel length (TL) (r = 0.5), indicating that enhanced vegetative growth is associated with both stem robustness and tassel development. This relationship suggests that leaf morphology plays a role not only in photosynthetic capacity but also in supporting reproductive structures, consistent with the conclusions of Hosseini *et al.,* (2025). Plant height (PH) was weakly associated with yield-related traits, showing only moderate correlations with number of tassel branches (NOTB) (r = 0.1) and NOS (r = 0.3), but negative associations with PD (r = –0.2) and seed weight (SW) (r = –0.2), implying that taller plants do not necessarily guarantee improved reproductive efficiency. This aligns with findings that excessive vegetative growth may divert assimilates away from reproductive sinks (et al., 2020). Tassel length (TL) had a significant negative correlation with NOTB (r = –0.5), highlighting a trade-off between elongation and branching, as also observed by Shivani, and Prasad, (2020). This suggests that genotypes with fewer tassel branches tend to develop longer tassels, which could influence pollen production efficiency. On the other hand, pith diameter (PD) was positively correlated with NR (r = 0.4), reinforcing its role in cob development and assimilate support, consistent with earlier reports that stem structural attributes are linked with ear productivity (Chauhan, 2022). Seed weight (SW) showed negative associations with NR and stem diameter (SD), suggesting a trade-off between kernel size and cob architecture, between kernel size and cob architecture, between kernel size and cob architecture, a trend also noted in previous studies (Hasan *et al.,* 2024). Overall, the correlation matrix emphasizes that traits contributing to cob structure (NR, NOS, NSR) and leaf morphology (LL, LW) are the most reliable indicators of yield potential. These findings indicate that indirect selection for NR and NSR, along with supportive vegetative traits, could accelerate genetic gain in maize breeding programs. Path coefficient analysis partitioned the genotypic correlations into direct and indirect effects of different traits on grain yield in maize (Table 5). Plant height (PH) exhibited a moderate direct effect on yield (0.3), while also maintaining positive indirect contributions through number of seeds per row (0.1) and number of rows per cob (0.0). This indicates that taller plants tend to support better reproductive development, as also reported by Hasan *et al.,* (2025). Number of leaves (NOL) showed a very low direct effect (0.1), but contributed indirectly through its positive association with number of rows (0.1). Leaf length (LL) had a strong negative direct effect (–0.6), though it still contributed indirectly via number of rows (0.2), suggesting that selection for leaf traits should be approached cautiously, consistent with Mohammed *et al.,* (2024). Leaf width recorded a small direct positive effect (0.2), with additional indirect support through plant height (-0.0), highlighting its structural contribution. Tassel length (TL) also showed a positive direct effect (0.2) but a notable negative indirect effect via

Fig 2: Correlation analysis for the twelve characters of fifteen maize genotypes

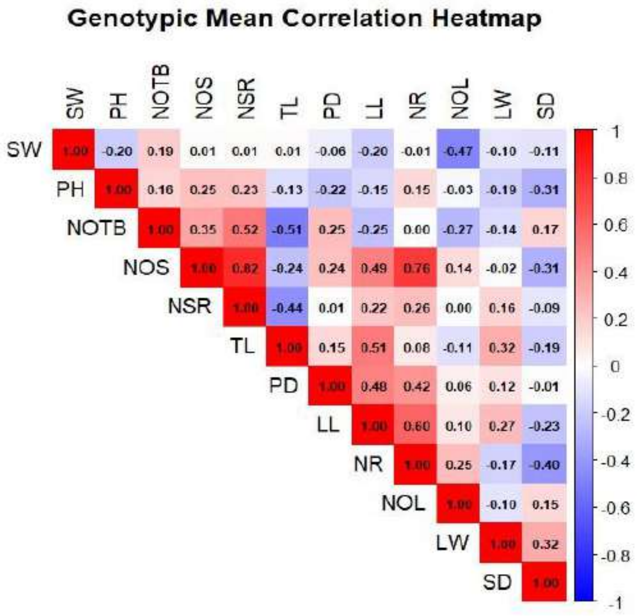


Table 5: Path analysis of thirty-two maize genotypes showing direct and indirect effects

