GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS STUDIES IN MAIZE (*Zea mays* L.)

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B.Sc. (Hons.) Agriculture

MASTER OF SCIENCE
IN
AGRICULTURE
(GENETICS AND PLANT BREEDING)

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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS STUDIES IN MAIZE (*Zea mays* L.)

By

K SHIVA

B.Sc. (Hons.) Agriculture

A thesis submitted to
Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani
in partial fulfilment of the requirement for the degree of

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IN
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2025

DECLARATION BY THE CANDIDATE

I hereby declare that the thesis entitled, **“GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS STUDIES IN MAIZE (*Zea mays* L.)”** submitted by me is based on the actual work carried out by me under the guidance and supervision of **Dr. Arun Ramrao Gaikwad**. The extent of information derived from the existing literature have been duly cited and referenced. The existing research work or its any part is not submitted anywhere else for the award of any degree or diploma.

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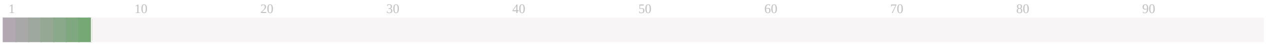

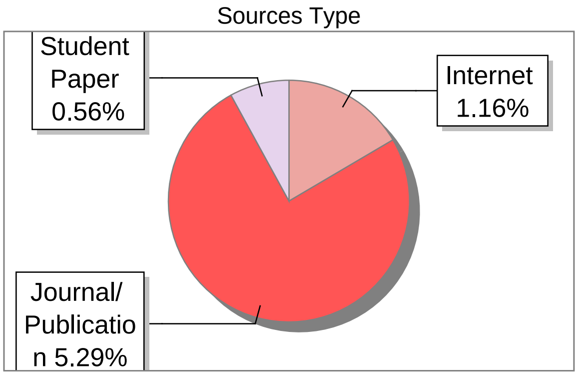

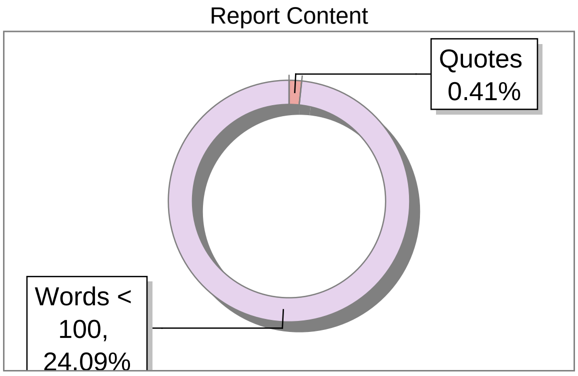

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Place: Parbhani

Date: 22/09/2025

K SHIVA

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ABBREVIATION

/	: Per
%	: Per cent
*	: Significant at 5 per cent
**	: Significant at 1 per cent
ANOVA	: Analysis of Variance
ASI	: Anthesis silking interval
b.s.	: Broad Sense
cm	: Centimeter
CV	: Coefficient of Variation
CD	: Critical Difference
d.f	: Degree of freedom
EMSS	: Error mean sum of squares
et al.	: et alia; and others
etc.	: et cetera; and more
Fig.	: Figure
g	: Gram (s)
G	: Genotypic
GA	: Genetic advance
GAM	: Genetic advance % mean
GCV	: Genotypic coefficient of variation
H^2	: Heritability broad sense
i.e.,	: In essence
kg	: Kilogram
Max	: Maximum
Min	: Minimum
MSS	: Mean sum of squares
No.	: Number
NS	: Non-significant
P	: Phenotypic

PCV	: Phenotypic Coefficient of Variation
RBD	: Randomized Complete Block Design
SD	: Standard Deviation
S. E	: Standard Error
S. Em±	: Standard Error of Mean
SPL	: Spike length
Sr. No	: Serial Number
via	: By the means of
Viz.	: Namely
X	: Mean
Σ	: Summation
σ^2	: Variance

THESIS ABSTRACT

THESIS ABSTRACT

1.Title of the thesis	:	Genetic Variability, Correlation and Path analysis studies in Maize (*Zea mays* L.)
2.Full name of the candidate	:	K SHIVA
3.Full name of the Research Guide	:	Dr. Arun Ramrao Gaikwad
4. Department	:	Genetics and Plant breeding
5.College / University	:	College of Agriculture, Parbhani
6. Degree to be awarded	:	M.Sc. (Agriculture)

The current study entitled, "Genetic Variability, Correlation and Path analysis studies in Maize (*Zea mays* L.)" was undertaken to obtain information on important genetic parameters in a set of fifty genotypes and three checks. Observations were recorded on twelve quantitative traits, namely days to 50% tasseling, days to 50% silking, anthesis silking interval, plant height (cm), ear height (cm), ear length (cm), ear girth(cm), number of grains per ear, hundred seed weight (g), grain yield per plant (kg), number of cobs per plant and shelling percentage. The study was carried out to analyze genetic variability, correlation, direct and indirect influence of various attributes on seed yield among all genotypes grown in randomized block design with two replications accomplished during *rabi* 2024-2025 at Wheat and Maize Research Unit, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani.

The analysis of variance revealed that the genotypes showed significant differences across all twelve traits studied, indicating substantial genetic variability among the germplasm accessions. This wide range of variation suggests considerable potential for selecting promising genotypes to improve grain yield. Based on performance across two replications, genotype V2201-51 exhibited the highest average grain yield per plant, followed by V2202-52, highlighting their suitability for use in hybridization programs aimed at yield enhancement. Genotypes V2199-5 and V2199-9 showed the earliest anthesis and silking, respectively, making them valuable candidates for developing early-maturing varieties. In terms of plant height, V2201-51 was identified as the shortest genotype, while the check variety Phule Maharshi was the tallest, suggesting their potential use in breeding programs targeting specific plant height preferences. Furthermore, V2202-44, Phule Maharshi, V2201-19, V2202-42, V2201-25, Phule Maharshi, V2202-44, and V2201-25 recorded the highest mean values for anthesis silking interval, ear height, ear length, ear girth, number of grains per ear, hundred seed weight, number of cobs per plant, and shelling %, respectively. These traits make these genotypes particularly promising for contributing to grain yield improvement.

