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Dissecting trait associations in maize (*Zea mays* L.) through phenotypic and genotypic correlation coefficient analysis

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Abstract

The improvement of grain yield in maize (*Zea mays* L.) relies not only on direct selection but also on understanding the interrelationships among yield and its contributing traits. This study was undertaken to estimate phenotypic and genotypic correlation coefficients among ten agronomic traits in nine diverse maize genotypes using data analyzed through RStudio (v4.5.1) with the ‘variability’ package (v0.1.0). The analysis of variance confirmed significant genetic variability among genotypes for all studied traits. Phenotypic correlation analysis revealed a highly significant and positive association between days to 50% tasseling and silking, indicating synchronized flowering. Grain yield per plot exhibited strong negative correlations with flowering time traits, suggesting the advantage of early maturity. Yield contributing traits such as ear length, ear girth, number of kernel rows per ear, and number of kernels per row were positively and significantly correlated with grain yield at both phenotypic and genotypic levels, emphasizing their potential as reliable indirect selection criteria. Conversely, traits like anthesis silking interval and test weight exhibited higher phenotypic than genotypic correlations with yield, reflecting a greater influence of environmental factors. These findings highlight that traits with strong and consistent genetic associations should be prioritized in selection programs for improving maize yield potential, while traits with environmentally influenced correlations require cautious interpretation and advanced breeding strategies.

Keywords: Phenotypic correlation, genotypic correlation, maize

1. Introduction

Maize (*Zea mays* L.) is a crucial cereal crop globally, ranked third after rice and wheat, with growing importance due to its role in food, feed, and industrial applications (Shettigar *et al.*, 2024) [28]. Improving grain yield, a complex quantitative trait influenced by multiple factors, requires a thorough understanding of the relationships among yield and its component traits (Chavan *et al.*, 2020) [7]. Correlation analysis is a pivotal tool to decipher these relationships by estimating the degree and nature of associations between traits, which aids breeders in indirect selection to improve yield under varying environmental conditions (Fadhli *et al.*, 2023) [9].

Phenotypic correlation coefficients measure the total association influenced by both genetic and environmental effects, whereas genotypic correlation coefficients reveal the true genetic relationship by excluding environmental noise (Searle, 1961; Chavan *et al.*, 2020) [27, 7]. This distinction is critical since phenotypic correlations can be misleading if environmental factors dominate, thus genotypic correlations provide a more reliable basis for selection decisions (Johnson *et al.*, 1955; Tucker *et el*, 2020) [14, 31]. For instance, (Shettigar *et al.* 2024) [28] observed that grain yield was positively correlated phenotypically with plant height, ear height, and ear per plant, while genotypic correlations highlighted anthesis and silking days as major contributors to yield. Several studies have documented significant correlations among phenological traits, particularly between days to 50% anthesis and silking, reflecting coordinated flowering that is essential for reproductive success (Azad *et al.*, 2012; Chase and Nanda, 1967) [2, 6]. Plant height and ear height often exhibit high positive correlation, contributing jointly to yield, as reported by (Hallauer *et al.* 2010) [11] and (Salami, 2002) [26].

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These interrelationships form the basis for indirect selection where improvement of one trait can positively influence others (Nzuve *et al.*, 2014) [21].

Correlation studies are further strengthened when coupled with genetic variability and morphological characterizations, which provide comprehensive insights into the breeding material (Islam *et al.*, 2020; Sabitha *et al.*, 2022) [13, 25]. Genetic variability assessments help in clustering genotypes into heterotic groups and exploiting complementary gene pools for hybrid breeding (Fufa *et al.*, 2005; Subramanian and Subbaraman, 2010) [10, 30]. Such integrative approaches enable efficient utilization of correlated traits to maximize yield gain.

Moreover, understanding correlations helps identify traits with direct and indirect effects on yield, which is essential for path coefficient analysis to dissect the causal relationships (Wright, 1929; Dewey and Lu, 1959) [32, 8]. This approach has been applied to maize to reveal how certain traits, though correlated, contribute differentially to yield (Chavan *et al.*, 2020) [9]. It supports breeders in formulating selection indices focusing on traits with the most influence. Environmental variation can modulate phenotypic correlations, making genotypic correlations indispensable for stable breeding outcomes (Fadhli *et al.*, 2023; Chavan *et al.*, 2020) [9, 7]. Selection based on genotypic associations thus enhances genetic gain by targeting inherent genetic factors rather than transient environmental influences (Johnson *et al.*, 1955; Burton, 1952) [14, 5].