	Plant height (cm)	Number of leaves	Leaf length (cm)	Leaf width (cm)	Tassel length (cm)	Number of tassel branches	Diameter (cm)		Seed weight (g)	Number of		
							stem	pith		seeds /cob	seeds / row	rows / cob
Plant height (cm)	**0.3**	-0.0	0.1	-0.0	-0.0	0.0	-0.0	0.0	0.0	-0.1	0.1	0.0
Number of leaves	-0.0	**0.1**	-0.0	-0.0	-0.0	-0.1	0.0	-0.0	0.0	-0.1	-0.0	0.1
Leaf length (cm)	-0.0	0.0	**-0.6**	0.0	0.1	-0.1	-0.0	-0.1	0.0	-0.3	0.1	0.2
Leaf width (cm)	-0.0	-0.0	-0.1	**0.2**	0.1	-0.1	0.0	-0.0	0.0	-0.1	0.0	0.0
Tassel length (cm)	-0.0	-0.0	-0.3	0.1	**0.2**	-0.2	-0.0	-0.0	-0.0	0.2	-0.3	0.0
Number of tassel branches	0.1	-0.0	0.1	-0.0	-0.0	**0.5**	0.0	-0.0	-0.0	-0.2	0.2	-0.0
Stem diameter (cm)	-0.0	0.0	0.1	0.0	-0.0	0.0	**0.1**	-0.0	0.0	0.1	-0.0	-0.0
Pith diameter (cm)	-0.1	0.0	-0.2	0.0	0.0	0.1	0.0	**-0.2**	0.0	-0.1	-0.0	0.1
Seed weight (g)	-0.1	-0.0	0.1	-0.0	0.0	0.1	-0.0	0.0	**-0.0**	0.0	-0.0	0.0
Number of seeds per cob	0.1	0.0	-0.2	0.0	-0.0	0.1	-0.0	-0.0	0.0	**-0.9**	0.5	0.3
Number of seeds per row	0.1	-0.0	-0.0	0.0	-0.0	0.2	-0.0	0.0	0.0	-0.7	**0.7**	0.1
Number of rows per cob	0.0	0.0	-0.3	0.0	0.0	-0.0	-0.0	-0.1	-0.0	-0.6	0.1	**0.4**

number of tassel branches (–0.2), confirming a trade-off between tassel elongation and branching, in line with Magar et al., (2021). Number of tassel branches exerted the highest positive direct effect (0.5) on yield, suggesting that branching contributes strongly to reproductive efficiency. Stem diameter (SD) had a positive direct effect (0.1), reflecting its importance in nutrient transport and plant robustness, which agrees with Chauhan et al., (2022). Pith diameter (PD), however, had a strong negative direct effect (–0.2), although it showed some positive indirect influence via number of rows (0.1). Seed weight (SW) had a small negative direct effect (–0.1), indicating its contribution is mostly indirect through traits like leaf length (0.1). Number of seeds per row (NOS) exerted the most pronounced negative direct effect (–0.9), though its strong positive indirect effect via number of seed rows (0.5) and number of rows per cob (0.3) suggests that seed distribution within the cob is a critical factor for yield. Similarly, number of seed rows (NSR) recorded a high positive direct effect (0.7), which was reinforced by positive indirect effects through NOS (0.5), confirming its central role in yield determination. Finally, number of rows per cob (NR) had a positive direct effect (0.4), supported by indirect effects through NOS (0.3), highlighting it as one of the most important yield attributes, corroborating the findings of Hasan *et al.,* (2025). Overall, the path analysis revealed that NOTB, NSR, NR, and SD are the key contributors to yield through their high positive direct effects, whereas traits such as LL and NOS negatively influenced yield directly but compensated indirectly through associated traits. These results suggest that selection focusing on tassel branching, number of seed rows, and number of rows per cob can significantly improve maize yield potential.

Hence, in conclusion, the present study revealed substantial genetic variability among the evaluated maize hybrids, with clear differences in performance for morphological and yield-related traits. Genotypes PBG-15, PBG-07 and PBG-06 consistently exhibited superior performance, though their strengths varied across parameters. High heritability estimates for plant height, tassel length, and tassel branches suggest that these traits are largely governed by additive genetic effects and can be effectively improved through selection. In contrast, traits with low heritability, such as stem diameter and number of leaves, require cautious improvement strategies. Correlation and path analysis highlighted the importance of seed rows, tassel branches, and rows per cob as key contributors to grain yield, both directly and indirectly. Overall, the study identified promising hybrids and key traits that can serve as reliable selection indices, thereby offering valuable insights for maize breeding programs aimed at yield improvement.