The correlation analysis revealed that grain yield per plant was positively associated with several traits, including plant height, ear height, number of grains per ear, 100 seed weight and shelling %. These findings suggest that selecting germplasm lines with higher average values for these traits could effectively enhance maize grain yield. To further understand the relationships, path coefficient analysis was conducted to separate direct and indirect effects. Traits such as, plant height, ear height, number of grains per ear, 100 seed weight and shelling % exhibited strong significant direct effects on grain yield per plant. In contrast, number of cobs per plant showed significant negative indirect effects on grain yield, indicated that a greater number of cobs per plant negatively influence productivity.

(**Keywords:** Maize, Variability, Heritability, Genetic advance as per mean, Correlation and Path coefficient)

INTRODUCTION

CHAPTER I

INTRODUCTION

Maize (*Zea mays* L.) is a member of the sub-family Panicoideae of the family *Poaceae* and tribe *Maydeae*. It is believed to be the native of Central America and Mexico and is evolved from teosinte (*Zea mexicana*). Maize, known as queen of cereals, globally occupies 1st rank in productivity among cereals with 5.82 t/ha followed by 4.66 t/ha of rice and 3.55 t/ha of wheat. Maize, being a C4 plant, is physiologically more efficient with higher per day productivity. It has wider adaptation over different environmental conditions and cultivated from latitude 58° N to 40° S, from mean sea level to higher than 3000 m altitude and in areas receiving 250 mm to 5000 mm yearly rainfall.

Maize (*Zea mays* L.) is the third most significant cereal crop in India after rice and wheat, playing a vital role in providing food, animal feed, fodder, fuel and serving as a key raw material for a variety of industrial products such as starch, oil, proteins, alcoholic beverages, sweeteners, cosmetics and biofuels. This crop is highly adaptable to diverse agro-climatic conditions, thriving from sea level up to elevations exceeding 3000 meters and is a major contributor to crop diversification efforts. At present, maize is cultivated across more than eight million hectares in India, yielding a total production of 16.8 million tons, with an average productivity exceeding 2000 kg per hectare. It accounts for about seven percent of the country's food supply. Maize holds significant value in India’s agricultural sector, being used for human consumption (26%), poultry feed (43%), livestock feed (11%), industrial applications (12%) and seed or other purposes (3%).

India witnessed a notable rise in maize cultivation during 2024-2025 (2nd Advance Estimates), with the total area reaching 107.28 lakh hectares, 84.37 lakh ha in *kharif* and 22.92 lakh ha in *rabi* reflecting maize’s growing importance in both rainfed and irrigated systems. Total production was estimated at 372.50 lakh tonnes, up from 376.65 lakh tonnes in 2023–2024, with 248.11 lakh tonnes from *kharif* and 124.38 lakh tonnes from *rabi*, indicating strong *rabi* performance due to expanded cultivation and improved hybrid adoption. National productivity rose to 3,472 kg/ha, with *kharif* at 2,941 kg/ha and *rabi* at 5,428 kg/ha. This growth highlights the impact of better irrigation, crop management and rising demand for maize in food, feed, industry and exports, pointing to further potential for technological and agronomic advancement. (Source: Ministry of Agriculture & Farmers Welfare, Govt. of India.)

Maharashtra emerged as a key contributor to maize cultivation in India during 2024-2025, with a total sown area of 15.93 lakh hectares 11.22 lakh ha in *kharif* and 4.72 lakh ha in *rabi* producing 42.66 lakh tonnes of maize. The state's overall productivity stood at 2,677 kg/ha, with 2,649 kg/ha in *kharif* and 2,744 kg/ha in *rabi*, reflecting consistent seasonal performance and slightly better output in r*abi* due to improved irrigation and pest control. While Maharashtra ranks among the top states in maize area and production, its productivity remains moderate compared to states like Tamil Nadu (6,379 kg/ha) and West Bengal (6,624 kg/ha), indicating potential for improvement through enhanced agronomic practices and better hybrid adoption. (Source: Ministry of Agriculture & Farmers Welfare, Govt. of India.)

Maize is considered a staple food across the globe largely due to its high nutritional content. It is particularly rich in starch and also provides essential proteins and oils. A typical maize grain consists of approximately 70% carbohydrates, 10% protein, 5-7% fat, 4% oil, 3-5% fibre and around 2% minerals. In addition to macronutrients, maize contains several important vitamins such as B-complex vitamins, folic acid, vitamin C and provitamin A (beta-carotene), which is converted into vitamin A in the human body. This vitamin is especially critical for maintaining healthy vision and acting as an antioxidant. Maize is also a good source of essential minerals like manganese, phosphorus, magnesium, zinc, copper, iron and selenium, though it has lower amounts of potassium and calcium. However, it naturally lacks sufficient quantities of tryptophan and lysine two essential amino acids required by the human body. A notable feature of maize is its wide variation in the types and levels of carotenoids (coloured pigments), particularly beta-carotene, which contributes to its nutritional value. For communities with limited access to fresh produce year-round, maize can serve as a key dietary source of vitamin A. Beyond its nutritional role, maize has a broad range of industrial uses. It is processed into products like starch, lactic acid, glucose, paper, rayon, plastics, textiles, adhesives, dyes, synthetic rubber, resins, artificial leather, boot polish, syrup, alcohol and acetic acid. Additionally, green maize ears are in high demand in urban markets and the crop is extensively used as feed for both poultry and livestock.

Yield is the primary focus of maize breeding programs. For successful crop improvement, it is essential for plant breeders to understand key genetic parameters such as variability, heritability, genetic advance and the correlation between yield and its contributing traits. These parameters are crucial for evaluating economically important quantitative characteristics in the crop. The success of developing new maize varieties or hybrids largely depends on the degree of genetic variability present in the initial breeding material. To assess this variability, breeders rely on measurements like the phenotypic and genotypic coefficients of variation (PCV and GCV), which help quantify the extent of variation in specific traits. A comprehensive analysis of the existing variability is a foundational step in initiating any varietal or hybrid development program. Therefore, examining both the type and magnitude of heritable genetic variation within the available germplasm is vital. A thorough understanding of the genetic diversity within the gene pool is highly valuable for launching a systematic breeding effort. The presence of considerable genetic variability in the base material significantly enhances the potential for developing superior maize cultivars.