The present study aims to estimate phenotypic and genotypic correlation coefficients among key agronomic traits and grain yield in nine maize genotypes. Identifying traits with significant positive genotypic correlations with grain yield will provide valuable insights for breeders to implement indirect selection strategies, ultimately enhancing maize productivity under diverse growing conditions.

2. Materials and Methods

2.1 Location, Experimental Design and Layout

The field experiment was carried out during the *Kharif* season of 2024 at the Agricultural Research Farm, G H Raisoni University, Saikheda. The study was laid out in a Randomized Complete Block Design (RCBD) with three replications to ensure statistical reliability. Each genotype was sown in individual plots measuring 3 × 3 meters, with a spacing of 60 cm between rows and 20 cm between plants, maintaining optimal plant population and uniform crop geometry for accurate evaluation.

2.2 Genotypes and Observations recorded

The experiment involved the evaluation of nine maize genotypes: Jawahar Makka-12, Jawahar Makka-11, Jawahar Makka-1018, Jawahar Makka-1016, Jawahar Makka-8, Chandan Makka-3, Chandan Makka-2, Chandan Makka-1, and a local Landrace. All genotypes were sourced from the Zonal Maize Research Institute, Chandgaon. Observations were recorded on five randomly selected plants from each replication, excluding the border rows to minimize edge effects. Data collection encompassed both pre and post harvest parameters, focusing on the following agronomic traits: Days to 50% Tasseling (DTT), Days to 50% Silking (DTS), Anthesis-Silking Interval (ASI), Plant Height (PH, in cm), Ear Length (EL, in cm), Ear Girth (EG, in cm), Number of Kernel Rows per Ear (NOKRPE), Number of Kernels per Row (NOKPR), Test Weight (TW, in gram), and Grain Yield per Plot (GYPP, in kilogram).

2.3 Software and Package

The statistical analysis was performed using RStudio (Version 4.5.1), incorporating the ‘variability’ package (version 0.1.0) for estimating genetic parameters. Microsoft Excel was additionally utilized for data organization and preliminary calculations. The analytical procedures included Phenotypic correlation coefficient and Genotypic correlation coefficent following the package provided by Popat *et al.* (2020) [23].

3. Results and Discussion

3.1 Phenotypic Correlation Analysis

The phenotypic correlation coefficients among the studied traits (Table 1, Fig 1 and Fig 2) revealed several significant associations that reflect both genetic and environmental factors influencing trait expression. A very strong positive correlation between days to 50% tasseling and days to 50% silking was observed (r = 0.99, $p<0.01$), indicating a tight synchronization of flowering times. This is consistent with earlier reports by Shettigar *et al.* (2024) [28], who found a similar strong association between anthesis and silking days, emphasizing their coordinated genetic control which facilitates simultaneous selection for flowering time in maize breeding programs. Such synchrony is critical for successful fertilization and yield stability, as also highlighted by Azad *et al.* (2012) and Chase & Nanda (1967) [2, 6].

Grain yield per plot exhibited significant negative correlations with flowering time traits (DTT: r =-0.79, DTS: r =-0.75), suggesting that genotypes with earlier flowering tend to have higher grain yield. This inverse relationship corroborates findings by Nzuve *et al.* (2014) [21] and Patel & Kumar (2016) [26], who reported that early maturity is often advantageous for adaptation to environmental stresses and results in improved yield. Chavan *et al.* (2020) [7] similarly observed that selection for early flowering traits can indirectly enhance yield under varying agro-climatic conditions.

Among ear related traits, positive phenotypic correlations were evident between ear length, ear girth, number of kernel rows per ear, and number of kernels per row, ranging from moderate to strong (r = 0.56 to 0.95). These associations highlight the coordinated development of ear morphology components, which collectively contribute to kernel set and grain filling, thereby influencing final grain yield potential. Similar findings were reported by Reddy *et al.* (2012) [24] and Niji *et al.* (2018) [20], who emphasized the significance of these traits as reliable indirect selection criteria for yield improvement. Furthermore, the strong phenotypic correlations among these ear traits align with the genetic diversity studies conducted by Al-Naggar *et al.* (2022) [1] and Hallauer *et al.* (2010) [11], underscoring the importance of these characters in hybrid performance.