References

1. Abegunde, I.O. 2023. Genetic variability of yield and yield related traits among drought tolerant maize genotypes. Agric. Trop. Subtrop., 56(1):1–9.
2. Ahmed, N., Chowdhury, A.K., Uddin, M.S. and Rashad, M.M.I. 2020. Genetic variability, correlation and path analysis of exotic and local hybrid maize (*Zea mays* L.) genotypes. Asian J. Med. Biol. Res., 6(1):8–15.
3. Akhtar, S., Abbas, A., Faisal, M., Raza, M.H., Samie, A. M. Yu and Lovell, A. 2023. Roles of personal, household, physical and institutional factors on farmers' efficiency of hybrid maize production: Implications for food security. Agricul., 13(9):1840.
4. Amegbor, I.K., A. van Biljon, N. Shargie, A. Tarekegne and Labuschagne, M.T. 2022. Heritability and associations among grain yield and quality traits in quality protein maize hybrids. Plants, 11(6):71

5. Chaudhary, C.S., S.N. Shah, Z. Chauhan and P. Rahevar 2022. Correlation study of yield attributing traits in maize (*Zea mays* L.). Int. J. Agric. Appl. Sci., 3(1):8–12.
6. Chauhan, Z., S.N. Shah, C.S. Chaudhary and Rahevar , P. 2022. Correlation study of yield attributing traits in maize (*Zea mays* L.). Int. J. Agric. Appl. Sci., 3(2):19–21.
7. Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat seed production. Agron. J., 51(9):515–518.
8. Dogar, M.W., Z. Hussain, M.I. Ashraf and Naveed, M. 2023. Evaluation of genetic variability in maize (*Zea mays* L.) based on yield and its attributed traits. Asian J. Biotechnol. Genet. Eng., 6(2):200–210.
9. Dragomir, V., B.I. Sebastian, B. Alina, P. Victor, L. Tanasa and Horhocea, D. 2022. An overview of global maize market compared to Romanian production. Rom. Agric. Res., 39(1):535–544.
10. Dudhe, M.Y., Jadhav, M.V., Sujatha, M., Meena, H.P., Rajguru, A.B., Gahukar, S.J. and Ghodke, M.K. 2024. WAASB-based stability analysis and validation of sources resistant to *Plasmopara halstedii* race-100 from the sunflower working germplasm for the semiarid regions of India. Genetic Resou. Crop Evolu. 71(4):1435-1452.
11. Erenstein, O., Jaleta, M., Sonder, K. Mottaleb, K. and Prasanna, B.M. 2022. Global maize production, consumption and trade: Trends and R and D implications. Food Secur., 14(5):1295–1319.
12. Fadhli, N., Farid, M., Azrai, M., Nur, A., Efendi, R. , Priyanto, S.B., Nasruddin, A.D. and Novianti, F. 2023. Morphological parameters, heritability and yield component correlation in hybrid maize. Biodiversitas, 24(1):205–209.
13. Falconer, D.S. 1981. Introduction to Quantitative Genetics. Longman, London.
14. Ferdous, T., Nur, I.J., Romel, M.H. and Bhuiyan, S.R. 2023. Genetic variability and heritability in F4 population of rice. Int. J. Appl. Sci. Biotechnol., 11(2):99–105.
15. Gautam, J., Adhikari, A., Ale, P., Dhungana, B., Adhikari, A. and Dhakal, K.H. 2022. Analysis of heritability and correlation for yield and yield attributing traits in maize hybrids. Int. J. Environ. Agric. Biotechnol., 7(1):100–110.
16. GOP. 2024–2025. Pakistan economic survey 2024–2025. Finance and economic affairs division, Ministry of Finance, Government of Pakistan, Islamabad.
17. Hamdi, A.A. and Al-Rawi, O.H. 2021. Evaluating the performance of maize lines and their half diallel crosses. IOP Conf. Ser. Earth Environ. Sci., 761(1):012073.
18. Hasan, N., Jone, M.J.H., Das, B. , Siddique, M.N.A. , Islam, Y. and Kashem, M.A. 2025. Genetic parameter analysis and evaluation of maize hybrids under local climatic conditions of Mymensingh, Bangladesh. Heliyon, 11(1):e36423.
19. Hosseini, S.M.S., Shiri, M., Mostafavi, K., Mohammadi, A. and Miri, S.M. 20 25. Genetic analysis and association detection of agronomic traits in maize genotypes. Sci. Rep., 15(1):399.
20. Huma, B., Hussain, M., Ning, C and Yuesuo, Y. 2019. Human benefits from maize. J. Appl. Sci. Res., 2(2):4-7.
21. Ilyas, M.,. Khan , S.A and Awan, S.I. 2019. Assessment of heritability and genetic advance in maize (*Zea mays* L.) under natural and water stress conditions. Sarhad J. Agric., 35(1):168–175.
22. Ishaq, M., Rahman, H., Hassan, G., Iqbal, M., Khalil, I.A., Khan, S.A. and Hussain, J. 2015. Genetic potential, variability and heritability of morphological and yield traits among maize synthetics. Electron. J. Biol., 11(4):187–191.

