



Comparative Evaluation of Yield Performance and Earliness in Maize (*Zea mays* L.) Hybrids under the National Uniform Yield Trial (NUYT)

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The objective of this study was to assess the performance of 12 maize genotypes, including one check genotype (genotype 1), for phenology, morphology, and yield traits in the field. A randomized complete block design with three replications was used. Observations were made for DFM, DFF, PH, EH, TPH, TEH, SP, yield (kg) and yield (kg/ha). Analysis of variance revealed significant differences for most traits, suggesting that there is a considerable amount of genetic variability. The differences among genotypes were statistically significant at ($P \leq 0.05$). Mean comparisons were performed using the LSD test at 5% probability level. Standard errors (\pm SE) were calculated for all measured traits, and confidence intervals (95%) confirmed the reliability of the observed differences among genotypes. Average performance revealed that several genotypes outperformed the check for important traits. Genotypes 3 and 7 were early flowering (DFM = 66 days; DFF = 68 days), while genotypes 4 and 11 were late flowering. PH ranged from 165 cm (check) to 235 cm (genotype 5), and EH from 110 to 150 cm. TPH and TEH were higher in genotype 5, while the lowest was in genotype 3. SP varied from 82.4% to 90.0% (genotypes 2 and 5, respectively). Genotypes differed in yield, with the highest yield (7.2 kg; 11946 kg/ha) in genotype 12, followed by genotypes 8 and 2, whereas the lowest yield was in genotype 3. Correlation studies showed that yield was positively correlated with PH, EH, and related traits, suggesting they could play a significant role in yield enhancement. In general, genotype 12 was the best performer, followed by genotypes 8 and 2. This research suggests that selection for plant architecture and yield components can lead to improved maize yield.

Keywords: Maize, Genetic Variability, Seed Yield, Forage Yield, Genotype Evaluation, Correlation Analysis

Introduction:

Maize (*Zea mays* L.) is one of the most important cereal crops and is a staple in global food, feed, and industry. Its adaptability and yield potential have enabled it to thrive across diverse agro-ecological environments. Maize is a staple food and feed crop and a valuable source of bio-industrial products worldwide, playing a crucial role in agriculture [1][2]. Maize has become a critical crop for developing nations, such as Pakistan, due to increasing demand from the poultry and feed industries and its importance to farmers' livelihoods. The increasing need for maize grain calls for ongoing yield and adaptation improvement through breeding approaches [3].

Maize grain yield is a quantitative trait that is controlled by several interacting traits, such as phenology, morphology, and yield. DFM and DFF play a key role in determining the reproductive success of maize, as the synchrony between tasseling and silking is essential for pollination and the kernel development. Any misalignment may lead to poor kernel set and yield loss [4][5]. Thus, assessing flowering traits is crucial for the selection of genotypes with consistent and effective reproductive efficiency across different environments.

Another critical aspect of maize yield is plant architecture, with traits such as PH and EH playing a vital role. These traits influence light interception in light interception, canopy architecture, and biomass production, and subsequently affect yield. Increased PH typically leads to higher biomass production, but very tall plants may be more prone to lodging, particularly with high levels of inputs. Likewise, EH plays a crucial role in plant balance and nutrient translocation [6][7]. Recent genetic analyses have shown that PH and EH are regulated by multiple quantitative trait loci and are highly correlated with yield performance, and are therefore critical traits for selection in breeding [8][9].

Other yield components, including TPH, TEH, and SP, play a role in determining yield. PP and PE per unit area affect yield potential, and SP affects the efficiency of biomass conversion. The genetic variability in these traits offers an opportunity to select better genotypes with improved productivity. Earlier research has highlighted the importance of improvement in yield components for increasing grain yield, as these traits are generally more heritable and stable than yield itself [10][11]. In addition, knowing the relationships between these traits (correlation and variance analysis) helps guide the breeding strategy.

Genetic variability among maize varieties is the key to successful breeding. Analysis of variance allows the decomposition of the total variability into genetic and environmental components, thus facilitating the identification of traits under substantial genetic influence. Analysis of mean performance also helps in the selection of the best genotypes, especially relative to the check varieties. Genotypes that perform better than the check for multiple traits are considered promising for further development and release [5].

Novelty Statement:

This research identifies genotypes with superior performance compared to the check for important phenological, morphological, and yield traits, with genotype 12 having the best overall performance. Additionally, it identifies important trait-yield associations, offering a basis for selection of superior maize genotypes for yield improvement.