Anthesis-silking interval (ASI) showed a strong positive correlation with test weight (TW) (r = 0.87), indicating that longer ASI might be associated with heavier kernels, which concurs with Meena *et al.* (2016) [18]. However, ASI displayed mostly non-significant or weak correlations with grain yield in our study, reflecting its complex interaction with environmental conditions, as also noted by Singh and Sharma (2018) [29] and supported by observations in Fadhli *et al.* (2023) [9]. This suggests that while ASI may influence kernel characteristics, its direct impact on yield may vary depending on environmental stressors.

It is important to note that phenotypic correlations, while informative, integrate both genetic and environmental variance, which may confound interpretation. Hence, genotypic correlations are essential to discern the true genetic associations among traits. Previous studies such as Chavan *et al.* (2020) [7] and Shettigar *et al.* (2024) [28] emphasize that genotypic correlations typically reveal stronger and more consistent relationships among yield contributing traits, facilitating more effective selection.

The phenotypic correlation analysis indicates that earlier flowering genotypes with favorable ear morphology traits have the potential to improve grain yield in maize. These findings reinforce the value of indirect selection using correlated traits and provide a basis for breeding programs aimed at yield enhancement under diverse environments, consistent with the genetic principles discussed by Burton (1952) [5] and Johnson *et al.* (1955) [14].

Table 1: Phenotypic correlation coefficient matrix.

	DTT	DTS	ASI	PH	EL	EG	NOKRPE	NOKPR	TW	GYPP
DTT	1 **									
DTS	0.98 **	1 **								
ASI	-0.26 NS	-0.1 NS	1 **							
PH	0.38 *	0.32 NS	-0.43 *	1 **						
EL	-0.49 **	-0.45 *	0.35 NS	-0.47 *	1 **					
EG	-0.69 **	-0.69 **	0.10 NS	-0.15 NS	0.71 **	1 **				
NOKRPE	-0.70 **	-0.73 **	-0.03 NS	-0.19 NS	0.61 **	0.92 **	1 **			
NOKPR	-0.48 *	-0.39 *	0.55 **	-0.47 *	0.86 **	0.60 **	0.46 *	1 **		
TW	-0.10 NS	-0.09 NS	0.54 **	-0.24 NS	0.23 NS	-0.01 NS	-0.20 NS	0.39 *	1 **	
GYPP	-0.77 **	-0.74 **	0.32 NS	-0.56 **	0.62 **	0.69 **	0.62 **	0.61 **	0.16 NS	1 **

Where, *, ** and NS indicates significant value of traits at $p<0.05$, $p<0.01$ and non significance, respectively.