Yield is a complex quantitative trait that is heavily influenced by environmental factors, making direct selection for yield alone less effective. Instead, selection should focus on the individual components that contribute to yield. The success of any breeding program relies on understanding both the direction and strength of the relationships between yield and its contributing traits. Correlation analysis plays a key role in identifying which traits, or combinations of traits, can serve as reliable indicators of high yield. It helps evaluate how various traits influence yield and interact with one another. Therefore, studying the correlation coefficients between grain yield and its associated traits is crucial for yield improvement. Both phenotypic and genotypic correlation coefficients provide insights into the strength and nature of the associations between different characteristics. This information is valuable for selecting traits that enhance yield and its related attributes. The concept of correlation was originally introduced by F. Galton in (1889) and further developed by R.A. Fisher in (1918). In correlation studies, multiple traits are examined to provide insight into indirect selection, which plays a crucial role in influencing the final outcome grain yield in any crop species. Indirect selection can be just as important as direct selection for yield improvement. To better understand these relationships, path coefficient analysis has become a valuable technique. It helps identify both the direct and indirect contributions of various traits to yield, offering a clearer understanding of the underlying factors responsible for strong correlations.

Path analysis uses standardized partial regression coefficients to break down the total correlation into direct and indirect effects, allowing for an evaluation of each trait's specific influence on yield. This method enables researchers to distinguish between traits that affect yield directly and those that exert influence indirectly through other associated traits. Unlike simple correlation analysis, which does not separate these effects, path analysis can reveal whether the observed relationship between an independent trait and grain yield is due to a direct impact or is mediated through other traits. The technique was first introduced by Wright in (1921) for genetic studies and later applied to crop improvement by Dewey and Lu in (1959).

Considering this background, the present investigation "Genetic Variability, Correlation and Path analysis studies in Maize (*Zea mays* L.)" carried out for 53 maize germplasm that included 50 hybrids of normal maize along with three commercial checks with the under-mentioned objectives to:

1. To study genetic variability for yield and yield attributing characters in maize.
2. To study correlation of grain yield and yield attributing characters.
3. To study the direct and indirect effect of yield contributing characters on grain yield.

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

The literature pertaining to various aspects of the current study entitled "Genetic Variability, Correlation and Path analysis studies in Maize (*Zea mays* L.)" has been reviewed under the following objectives.

2.1 To study genetic variability for yield and yield attributing characters in maize.

2.2 To study correlation of grain yield and yield attributing characters.

2.3 To study the direct and indirect effect of yield contributing characters on grain yield.

2.1 To study genetic variability for yield and yield attributing characters in maize.

The entire success of the plant breeding programme in any crop largely depends upon the presence of wide range of variability in respect of economic characters in the population. Presence of variability is the preliminary requirement for effective selection of a particular genotype.

Muhammad *et al.* (2008) evaluated twenty 3-way crosses and two controls were evaluated and it was observed that days to 50% tasseling, days to 50% silking and grain yield per plant exhibited relatively higher broad-sense heritability.

Chauhan *et al.* (2010) assessed 20 baby corn cultivars to study variability and genetic advance across 20 quantitative traits. High genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for traits such as days to first and last cob picking, cob yield per plant, ear yield per plant, harvest index and tassel weight per plant. Traits including stalk weight, biological yield, cob yield per plant, ear yield per plant, fodder yield per plant and plant height exhibited high heritability along with high genetic advance, suggesting that these traits are primarily influenced by additive gene effects. In contrast, days to first and last cob picking intervals and cob weight showed low heritability and genetic advance.

Rafique *et al.* (2010) examined three testers and ten maize inbreds to create thirty offspring lines. The study was carried out using a randomized block design. The ANOVA analysis's findings showed that all of the examined attributes showed clear variance. Significant differences were observed 100 grain weight, ear height, ear diameter, ear length and grain yield.

Shanthi *et al.* (2011) conducted an experiment to assess genetic variability parameters in Quality Protein Maize (QPM) genotypes across two locations Hyderabad and Allahabad and during two Kharif seasons, 2003 and 2004. The study focused on various economic traits including grain yield, growth, maturity and quality-related parameters. The experimental material included 10 parent lines, 45 single cross hybrids and two standard checks (Shaktiman-2 and DHM-105), evaluated in a randomized block design with three replications. Among the 26 traits studied, grain yield and related traits such as total anther dehiscence period, total silk appearance period, active pollination period, cob weight, number of seeds per cob, protein yield and oil yield showed high genotypic and phenotypic coefficients of variation (GCV and PCV), along with heritability exceeding 85% and high genetic advance. These results suggest that the observed genetic variation is largely due to additive gene action, indicating good potential for improving these traits through direct selection.

Bello *et al.* (2012) assessed ten open-pollinated maize varieties for genetic parameters at the Teaching and Research Farm of Ilorin University, Nigeria. The analysis revealed that traits such as grain yield, 100-seed weight, number of grains per ear, ear weight, plant height and ear height exhibited high and significant phenotypic and genotypic coefficients of variation (PCV and GCV), along with high heritability and high genetic advance. These findings suggest that these traits are largely governed by additive gene action, indicating good potential for improvement through effective selection.

Nagaraju (2012) observed significant genotypic variation among the 41 genotypes across all fifteen traits. Both genotypic and phenotypic coefficients of variation were highest for grain yield per plant, followed by anthesis-silking interval, ear height, number of grains per row, harvest index, plant height, 100-grain weight and number of cobs per plant. Thirteen traits including grain yield per plant, harvest index, number of grains per row, ear height, plant height, number of cobs per plant, 100-grain weight and anthesis-silking interval exhibited high heritability along with high genetic advance, suggesting that these traits are largely controlled by additive gene action, making selection an effective method for their improvement.

Reddy *et al.* (2012) evaluated 45 F1 hybrid lines, which were developed through diallel crosses involving 10 parent lines (excluding reciprocals). The variability analysis across the studied traits revealed that environmental influences were prominent, as the genotypic coefficient of variation (GCV) values were consistently lower than the phenotypic coefficient of variation (PCV) values for all traits examined. Among the traits, ear height recorded the highest GCV and PCV, followed by grain yield per plant, 100-seed weight, number of kernels per row, ear girth and ear length. Traits such as grain yield per plant, ear length, plant height and number of kernels per row exhibited both high heritability and substantial genetic advance, indicating strong genetic potential for improvement through selection.