Future Prospects:

In recent decades, there has been a greater focus on the development of high-yielding maize genotypes with early maturity, desirable plant architecture, and yield components. These types of genotypes will have better adaptation to environmental stresses and yield stability. Thus, the field performance of maize genotypes needs to be evaluated rigorously to select

superior lines and to quantify the role of various traits in determining yield. In this study, several maize genotypes, including a check variety, were evaluated for their performance in terms of important phenological, morphological, and yield traits. The results of this study will help identify superior genotypes for breeding maize.

Objectives:

To evaluate the comparative performance of maize (*Zea mays* L.) hybrids for yield under National Uniform Yield Trial (NUYT) conditions.

To assess earliness-related traits (days to 50% tasseling and silking) among different maize genotypes.

Materials and Methods:

This experiment was carried out at the Maize Research Station, Ayub Agricultural Research Institute, Faisalabad. The main objective of the study was to assess the field performance of various maize hybrids. Twelve maize genotypes, including a check (genotype 1), were used in the experiment (Table 1). The selection of 12 maize genotypes, including one check, was based on their diverse genetic background, representation in the National Uniform Yield Trial (NUYT), and their potential for variability in yield and earliness traits. This number was considered sufficient to capture meaningful genetic variation while maintaining experimental precision and manageability under field conditions (Figure 3).

Table 1. The hybrids of maize evaluated in the national uniform yield trial for earliness and yield-related characters

Serial No	Genotype
1	YH-5427 (Check)
2	LS-2021
3	AS-5144
4	SB-6222
5	SW-9481
6	HMC-9091
7	TGT-6325
8	SF6325
9	SF-6810
10	SB-6223
11	HS-3939
12	TR-1725

A Randomized Complete Block Design (RCBD) with three replications was adopted for the experiment to reduce the effect of environmental variability. The seed of all genotypes was treated with imidacloprid 30.7% w/w and tebuconazole 1.07% w/w before sowing. Each genotype was sown in plots with row-to-row and plant-to-plant spacing of 75 cm and 25 cm, respectively, to maintain a healthy plant population. The soil was fertile clay loam, and all plots were given the same agronomic management. The recommended dose of fertilizers NPK @ 200:120:100 kg ha⁻¹ (N:P₂O₅:K₂O) was applied from urea, DAP, and muriate of potash. Four irrigations were provided throughout the season at key growth stages such as germination, vegetative stage, tasseling, and grain filling. Irrigation, fertilization, and weed control were kept the same for all treatments to ensure unbiased comparison among different genotypes Figure 1.

The mean, maximum, and minimum temperatures during the cropping season are presented in Figure 1 A steady increase in temperature was observed from February to June,

with both maximum and minimum temperatures peaking in June. The mean temperature followed the same upward trend, reflecting seasonal warming. A slight decline was observed in July, likely due to the onset of the monsoon season.

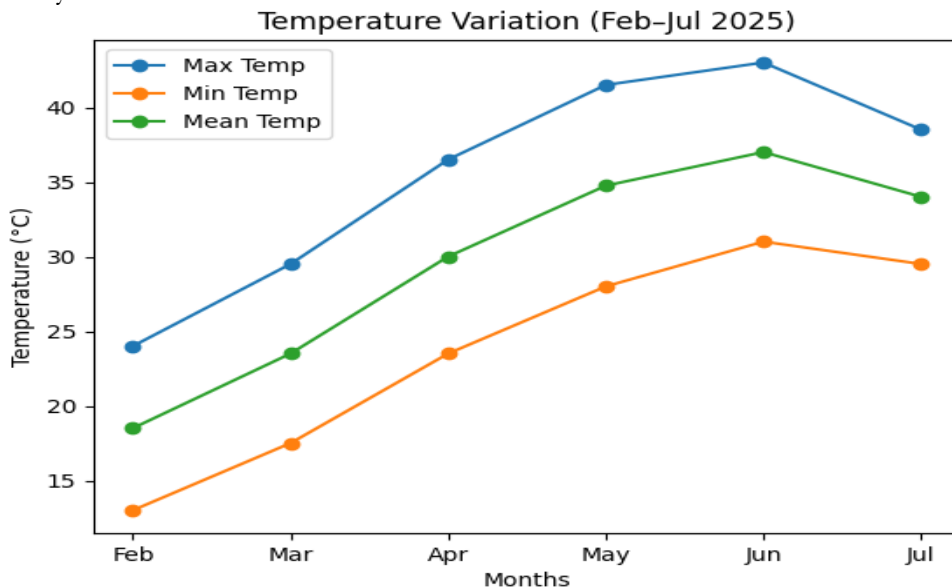


Figure 1. The mean temperature, the highest temperature, and the lowest temperature of the months of the season from February to July