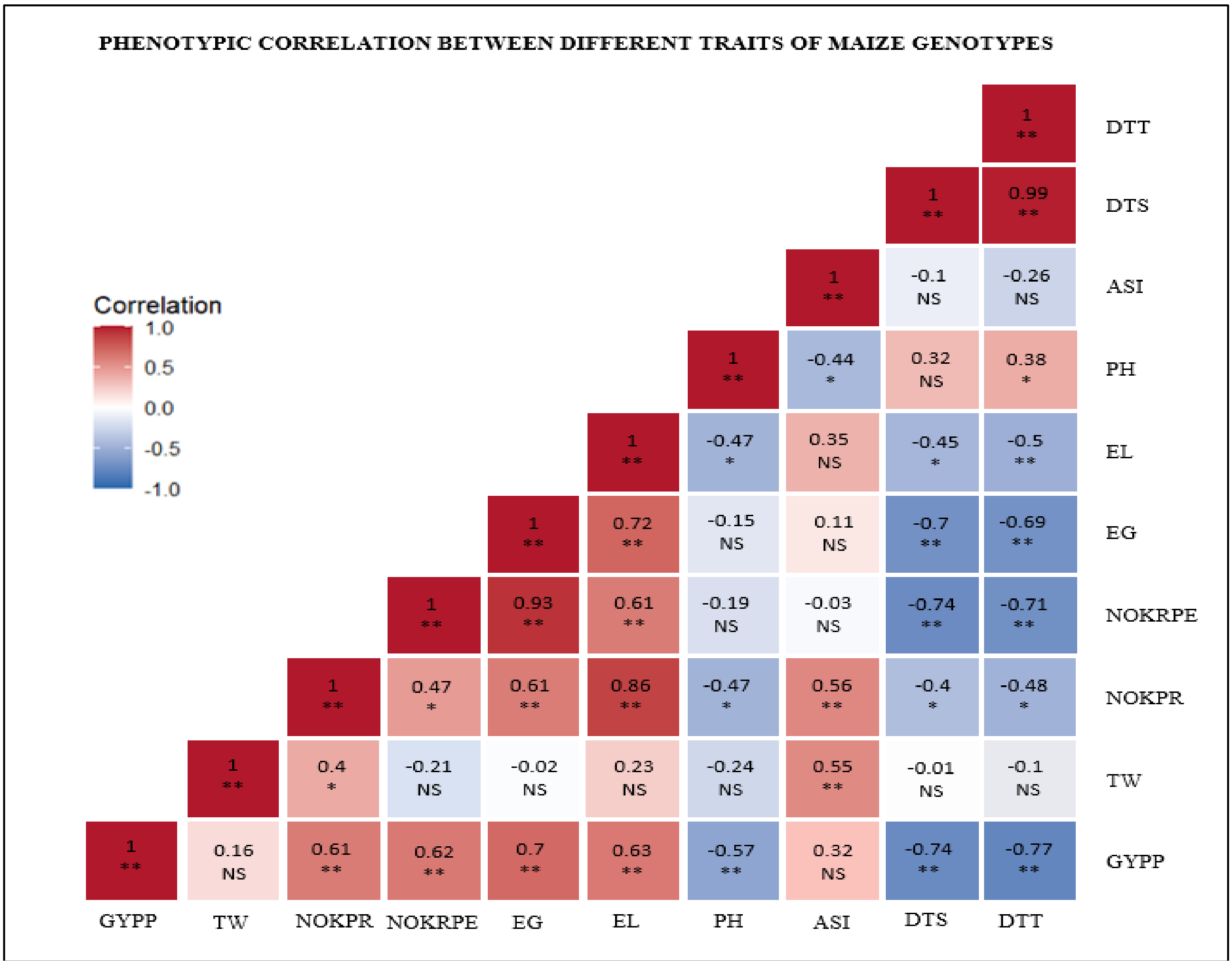

Fig 1: Phenotypic Correlation Heatmap Between Agronomic Traits in maize

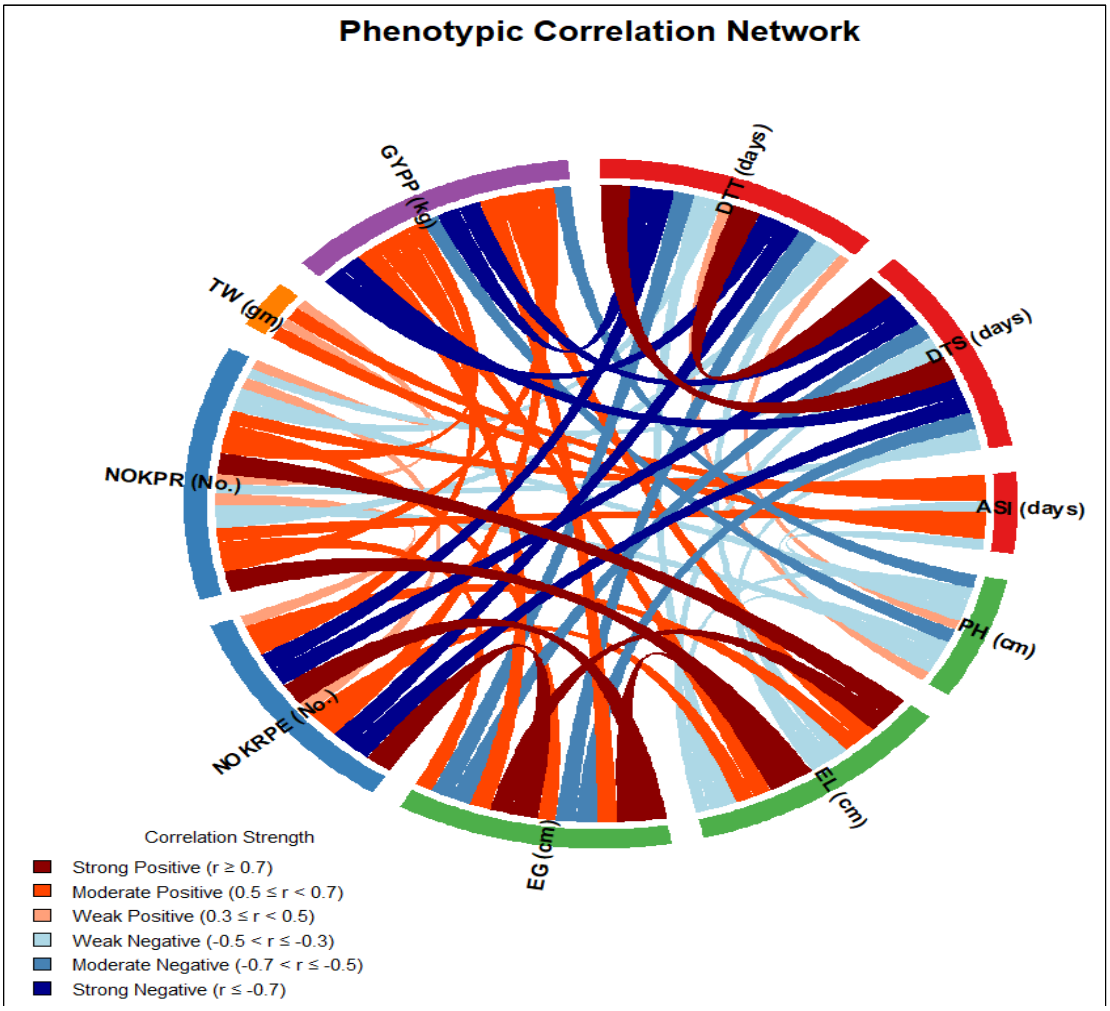

Fig 2: Chord diagram of Phenotypic Correlations Among Agronomic Traits in maize

3.2 Genotypic Correlation Analysis

Genotypic correlation coefficients represent the true genetic associations between traits by removing environmental effects, thus offering a clearer insight into the inheritance patterns of key agronomic characters (Burton, 1952; Johnson *et al.*, 1955) [5, 14]. The result (Table 2 and Fig 3) consistent with phenotypic observations, days to 50% tasseling and days to 50% silking exhibited a very high and significant genotypic correlation ($r = 0.98$, $p<0.01$), reaffirming the strong genetic linkage between these flowering traits (Azad *et al.*, 2012) [2]. This relationship underscores the potential of simultaneous selection for flowering time to accelerate breeding progress.

Grain yield per plot demonstrated significant negative genotypic correlations with both days to 50% tasseling and days to 50% silking, indicating that early maturity genotypes tend to possess inherently higher yield potential. These results align with the findings of Shettigar *et al.* (2024) [28], who reported similar trends in maize hybrids evaluated under diverse agro-climatic conditions. Such negative correlations imply that earliness confers an adaptive advantage by enabling plants to escape terminal drought stress and optimize the grain filling period.