Panwar *et al*. (2013) studied genetic variability and the relationships between grain yield and its contributing traits in eighty-three maize (*Zea mays* L.) genotypes. The study revealed minimal differences between the genotypic and phenotypic coefficients of variation for all traits, suggesting that environmental influence on these traits was limited and they were predominantly controlled by genetic factors. High heritability along with high genetic advance was recorded for traits such as grain yield per plant, number of leaves per plant, 100-seed weight, harvest index and ear length, indicating that these traits are mainly governed by additive gene action.

Rajesh *et al*. (2013) studied sixty-five maize germplasm lines to evaluate various traits for genetic variability. Traits such as number of seeds per row, plant height, ear length, 100-seed weight and grain yield exhibited moderate to high values of both phenotypic and genotypic coefficients of variation (PCV and GCV), suggesting considerable variability and potential for genetic improvement through selection. Notably, high GCV values were observed for number of seeds per row, grain yield, ear length, ear height and 100-seed weight, indicating strong prospects for identifying promising lines to be utilized in future crop improvement programs.

Lal and Singh (2014) demonstrated various morphological and quality traits in Quality Protein Maize (QPM) lines revealed significant genetic variability. High

Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were noted particularly for seed yield per plot, followed by traits such as plant height, cob length, cob girth, cob height, 1000-grain weight and number of grains per row. In contrast, traits like days to 50% silking, lysine content, number of rows per plant, protein content, tryptophan concentration and number of grains per row showed low heritability and genetic advance, suggesting that non-additive gene action plays a dominant role. This indicates a strong environmental influence on these traits, making genetic improvement more challenging.

Sharma *et al*. (2014) evaluated twenty distinct maize genotypes in order to estimate the level of genetic diversity for yield and kernel quality metrics. Genetic variability components showed that the phenotypic coefficient of variation (PCV) was greater than the equivalent genotypic coefficient of variation (GCV). Test weight, grains per cob, cob length, grains per row, kernel yield per plant and harvest index were determined to be important criteria in selection programs designed to increase maize output.

Ghimire and Timsina (2015) evaluated 14 genotypes of maize in order to investigate genetic variation in yield and traits associated with yield. Grain yield per hectare, days to silking and days to tasseling were all highly heritable (>0.6) in this research. Higher GCV and GAM on these traits suggest effective indirect selection for a higher grain production per hectare. Significant GAM and GCV were discovered for ear weight, ear height and grain output per hectare.

Kapoor and Batra (2015) examined correlation, route coefficients and genetic variation. The genotypes of each attribute varied significantly. Significant environmental influences were indicated by the phenotypic coefficients of variation (PCV) calculations, which were consistently higher than the genotypic coefficients of variation (GCV). High estimates of GCV and PCV were found for plant height, number of seeds, dry matter yield, leaf length, stem girth, number of cobs and green fodder yield; this implies that selection based on these characteristics may successfully isolate favourable genotypes.

Rahman *et al.* (2015) evaluated nine maize genotypes for genetic diversity. Data on seven morphological features was obtained. Significant variance between maize genotypes has been demonstrated through statistical analysis. the highest genotypic and phenotypic coefficients of variation were found for yield/plant. The genetic advance was greatest for 1000-kernel weight followed by the number of kernels per ear.

Sandeep *et al.* (2015) conducted an experiment during the Kharif season of 2013 at the College Farm, College of Agriculture, PJTSAU, Rajendranagar, Hyderabad, to assess genetic variability in sixty maize inbred lines. The study found that for all traits, the genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV), suggesting the influence of environmental factors. Traits such as grain yield per plant and ear height showed high PCV and GCV along with high genetic advance, indicating strong genetic potential for improvement. A minimal difference between PCV and GCV was observed for shelling percentage, implying that this trait is less affected by environmental variation.

Bhusal *et al.* (2017) calculated the degree of trait correlation and genetic diversity in fifty-five genotypes of maize. Significant variations in the genotypes for the 18 traits under study were found by analysis of variance. Grain yield per plant, biological yield per plant and cob weight all showed strong genotypic and phenotypic coefficients of variation, along with high heritability and genetic advancement.

Kharel *et al.* (2017) examined the genetic traits and relationships between yield metrics in maize genotypes. In contrast to the negative correlations found for days to 50% silking, leaf angle and days to 50% tasseling, the number of kernels row-1 (0.94) exhibited a positive and highly significant correlation with grain yield plant-1, followed by ear length, 100-kernel weight, ear girth, SPAD chlorophyll, plant height and ear height. The number of kernels row-1, ear length, 100-kernel weight and ear girth showed a very significant positive inter-se association with all yield variables, with the exception of days to 50% tasseling, days to 50% silking and leaf angle.

Sravanti *et al.* (2017) studied forty-two maize genotypes for genetic advance, heritability and variability for twelve yield-related characters. The analysis of variance showed that the genotypes under investigation varied significantly. Among all the parameters examined, ear height had the highest PCV and GCV, whereas days to maturity had the lowest PCV and GCV. The prevalence of additive gene action in generating the traits was demonstrated by the significant genetic and high heritability of ear height and grain production per plant. In order to boost the yield, direct selection of these features would be effective and attention should be paid to them.

Beulah *et al.* (2018) evaluated 11 genotypes and, based on analysis of variance, heritability and genetic advance, reported highly significant variation across all traits studied. For every trait, the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV). Very high heritability was observed for traits such as anthesis-silking interval, grain yield, plant height, cob height, days to maturity and the number of grain rows per cob, while the remaining traits exhibited moderate heritability. Field weight and grain yield per plot showed a high genetic advance, whereas other traits demonstrated very low genetic advance.

Dar *et al.* (2018) conducted a field experiment during the 2017 Kharif season at the Budgam Dryland Agriculture Research Station (DARS) under natural rainfed conditions. Thirteen maize varieties were evaluated using a randomized block design with three replications. The study revealed that the highest genotypic and phenotypic coefficients of variation were observed in days to 50% anthesis, days to 50% silking and the anthesis-silking interval, while the number of cobs per plant exhibited the lowest variation.