The rainfall pattern during the cropping season is presented in Figure 2. The graph shows low to moderate rainfall from February to May, with a slight fluctuation, and the lowest rainfall occurred in May. A sharp increase is observed in June, followed by a peak in July, indicating the onset and intensification of the monsoon season.

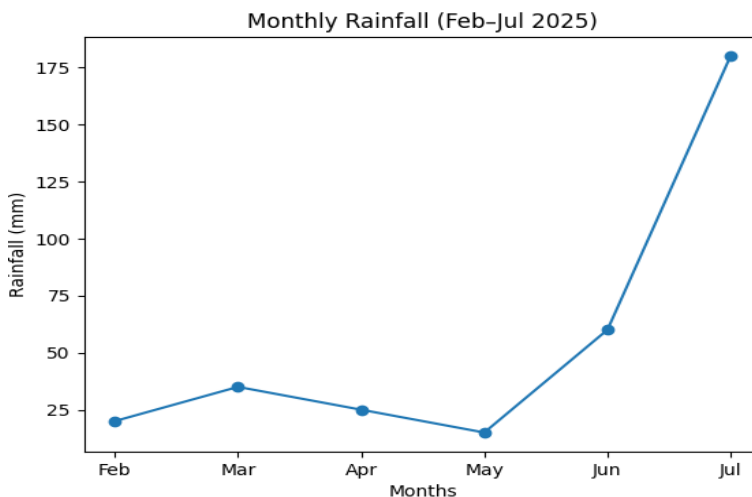


Figure 2. Rainfall scenario during the growth period showing variation in precipitation during the growth period

Information was collected on different phenological, morphological, and yield attributes from randomly selected plants in each plot.

Days to male flowering (DFM) and female flowering (DFF):

They were recorded as the number of days from sowing to 50% tasseling and silking.

Plant height (PH) and ear height (EH)

Plant height (PH) was measured in centimeters from the ground to the tip of the tassel at maturity, and ear height (EH) was measured from the ground to the node of the uppermost ear.

Total number of plants harvested (TPH) and total number of ears harvested (TEH):

These were recorded at harvest time for each plot. Shelling percentage (SP) was calculated as the ratio of grain weight to total ear weight × 100

Grain yield (Yield /kg and Kg/ha):

This was measured after harvesting, drying, and threshing of ears and then converted to yield per hectare (kg/ha) through conversion factors depending on plot size.

Statistical Analysis:

The data were analyzed statistically using analysis of variance (ANOVA) at a significance level of 0.05, suitable for the RCBD to assess the statistical significance of treatment differences. The means were compared to determine the performance of genotypes, especially vis-à-vis the check variety. Bivariate correlation analysis was also conducted to determine the associations between traits and yield. Statistix 8.1 was used for statistical analysis.