Interestingly, grain yield exhibited a moderate negative genotypic correlation with plant height ($r =-0.56$), deviating from some prior studies where positive associations were reported (Hallauer *et al.*, 2010; Chavan *et al.*, 2020) [7]. This divergence may reflect genotype × environment interactions or differences in the genetic background of the studied germplasm (Nzuve *et al.*, 2014) [21]. It also suggests that reduced plant stature may favor assimilate partitioning toward grain yield in the tested environments.Among ear related traits, a notably high positive genotypic correlation was observed between number of kernel rows per ear and ear girth ($r = 0.92$), highlighting their shared genetic control and combined influence on yield enhancement (Nair *et al.*, 2018; Reddy *et al.*, 2012) [29, 24]. This finding corroborates earlier reports by Begum *et al.* (2016) [3] and Magar *et al.* (2021) [17] that underscore the importance of these yield components in determining grain production efficiency.

Conversely, anthesis-silking interval exhibited weak or non significant genotypic correlations with grain yield and other yield related traits, suggesting that its genetic architecture may involve non-additive gene effects and be highly influenced by environmental fluctuations (Bello *et al.*, 2012; Hefny, 2011) [4, 12]. This complexity necessitates employing advanced breeding techniques, such as hybrid development and marker assisted selection, to improve anthesis silking interval effectively. Overall, the genotypic correlation analysis highlights the critical traits flowering time, ear components, and plant architecture that should be prioritized for indirect selection to accelerate genetic gains in maize breeding programs. These results complement previous genetic diversity and correlation studies (Shettigar *et al.*, 2024; Chavan *et al.*, 2020; Fadhli *et al.*, 2023) [28, 7, 9] and provide a robust foundation for developing high yielding, early maturing maize cultivars adapted to specific environmental contexts.