Tadesse *et al.* (2018) discovered significant variations between genotypes for every variable examined, with the exception of tassel size. All of the qualities under study had genotypic coefficients of variation (GCV) that were lower than phenotypic coefficients of variation (PCV), suggesting that the environment has a major influence in how the traits are expressed. Grain yield, thousand kernel weight, ear height, ear diameter, anthesis and silking interval and plant appearance all had high PCV and GCV estimations. Plant height, ear length and 1000-kernel weight all showed high heritability and high genetic advancement, suggesting that additive gene effects predominate in controlling the traits. Efficient selection based on these traits would be highly beneficial for improving inbred lines.

Rahim (2019) evaluated the morpho-biochemical trait variability in 18 open-pollinated maize accessions and found substantial variance and covariance findings for every morpho-biochemical trait, indicating a large amount of variation among the maize accessions.

Teron *et al.* (2020) discovered notable variance for every characteristic with the exception of dry matter percentage, crude protein content, leaves per plant and leaf-stem ratio. For every character, the phenotypic coefficient of variation estimates was greater than the genotypic variation estimates, indicating that the environment had an impact on the characteristics. High heritability and high genetic advancement were found in dry matter yield, green forage yield, per-day productivity of dry matter yield and green forage yield, leaf area, ears per plant, leaf breadth, leaf length, plant height, ear height, stem diameter and total carbohydrate content. These traits were found to be controlled by additive gene action and could also be used as selection criteria in forage breeding programs.

Saritha *et al.* (2024) carried out investigation to assess the genetic variability, heritability and genetic advance in twenty- six maize lines for agro morphological characters. The analysis of variance revealed the presence of significant variation among maize populations under study and the variability studies indicate the estimates of phenotypic coefficient of variation were slightly higher than its genotypic coefficient of variation for all the traits indicating there is less influence of environment. Among all the characters under study, yield exhibited highest phenotypic coefficient of variation (58.20) and genotypic coefficient of variation (57.89) whereas lowest PCV (5.97) and GCV (5.52) were recorded for days to 50% silking. High heritability with high genetic advance as percent of mean were recorded for plant height, ear height, cob length & girth, no. of kernel rows, no. of kernels per row, 100 - seed weight and yield which indicated the preponderance of additive gene action in controlling these traits. Emphasis should be given on these characters, while selection is made to improve yield potential.

Antony *et al.* (2024) examined genetic analysis of variability, heritability and character association was studied among 25 maize inbred lines for eleven traits. The ANOVA indicated significant variation existed among the inbred lines chosen for the study for all the traits. Wide range of variability was observed for all the traits among them grain yield varied from 16.03 to 62.52 q/ha with an average mean value of 45.75 q/ha. Phenotypic variance was higher compared to genotypic variance and highest phenotypic variance was observed for plant height followed by grain yield. However, the difference between phenotypic and genotypic variance was very narrow for majority of the traits. Similarly, phenotypic coefficient of variation (PCV) was marginally higher than genotypic coefficient of variation (GCV) and highest GCV and PCV was recorded for grain yield (37.03, 38.12) followed by ear height (24.12, 26.48) indicating that these characters are under genetic control have high potential for selection.

Gogoi *et al.* (2025) evaluated 22 maize genotypes using an RBD design with two replications to assess genetic variability, trait associations and path analysis for 13 quantitative traits. High phenotypic and genotypic variation was observed for ear height. Traits like ear height, 100-kernel weight, tassel length, kernels per row, ear length, kernel rows per ear and plant height showed high heritability with high genetic advance. Grain yield per plant was significantly and positively correlated with shelling percentage (both levels) and with ear diameter, kernel rows per ear and kernels per row (genotypic level). Path analysis indicated that days to 50% pollen shed had the highest positive direct effect, while days to 50% silk had the highest negative effect on yield. Key yield determinants identified were ear diameter, kernel rows per ear and kernels per row, suggesting their selection can improve yield.

2.2 To study correlation of grain yield and yield attributing characters:

Correlation study indicates the degree of interdependence of plant characters, which is an important tool in selection of a pertinent genotype. Therefore, information on association between characters is quite useful to plant breeders to formulate their breeding and selection strategies. The correlations provide information about inter-relationship among yield and its components. The information on character association may be used in the prediction of correlated response to directional selection, construction of selection indices and identification of some characters which may have no value by themselves, but are useful as indicators of the more important ones under consideration (Johnson et al. 1955).

Malik *et al.* (2005) examined 36 maize hybrids along with their parental lines using a randomized complete block design with two replications to analyse genetic correlations among various traits. The study found that grain yield per plant had a significant positive correlation with ear height, number of leaves per plant, leaf length, leaf width, leaf area, ear weight and number of kernel rows per ear. Conversely, days to 50% silking, days to 50% tasseling and grain moisture at harvest showed negative correlations with grain yield. Among all traits, kernel rows per ear had the strongest positive correlation with grain yield (r = 0.76), followed by leaf area (r = 0.69), plant height (r = 0.67) and number of leaves per plant (r = 0.43). The high positive genetic correlations between plant height, leaf area, number of leaves, ear weight, kernels per row and grain yield suggest that selecting for these traits could effectively enhance maize grain yield.

Hemavathy *et al.* (2008) studied genetic variability and correlations in 42 inbred lines of maize. The data were recorded on seed yield and six yield related traits. Grain yield was found to be positively correlated with cob length kernel rows/cob and kernels/row and 100 seed weight. Grain yield and cob length estimates combined with high genotypic co-efficient of variation and high heritability were indicating additive gene action controlling these traits. Cob breadth had high positive indirect effects through kernel rows/cob; and low negative indirect effects through kernel rows/cob and 100 seed weight. Kernel rows/cob, kernels/row and 100 seed weight had significant positive correlation with grain yield.

Wannows *et al.* (2010) found a positive and significant correlation between grain yield and traits such as kernel number per row (0.589), ear length (0.465) and leaf area index (0.497). To determine the relative contribution of various traits to grain yield, a path coefficient analysis was conducted. This analysis revealed that plant height, leaf area index, ear diameter and physiological maturity exhibited strong and positive direct effects on grain yield per plant.

Jawaharlal *et al.* (2011) found that there was a substantial and positive correlation between grain output and the number of seed rows per ear, plant height, number of seeds per ear, ear height, ear girth, number of seeds per row and 100-seed weight. Grain yield was most positively correlated with plant height, ear height, ear girth, number of seeds per row, 100 seed weight and number of seed rows per ear. Grain yield was shown to have a high negative genotypic connection with days to 50% silking and days to 50% tasselling.