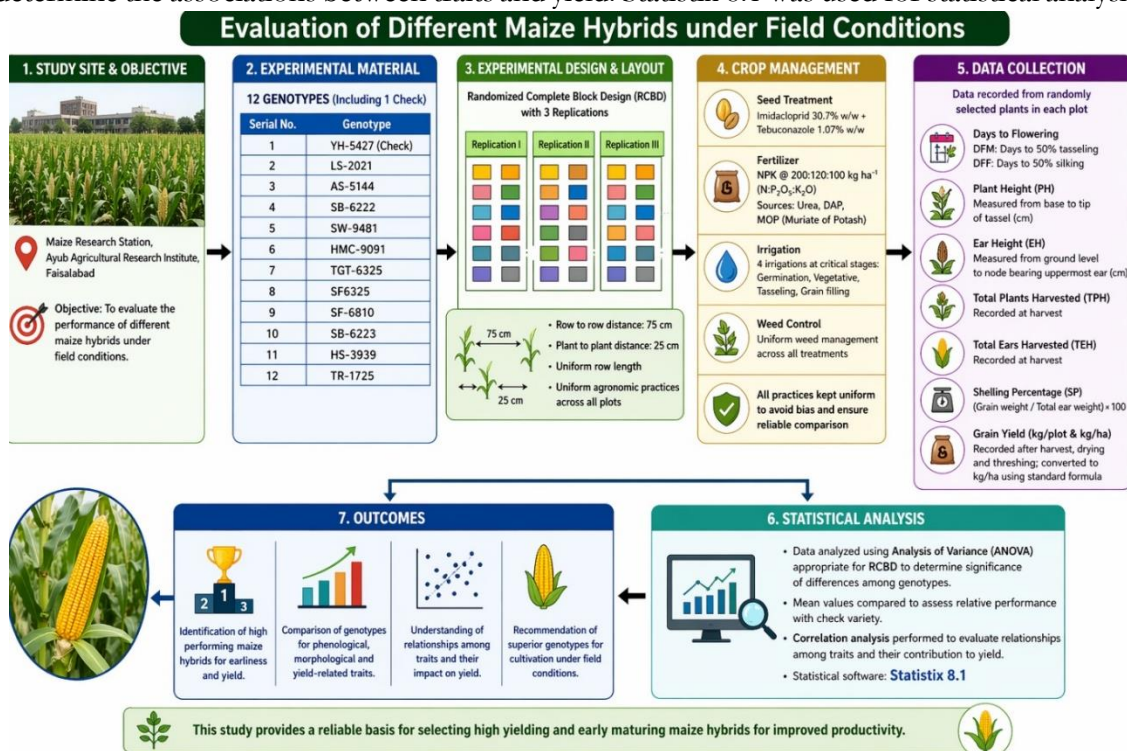


Figure 3. Flow chart showing Study location, experimental material and design, crop management, data collection, statistical analysis, and outcomes of research

Results and Discussion:

Analysis of Variance:

The MSS for DFM (5.21**) and DFF (5.23**) were highly significant, suggesting that the genetic variation among genotypes for flowering traits is large. The comparable level of variation in DFM and DFF also indicates a high degree of coordination between male and female flowering, an an important trait for pollination and seed production.

There were also significant variations in PH (580.80*) and EH (304.29*), indicating good genetic variability in plant structure. The greater MSS value for PH compared to EH suggests higher genetic variability for the plant height trait. EH is a structural trait that depends on PH; thus, the variation in PH and EH indicates some potential for selection in breeding programs that aim to improve plant structure.

The MSS for NPH (60.02) was not significant, suggesting that there was little variation among genotypes for this trait. This implies that NPH might have been more environmentally

influenced, and hence may be less useful for selection. On the other hand, the MSS for NEH (59.60*) was significant, suggesting that the number of ears harvested differed significantly among the genotypes and could be improved by selection.

Shelling percentage (SP) (7.02*) showed significant variation, suggesting genetic differences in grain recovery. This is crucial for yield, and its significant variation implies that it can be improved by selection.

There was significant variation among genotypes for yield attributes. The MSS values for yield (3.35*) and YIELD (k/ha) (9274331*) were significant, indicating that genetic variability exists for yield. The extremely high MSS value for yield (k/ha) suggests large variability in yield under field conditions. In summary, the variation observed in yield and its components indicates that selection for high-yielding genotypes can be made.

Table 2. MSS values of yield and earliness-related characters in the national uniform yield trial

SR no	Character name	MSS (GEN)
1	Days to Flowering (Male)	5.21**
2	Days to Flowering (Female)	5.23**
3	Plant height	580.80*
4	Ear height	304.29*
5	No of Plants Harvested	60.02
6	No of Ears Harvested	59.60*
7	Shelling (%)	7.02*
8	Yield (kg)	3.35*
9	Yield (k/ha)	9274331*

Mean Data Representation:

The average performance of the genotypes varied compared with the check (genotype 1) for all traits. For flowering characters, the check had DFM and DFF of 70 and 72 days, respectively. Genotypes 3, 7, 8, and 12 were early flowering for both DFM (66-67 days) and DFF (68-69 days) compared with the check. On the other hand, genotypes 4 and 11 were later than the check (71-73 days), while the rest were either similar or slightly earlier in flowering (Figure 4).

Regarding PH, the check had the lowest value (165 cm), and all genotypes were higher, with the highest PH in genotype 5 (235 cm) and genotype 12 (220 cm). Similarly, EH of the check (115 cm) was lower than most genotypes, and the highest EH was observed in genotypes 7 (150 cm) and 5 (145 cm), indicating plants with higher ear placement than the check.