Table 1: Genotypic correlation coefficient matrix.

	DTT	DTS	ASI	PH	EL	EG	NOKRPE	NOKPR	TW	GYPP
DTT	1 **									
DTS	0.99 **	1 **								
ASI	-0.33 NS	-0.22 NS	1 **							
PH	0.38 NS	0.32 NS	-0.67 *	1 **						
EL	-0.51 NS	-0.48 NS	0.46 NS	-0.49 NS	1 **					
EG	-0.72 *	-0.75 *	-0.03 NS	-0.16 NS	0.77 *	1 **				
NOKRPE	-0.74 *	-0.79 *	-0.20 NS	-0.19 NS	0.66 NS	0.95 **	1 **			
NOKPR	-0.51 NS	-0.44 NS	0.77 *	-0.49 NS	0.89 **	0.70 *	0.56 NS	1 **		
TW	-0.13NS	-0.03 NS	0.87 **	-0.29 NS	0.26 NS	0.03NS	-0.26 NS	0.38 NS	1 **	
GYPP	-0.79 *	-0.75 *	0.53 NS	-0.57 NS	0.63 NS	0.75 *	0.66 NS	0.65 NS	0.20 NS	1 **

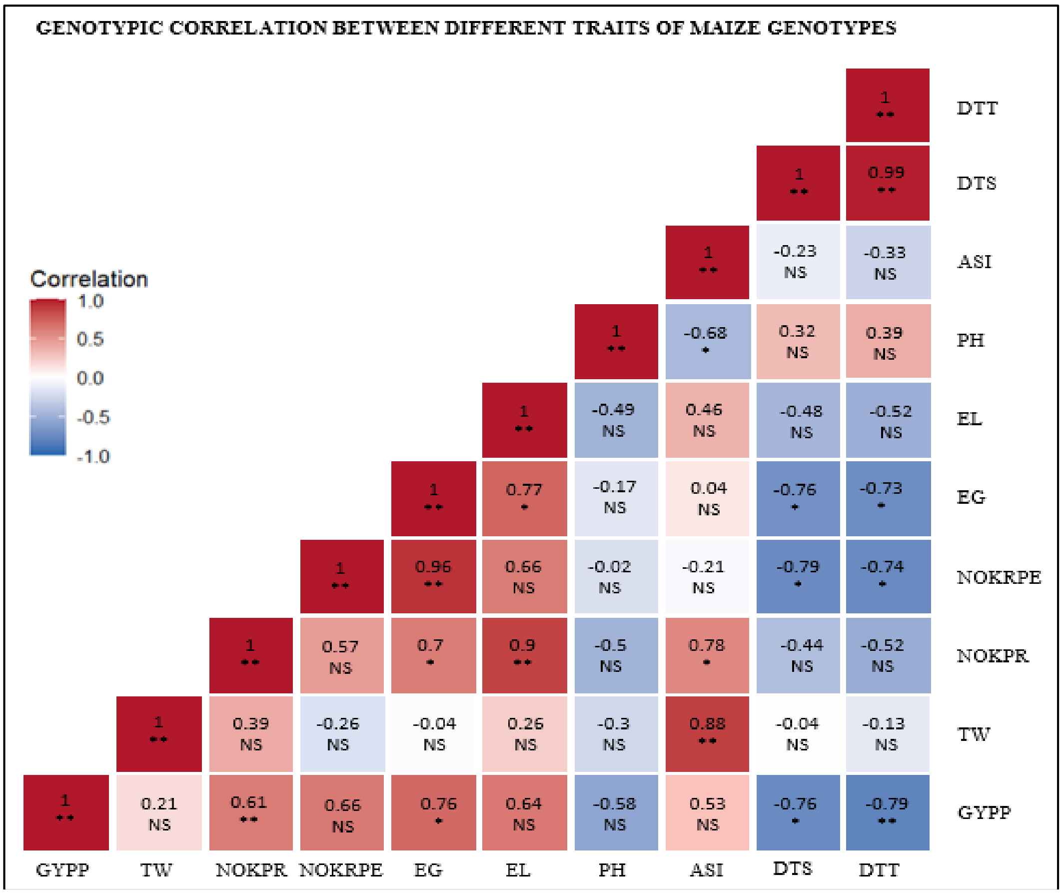

Fig 3: Genotypic Correlation Heatmap between Agronomic Traits in maize

3.3 Comparison of Phenotypic and Genotypic Correlations: Concordant and Discrepant Associations

The comparative analysis of phenotypic and genotypic correlation coefficients provides valuable insights into the extent to which observed trait associations are governed by genetic factors as opposed to environmental influences. This distinction is crucial for breeders aiming to identify stable and heritable traits for selection.