Selvaraj and Nagarajan (2011) found that while days to tasseling and days to silking had a non-significant positive association with grain yield, ear length, plant height, ear height, number of grains per row, starch content, ear girth, hundred grain weight, number of grains per ear and carotene content had a significant positive association with grain yield. Grain yield was negatively correlated, but not significantly, with the number of rows per ear and the content of crude protein. The number of grains per row and ear length were the two factors that were most correlated with grain production.

Sumalini and Manjulatha (2012) found that, with the exception of days to 50% silk emergence, there is a substantial and positive correlation between grain yield and every attribute that was studied. Ear girth showed the most positive genotypic association with grain yield, followed by ear length and kernels per row.

Amini *et al.* (2013) investigated the relationships between seed yield and its contributing traits in maize by evaluating six generations in a randomized complete block design with three replications during the 2009 cropping season. The correlation analysis revealed that, in most cases, genotypic correlations between traits were higher than phenotypic ones. Notably, plant height showed a strong positive genotypic correlation with seed yield. Path coefficient analysis further indicated that yield components had a strong positive direct influence on seed yield per plant. Although ear seed weight exhibited a very strong positive direct effect on seed yield per plant, it was negatively correlated with overall seed yield due to significant negative indirect effects on other yield-related traits.

Nzuve *et al.* (2014) evaluated 42 maize hybrids were examined in order to identify the genetic traits that contribute to grain yield inheritance and related component qualities. The results of this investigation showed a significant and positive relationship between plant and ear height and grain yield.

Vida (2014) reported a significant and positive correlation was observed between forage yield and several traits, including stem diameter, ear weight, kernel number per row, ear length, days to silk emergence and days to physiological maturity. In the regression analysis, stem diameter, ear weight and plant height remained in the final model, indicating their strong influence on forage yield. Path analysis further highlighted ear weight as a key selection criterion due to its strong positive direct effect on forage yield. Stem diameter and plant height were also identified as important traits for selection in forage corn breeding programs.

Kumar *et al.* (2015) investigated 24 maize inbreds for correlation studies amongst 11 quantitative traits. Positive and significant phenotypic correlations were recorded for grain yield with plant and ear height, ear length and diameter, number of kernel row per ear and kernels per row and 100 kernels weight except maturity traits which, showed negative association with grain yield.

Patil *et al.* (2016) found highly significant positive correlation between grain yield per plant and traits such as ear circumference, number of kernels per row, ear length and plant height. Path analysis further revealed that days to maturity, plant height, ear length, number of kernel rows per cob and 100-grain weight had strong direct effects on grain yield, indicating a true and consistent relationship among these traits.

Reddy and Jabeen (2016) determined that the genotypic correlations were stronger than the phenotypic connections after comparing the magnitudes of the two correlations. Plant height, ear weight, ear girth, ear length, 100-kernel weight and number of kernels per row were all shown to be significantly and favorably correlated with grain yield.

Izzam *et al.* (2017) conducted an experiment using 22 genotypes comprising 20 hybrids and two local checks. Hybrid-1 performed better for yield and yield associated traits under the tested agro-climatic conditions. Grain yield had significant and positive correlation with ear length (r=0.45) and non-significant but positive correlation with plant height (r=0.23), ear height (r=0.41), flag leaf area (r=0.03) kernel rows per cob (r=0.05) and 100 kernel weight (r=0.21). The positive correlations suggested that the desired characters in these hybrids could be improved simultaneously in further maize breeding programs.

Arsode *et al.* (2018) studied twenty-four crosses which were developed from crossing between eight maize inbreds with three maize inbred testers. In this investigation, trait association was studied to evaluate the correlation among yield and other traits responsible for it. it was observed that Grain yield/plant showed substantial and positive correlation with ear length, days to maturity, number of seeds per row, ear height, plant height, ear girth, hundred seed weight and number of seed rows /ear and negative correlation with days to 50 % silking and days to 50 % tasseling.

Kandel *et al.* (2018) examined the path coefficient and correlation in 20 inbred lines of maize. For every attribute examined, the analysis of variance showed that there were substantial differences between all of the lines. The following variables showed significant and negative correlations with grain yield: tassel blast, anthesis silking interval, leaf area index and leaf firing; shelling percentage; cob length; silk receptivity and diameter; number of kernel row-1; number of kernel ear-1; number of kernel row; SPAD chlorophyll; and thousand kernel weight.

Ahmed *et al.* (2020) reported that grain yield showed positive value of correlation with number of kernelper ear, cob diameter, number of rows/ cob and ear length. Highest value of correlation was obtained for number of kernels per ear and days to tasseling with grain yield. Whereas, ear height and days to silking showed negative correlation with grain yield. This study revealed that number of rows cob, number of kernels/per cob, ear height, 1000-seeds weight can be used for effective selection for improving the grain yield.

Olawamide and Fayeun (2020) estimated path coefficient of grain yield and its contributing Characters having these qualities could be chosen to boost maize grain output. Path analysis at the phenotypic and genotypic levels revealed that field weight and the quantity of collected cobs had a favorable direct relationship on grain output. According to this research, increasing the number of plants per plot is crucial for raising grain output. Therefore, field weight and the quantity of collected cobs are variables that might be considered to boost maize grain yield.

Amegbor *et al.* (2022) evaluated different genotypes to estimate the heritability of grain yield and its related traits, as well as quality traits and determine the association between quality protein maize (QPM) with non-QPM crosses Significant genotypic and phenotypic correlations were recorded for grain yield with protein content (rG = 0.38; rP = 0.25) and tryptophan with oil content (rG = 0.58; rP = 0.25) and negative rG and rP correlations were found for protein with tryptophan content and grain yield with tryptophan content.