For TPH and TEH, the check had the lowest values (35 and 25, respectively). Most genotypes had higher values than the check, with the highest TPH (49) and TEH (39) in genotype 5, followed by genotypes 8 and 9, suggesting improved plant stand and ear production. But genotype 3 had lower values than the check for both traits.

The SP of the check was 88.8%, which was equalled or exceeded by genotypes 2 and 5 (90.0%), with most other genotypes showing slightly smaller SP (minimum in genotype 9: 82.4%).

The yield trait showed improvement in some genotypes over the check. The check recorded 4.7 kg and 7823 kg/ha, which were surpassed by genotypes 2, 4, 5, 6, 8, 9, and 12. Genotype 12 exhibited the highest yield (7.2 kg and 11946 kg/ha), followed by genotype 8 (6.4 kg and 10615 kg/ha) and genotype 2 (6.0 kg and 10036 kg/ha), showing good performance. However, genotype 3 was inferior with the lowest yield (3.2 kg and 5410 kg/ha), even inferior

to the check. In general, most genotypes performed better than the check, with genotype 12 being the best in yield and other characteristics.

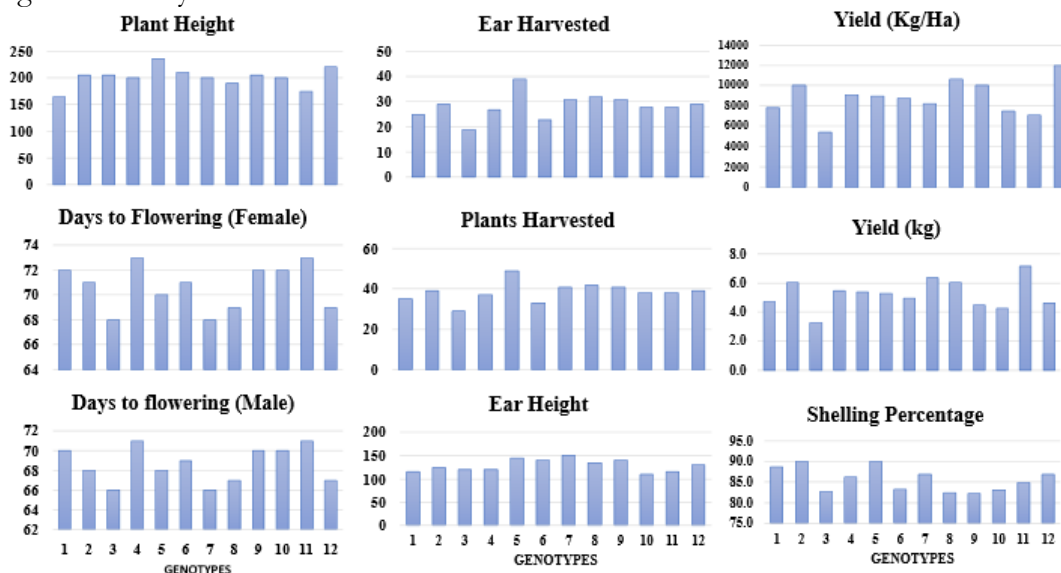


Figure 4. Comparative performance of 12 maize genotypes for key agronomic and yield-related traits, and earliness traits in National Uniform Yield Trial

Correlation Analysis:

DFM had a very strong and significant positive correlation with DFF ($r = 0.9914, p = 0.000$), suggesting that DFM was highly correlated with DFF. This indicates that genotypes that flower early (or late) for DFM are likely to flower early (or late) in DFF.

EH was highly positively correlated with PH ($r = 0.5957, p = 0.0001$), and TEH was positively correlated with PH ($r = 0.3613, p = 0.0304$). Likewise, TPH was highly positively correlated with TEH ($r = 0.9997, p = 0$), and also had a significant positive correlation with PH ($r = 0.3609, p = 0.0306$).

Yield (kg) and kg/ha exhibited highly significant positive correlations with TEH ($r = 0.7169, p = 0$) and TPH ($r = 0.7159, p = 0$), along with a significant positive association with PH ($r = 0.4224, p = 0.0103$). This suggests that yield is highly correlated with the traits of THE, TPH, EH, and PH, especially where the relationships are strongest.