23. Islam, S., Ferdausi, A., Sweety, A.Y., Das, A., Ferdoush, A. and Haque, M.A. 2020. Morphological characterization and genetic diversity analyses of plant traits contributing to grain yield in maize (*Zea mays* L.). J. Biosci. Agric. Res., 25(1):2047-2059.
24. Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. Agron. J., 47(7):314–318.
25. Kumawat, G., Shahi, J.P. and. Choudhary, M.K. 2020. Genetic parameters, correlation and path coefficient analysis in maize hybrids under waterlogging conditions. Range Manag. Agrofor., 41(2):227–234.
26. Kwon, S.H. and Torrie, J.H. 1964. Heritability and interrelationships among traits of two soybean populations. Crop Sci., 4(2):196–198.
27. Magar, B.T., Acharya, S., Gyawali, B., Timilsena, K., Upadhyay, J. and Shrestha, J. 2021. Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. Heliyon, 7(11):e09905.
28. Mohammed, M.S., Towfiq, S.I., Hassan, H.N. and Jumaa, M.E. 2024. Correlation and path analysis of agronomic traits and their impact on kernel yield in F_2 maize hybrids. Passer J. Basic Appl. Sci., 6(2):543–552.
29. Mohammedali, A.M., Mohamed, O.A., Abdalla, M.G., Taha, K. and Ahmed, E. 2021. Genetic variability, heritability and genetic advance estimates in maize varieties in Sudan. Int. J. Food Sci. Agric., 5(1):85–90.
30. Ravi, S. and Patel, R. 2024. Genetic variability and diversity analysis in maize (*Zea mays* L.). Pharma Innov. J., 13(9):105–109.
31. Rawi, O.H.A., Shaheen, M.R.A. and Abdulkafoor, A.H. 2018. Estimation of genetic parameters in Iraqi maize inbred lines and their full diallel crosses. Plant Arch., 18(2):2257–2262.
32. Sangare, S., Menkir, A., Ofori, K. and Gracen, V. 2019. Studies on estimation of heterosis for striga resistance in maize test crosses in Mali. J. Genet., Genomics, Plant Breed., 3(3):1-8.
33. Shakarchy, W.A., Taweel, M.A., Shamil, A.H. and Zubaidy, K.A. 2023. Heritability, genetic advance and genetic parameters of maize genotypes under different plant densities. Euphrates J. Agric. Sci., 15(2):240–251.
34. Shikha, K., Shahi, J.P. and Singh, S. 2020. Path coefficient analysis in maize (Zea mays L.) hybrids. J. Pharmacogn. Phytochem., 9(2):278–282.
35. Shivani, D., and Prasad, V. 2020. Correlation and path analysis in maize (*Zea mays* L.). J. Genet., Genomics, Plant Breed., 1(2):1–7.
36. Singamsetti, A., Zaidi, P.H., Seetharam, K., Vinayan, M.T., Olivoto, T., Mahato, A. and Shikha, K. 2023. Genetic gains in tropical maize hybrids across moisture regimes using multi-trait index selection. Front. Plant Sci., 14(1):1147424.
37. Singh, A.K. 2023. Early history of crop introduction into India: American cereal maize (*Zea mays* L.). Indian J. Genet. Plant Breed., 83(1):1–7.
38. Singh, R.K. and Chaudhary, B.D. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, India.
39. Steel, R.G.D., Torrie, J.H. and Dickey, D.A. 1997. Principles and procedures of statistics: A biometrical approach. 3rd ed. McGraw-Hill, New York.
40. Syahruddin, K. and Suwardi 2023. Genetic variability, heritability and correlation of hybrid maize agronomic traits adapted to dry land. IOP Conf. Ser. Earth Environ. Sci., 2(1):153–156.
41. Taiwo, O.P., Nwonuala, A.I. , Isaiah, B.F. , Olawamide, D.O. and Agbugba, I.K. 2020. Correlation and path coefficient analysis of grain yield and its contributing traits in maize. Int. J. Plant Soil Sci., 32(1):7–13.

42. Wang, Y., Zhang, G., Li, R., Wang, K., Ming, B., Hou, P. and Li, S. 2023. Pathways to increase maize yield in Northwest China: A multi-year, multi-variety analysis. Eur. J. Agron., 49(1):126–134.
43. Wright, S. 1921. Correlation and causation. J. Agric. Res., 20(7):557–585.
.
44. Zhi, Y., Li, X., Wang, X., Jia, M. and Wang, Z. 2024. Photosynthesis promotion mechanisms of artificial humic acid depend on plant type: A hydroponic study on C_3 and C_4 plants. Sci. Total Environ., 917(1):1.