Reddy *et al.* (2022) estimated genetic variability, genetic advance, correlation and direct and indirect effects of yield contributing traits on yield. The correlation coefficient indicates there is a significant positive correlation between grain yield and cob weight, number of cobs per plant, number of kernels per row, number of kernel rows per cob, 100 kernel weight, cob length, cob girth, plant height, ear height, shank weight and tassel length at the phenotypic level

Al-Rawi *et al.* (2024) evaluated 60 hybrids in randomized complete block design (RCBD) with three replicates. The analysis of variance results revealed statistically significant differences among all studied traits. The values of genetic variance were higher than the environmental variance for all studied traits except for plant height. The highest broad-sense heritability (0.956) appeared in grain yield per plant, followed by the days from planting to 50% silking (0.803). A significant positive genetic and phenotypic correlation was apparent between grain yield, 100-grain weight and the number of grains per row, while a negative genetic correlation between grain yield and the number of days from planting to 50% silking occurred.

Duvvada *et al.* (2024) conducted an experiment at a farmer's field of Chella, Kamarapara, West Bengal, during pre-kharif season of 2022. The treatments consisted of 2 levels of tillage practices and 7 levels of SSNM treatments. The experimental finding revealed no significant difference between grain and stover yield with different tillage treatments. Whereas significantly higher grain and stover yield `was seen with SSNM through NE, lower grain and stover yield was recorded with control. Correlation studies revealed that plant height, dry matter accumulation, crop growth rate, cob girth, cob length, number of grain rows per cob and number of cobs were highly significant and positively correlated with grain yield.

2.3 To study the direct and indirect effect of yield contributing characters on grain yield.

Path coefficient analysis permits partitioning of the correlation coefficients into direct and indirect effects of a set of independence variables on the dependent variable and gives more realistic contribution. This technique was originally developed by Wright (1921) but was first used for plant selection by Dewey and Lu (1959). To use this path coefficient analysis, it required cause and effect situation among the variables in any crop. Grain yield has been associated with a number of yields contributing characters and these characters themselves are inter-related. The available literature on path analysis for seed yield with their component traits in maize is briefly reviewed below.

Saidaiah *et al.* (2008) conducted a path coefficient analysis involving 11 traits across 40 maize hybrids, 14 parental lines and 2 check varieties during the 2004–05 season. The analysis indicated that 100-kernel weight exerted the highest positive direct effect on grain yield, followed by plant height and the number of leaves above the ear. Additionally, traits such as plant height, ear height, number of leaves above the ear, chlorophyll content at 50% silking, flag leaf area, ear length, ear girth and 100-kernel weight contributed positively to grain yield through indirect effects.

Satyanarayana *et al.* (2008) found that in research that looked at path analysis on forty maize genotypes for eleven different factors, hundred seed weight had the largest positive and direct effect on grain output. Grain yield was positively impacted directly by the number of leaves above the ear and plant height and positively indirectly by variables such as flag leaf area, ear width, hundred seed weight, ear length, chlorophyll content at 50% silking, ear height and number of leaves above the ear. Grain yield is influenced by several yield-contributing features, both directly and indirectly.

Nemati *et al.* (2009) carried out a study at the agricultural research farm of Mohaghegh Ardabili University in 2007. Path analysis results revealed that the number of kernels per ear had the strongest positive correlation with grain yield (r = 0.53). Conversely, both grain yield and kernel yield showed significant negative correlations with grain thickness per ear (r = -0.33 and r = -0.52, respectively). A significant negative correlation was also observed between grain protein content and grain thickness (r = -0.52). The path coefficient analysis suggested that selecting maize cultivars with a higher number of kernels per ear can enhance grain yield. Additionally, kernel length and the number of kernels per row were found to influence grain yield, indicating their potential value in maize breeding programs aimed at developing superior cultivars.

Bello *et al.* (2010) examined the relationship between grain yield and other agronomic factors using ten different types of maize. They found that the number of grains per ear, days to 50% silking and 100 grain weight had the greatest direct impact on total grain yield, while the number of grains per cob via ear height had the highest moderate indirect negative impact. Grain quantity per cob, days to flowering, cob and plant height and 100 grain weight may also be important selection factors for open pollinated types and hybrids to increase their potential production, according to the results.

Raghu *et al.* (2011) observed that the number of kernel rows/ear, plant height and 100 kernel weight had the most significant direct effects on kernel yield, followed by cob girth. Grain yield was positively impacted indirectly by the weight of 100 kernels per cob, the number of seed rows per cob and the number of seeds per row. The study's yield-contributing features affected the expression of the dependent trait, or grain yield, both directly and indirectly.

Bharathiveeramani *et al.* (2012) evaluated 144 maize inbreds for 15 different quantitative characteristics and shown that the weight of the seeds per 100 and the number of kernels per row had a highly substantial direct effect on grain production. While the number of grain rows/cob, the number of kernels per row and the weight of 100 seeds all showed a strong direct impact on grain output, the total number of leaves had a modest one. Grain yield was negatively impacted by the remaining characteristics.

Zarei *et al.* (2012) found that the cob length, kernel length, 100 grain weight, total number of kernels/cobs and cob percentage of the ear all had favorable direct effects on grain production after evaluating the path analysis of 11 corn hybrids. Grain yield was most directly impacted by the quantity of kernels per cob, then by the weight of 100 grains. Cob length and 100 grain weight, as measured by the number of kernels per cob, on the other hand, had the most indirect effects. Through the number of kernels per row and the number of kernel rows per cob, the comparatively large positive direct effect of 100 grain weight on grain yield was somewhat offset by its negative indirect effects.

Hepziba *et al.* (2013) examined 70 divergent inbreds gathered from various regions and found that the number of kernel rows/cob had the greatest beneficial direct effect, followed by cob length. Positive indirect effects through cob length, number of kernel rows per cob, plant height and days to 50% silking are responsible for the strong correlation between grain production per plant, hundred kernel weight and number of kernels per row.

Nataraj *et al*. (2014) based on path analysis reported that ear weight, number of kernel rows per ear, number of kernels per row and 100-kernel weight had the strongest significant positive direct effects on grain yield per plant. Plant height, ear height and ear diameter also contributed positively, though to a lesser extent, while the remaining traits showed a negative direct influence on grain yield per plant.

Jakhar *et al.* (2017) reported that days to 75% brown husk had the strongest positive direct effect on grain yield, followed by tassel length, cob length without husk, days to 50% tasselling and leaf width. In contrast, cob height and days to 50% silking exhibited negative direct effects on yield, suggesting the potential value of indirect selection. Days to 50% tasselling showed a significantly positive indirect effect on yield, along with days to 75% brown husk and leaf width. However, traits such as 100-seed weight, tassel length and cob length with husk demonstrated negative indirect effects on yield.