	DFF	DFM	EH	TEH	PH	TPH	SP	YIELD
DFM	0.99*							
EH	0.12	0.15						
THE	-0.29*	-0.28	0.04					
PH	0.0188	0.02	0.59*	0.36*				
TPH	-0.30	-0.29	0.04	0.99*	0.36*			
SP	0.0523	0.05	-0.03	0.12	0.05	0.12		
YIELD (Kg)	-0.28	-0.29	0.11	0.71*	0.42*	0.71*	0.15	
YIELD (Kg/ha)	-0.29	-0.30	0.11	0.71*	0.42*	0.71*	0.15	0.99**

Discussion:

The relative performance of genotypes compared to the check (genotype 1) showed great variability in phenological, morphological, and yield traits, suggesting high genetic diversity and capacity for selection [12][13]. The early flowering of genotypes 3, 7, 8, and 12 relative to the check indicates their potential adaptation to environments with a shorter

growing period. Earlier genotypes in maize are often more adaptive to stress environments and yield stably, as long as DFM and DFF are harmonized to allow effective pollination [4][9][14][15].

The high degree of synchrony between DFM and DFF in this study ensures stable reproductive development of the genotypes. The increased PH and EH of most genotypes over the check underlines the role of plant architecture in yield. Genotypes 5 and 12 had higher PH, and 7 and 5 had higher EH than the check, suggesting improved vegetative growth. These characteristics have a great impact on light capture, biomass accumulation, and plant efficiency [16]. However, high PH can result in lodging, affecting yield. It has been confirmed that both PH and EH are quantitative traits and are highly genetically controlled and closely related to maize productivity [17].

The increased values of TPH and TEH in some genotypes, especially in genotypes 5 and 8, compared to the check, show that they have better stand establishment and ear setting ability. The number of effective plants and ears per unit area is the major determinant of yield in maize and is therefore an important selection trait [18]. Genotype 3's lower values for these traits are responsible for its lower yield, showing the influence of yield components on yield. Genotypes also had variable SP, with some higher than the check. A higher SP value implies good grain recovery and efficient conversion of ear biomass into grain yield. It is related to economic yield and can be used as an important selection criterion in maize breeding [19].

Yield performance distinguished high-performing genotypes from the check. Genotypes 12, 8, 2, and 9 were superior to the check in yield (kg) and yield (kg/ha), with the highest yield being achieved by genotype 12. This can be explained by the combined impact of desirable agronomic traits such as normal flowering, better plant architecture, higher TPH and TEH, and acceptable SP. Yield is a complex trait that is a result of several components, and improving these traits increases yield [20]. Earlier studies have shown that PH, EH, and yield components play a vital role in grain yield by influencing biomass production and resource use efficiency.

In conclusion, the findings suggest that various genotypes outperformed the check in major agronomic traits, including yield and yield components, and therefore can be selected for breeding. The results highlight the effectiveness of indirect selection for yield under a wide range of environments through the selection of phenology, plant architecture, and yield components. The analysis of variance showed that most traits significantly differed among the genotypes, suggesting considerable genetic variation that can be used to improve maize productivity [21]. The significant genetic variation for DFM and DFF implies the presence of genetic factors with major effects on flowering time. The strong correlation between these two traits suggests coordinated flowering, critical for effective pollination and grain formation. This is consistent with recent research, which reported that flowering traits play a critical role in reproductive success and yield performance across different environments. The high variability in PH and EH suggests a high degree of diversity in plant stature.

The positive correlation among PH, EH, and yield traits, as they are often controlled by common genetic factors affecting plant growth and development. Appropriate plant height and ear height are crucial for light interception, increased efficiency, and ultimately greater yield. The variation found in this study suggests that SP can be improved by selection; this is confirmed by recent field experiments. The high variability in yield and yield-related traits indicates that high-yielding genotypes can be selected.

Correlation analysis showed significant associations between flowering, plant architecture, and yield traits in maize, highlighting their significance in breeding programs. Flowering synchrony is an important breeding goal to ensure efficient pollination and kernel formation, which in turn supports grain yield under different environmental conditions. Plant height (PH) and ear height (EH) were positively correlated, indicating their genetic and functional interdependence as important components of plant architecture. Positive correlations between yield, plant height, and ear height indicate that plant structure is important for yield.

YIELD was highly correlated with EH~01 and PH~01, suggesting that plants with ideal plant height and ear height have better yield potential. In summary, the findings show that flowering synchronization and plant architectural traits have a significant impact on yield in maize. The results indicate that indirect selection for yield through these traits can be successful.

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