3.3.1 Concordant Correlations

Traits such as days to 50% tasseling and days to 50% silking demonstrated strong positive correlations at both phenotypic and genotypic levels, underscoring their stable genetic linkage and coordinated expression (Kumara *et al.*, 2011) [16]. Similarly, the significant negative correlations observed between grain yield and flowering time traits were consistent across phenotypic and genotypic analyses, reinforcing the utility of early flowering as an indirect selection criterion for enhancing yield potential. Additionally, ear traits including the number of kernel rows per ear and ear girth exhibited strong concordant positive correlations, highlighting their integral role in yield determination and supporting their use as reliable selection targets (Patel *et al.*, 2017) [22].

3.3.2 Discrepant Correlations

Conversely, certain traits such as anthesis-silking interval and test weight showed notably higher phenotypic correlations compared to genotypic correlations, suggesting that environmental factors substantially influence these associations and may inflate phenotypic estimates. Similarly, plant height and ASI exhibited weaker genotypic correlations relative to their phenotypic counterparts, further emphasizing the impact of environmental variability on trait expression (Singh *et al.*, 2018) [29]. These discrepancies highlight the necessity for cautious interpretation of phenotypic correlations in breeding programs, as reliance solely on phenotypic data may lead to suboptimal selection decisions (Burton, 1952) [5].

3.4 Implications for Breeding

The identification of high and consistent genotypic correlations between grain yield and key agronomic traits such as early flowering and ear morphology underscores their potential as effective indirect selection criteria in maize breeding. Utilizing these traits can expedite genetic gain by shortening breeding cycles and enhancing selection efficiency (Nair *et al.*, 2018) [19]. Concordantly correlated traits are less susceptible to environmental variation, making them dependable targets for phenotypic selection (Singh *et al.*, 2018) [29]. On the other hand, traits exhibiting discrepant correlations, including ASI and test weight, demand more sophisticated selection strategies. Integration of molecular marker assisted selection, coupled with multi-environmental evaluations, is essential to accurately capture the genetic potential of such environmentally sensitive traits (Bello *et al.*, 2013) [4]. Therefore, a combined approach leveraging both phenotypic and genotypic correlation analyses offers a robust framework to optimize breeding decisions aimed at yield enhancement and stability under diverse environmental conditions.

4. Conclusion

The present study provides a comprehensive evaluation of the phenotypic and genotypic correlations among critical agronomic and yield contributing traits in maize, offering valuable insights for breeding strategies aimed at yield enhancement. The consistently high and significant positive correlations between days to 50% tasseling and days to 50% silking at both phenotypic and genotypic levels confirm their tight genetic linkage and coordinated phenological expression. This reinforces the importance of synchronized flowering as a pivotal breeding target for improved adaptation and yield stability.

The strong negative correlations observed between flowering time traits and grain yield per plot highlight the adaptive advantage of early maturity in optimizing yield potential, especially under environments with limited growing periods. Yield related ear traits including ear length, ear girth, number of kernel rows per ear, and number of kernels per row demonstrated robust positive correlations with grain yield consistently across phenotypic and genotypic levels. These findings validate these traits as reliable indirect selection indices due to their predominant control by additive gene effects, facilitating sustained genetic gain through conventional breeding approaches. Conversely, traits such as anthesis silking interval and test weight exhibited relatively higher phenotypic than genotypic correlations with grain yield, suggesting substantial environmental modulation in their expression. For these traits, multi-environment trials and integration of molecular marker assisted selection may be essential to achieve precise and stable genetic improvement.

This investigation underscores the critical importance of discerning genetically stable trait associations for effective maize breeding. Prioritizing traits with strong and consistent genotypic correlations to grain yield such as kernel row number, ear length, and ear girth can significantly enhance selection efficiency and accelerate progress in maize improvement programs. The strategic exploitation of these genetically robust correlations will support the development of high yielding, well adapted maize cultivars under diverse agroecological conditions.

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