Rani *et al.* (2017) through path analysis of 21 maize hybrids, found that cob length, number of kernel rows, 100-kernel weight and harvest index had significant positive correlations with grain yield at both the genotypic and phenotypic levels. The path analysis further revealed that biological yield and harvest index had the strongest positive direct effects on grain yield per plant and per hectare, followed by ear length, plant height and grain protein content.

Prakash *et al.* (2019) conducted an experiment to study the path analysis for grain yield and grain yield contributing traits in maize. Hundred maize inbred lines obtained were raised along with five checks in augmented block design II and observations were recorded on twenty morphological traits. Thus, selection for these traits could bring about an improvement in yield attributes of maize. Path analysis for the attributed traits revealed the direct influence of cob girth followed by number of kernels per row, shelling percentage, days to 50 percent silking and ear height on grain yield. Hence, these traits could be used as an effective selection indicator to identify the elite genotypes from a population.

Sukumar *et al.* (2019) reported that results of path coefficient analysis directed that anthesis silking Interval, hundred-seed weight imparted the maximum positive and direct effects both at phenotypic and genotypic levels and therefore, these parameters play a major role while developing maize hybrids with high grain yields through various breeding programs.

Ubi *et al.* (2019) reported that traits like grain yield per plant, ear length, ear height, test weight and cob diameter exhibited high genotypic and phenotypic coefficients of variation (GCV and PCV), along with high heritability and substantial genetic advance. Path coefficient analysis showed that test weight, followed by the number of grains per row, kernel rows per ear, ear length and ear diameter, had the most significant direct influence on grain yield per plant. Additionally, many traits exerted notable positive indirect effects through test weight, number of kernel rows per ear and number of kernels per row.

Chaurasia *et al.* (2020) evaluated thirty-one genotypes comprising seven inbred lines, their twenty-one F_1's developed through diallel mating scheme and three hybrids as a check. Analysis of variance for design of experiment for fourteen quantitative characters revealed that mean squares due to genotypes were highly significant for all the characters studied. Path coefficient analysis at phenotypic level revealed that the trait, days to 50 per cent silk (2.469) had the highest positive direct effect on grain yield per plant followed by grains per plant (1.019), 1000-kernel weight (0.383), ear height (0.086), ear length (0.085), kernel rows per ear (0.065), ear diameter (0.025) and days to 50 per cent physiological maturity (0.024). Hence, direct selection all for these traits will be effective.

Yahaya *et al*. (2021) studied to estimate the direct and indirect effects of four agronomic traits on maize grain yield by the application of simple coefficient correlation and path coefficient analysis in two experimental fields. The path coefficient analysis revealed that plant height made the highest direct contribution to grain yield followed by 1000-grain weight with a direct contribution of 0.4290. The path analysis further disclosed these characters to be the most important components of grain yield. Both correlation and path coefficient analyses have established cob diameter as a less reliable agronomic trait than the other three variables included in the maize yield component analysis.

Singh *et al.* (2022) evaluated different genotypes by considering grain yield as a complex character so direct selection for yield as such can be misleading. Keeping in view, the present study aimed to assess the path coefficient analysis with correlation coefficient technique to establish the direct and indirect relationship between the yield and its component. Highest positive direct effect on 5 ear weight was noticed by shelled grain weight (1.108) followed by phenols (0.115), internodal length (0.106) and days to 50 percent anthesis (0.102) indicating that the selection for these characters were likely to bring about an overall improvement in grain yield directly.

Tejaswini *et al.* (2022) evaluated twenty-eight experimental hybrids along with eight inbred lines and one commercial check to determine correlation and path analysis for yield and yield attributing traits. The experiment was conducted in randomized block design with three replications. Path coefficient analysis exhibited that days to 50% silking had highest positive direct effect on grain yield per plant followed by hundred grain weight, ear girth, number of kernels per row, number of kernels per row and plant height at phenotypic level and genotypic levels.

MATERIAL AND METHODS

CHAPTER III

MATERIAL AND METHODS

The details of the materials used, experimental procedure followed and techniques adopted during the course of the investigation are presented in this chapter. The present investigation entitled "Genetic variability, correlation and path analysis studies in Maize (*Zea mays* L.)" was conducted at experimental farm of Wheat and Maize Research Station, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani during *Rabi* 2024-25. The experimental site is located in Agro-climatic zone-IX (Central Plateau-Western Maharashtra) of Maharashtra state. Geographically Wheat and Maize Research station is situated at 19°14'30.0"N latitude and 76°47'02.0"E longitude with an altitude of 421 meters above mean sea level. The soil of experimental site is Greyish black clay loam.

3.1 EXPERIMENTAL DETAILS

The experimental details for field layout and conduction of experiment are as under:

1. Name of the experiments	"Genetic Variability, Correlation and Path analysis studies in Maize (*Zea mays* L.)"
2. Location	Experimental Farm of Wheat and Maize Research Station, Vasantrao Naik Maratwada Krishi Vidyapeeth, Parbhani.
3. Season and year	*Rabi* 2024-2025
4. Number of genotypes	50 + 3 (checks)
5. Experimental design	Randomized block design (RBD)
6. Replication	2
7. Spacing	60 × 20 cm
8. Plot size	6 m × 0.40 m
9. Fertilizer dose	120 kg N: 60 kg P: 40 kg K (kg ha_{-1})
10. Package of practice	All the recommended agronomic practices ware followed as per standard practices.

3.2 EXPERIMENTAL MATERIALS

The experimental material comprised of 50 genotypes along with 3 checks (Local Check 1-3) which were obtained from CIMMYT (International Maize and Wheat Improvement Centre). The list of genotypes is given below in Table 3.1.

Table 3.1 Details of genotypes Variety/Cultivar Name and their source

Sr. No	GENOTYPES	PEDIGREE
1	V2197-23	HYDTSyn16HG(A)-5-2-1(DM)-B2-BB
2	V2198-1	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*4/(CA34505xCA00302)-B-2-1-B-1-BB(T)-B3-#15-2-B-1-B*4)-B-12(18r)-BBB
3	V2198-3	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*4/(CA34505xCA00302)-B-2-1-B-1-BB(T)-B3-#15-2-B-1-B*4)-B-5-B<20r>-BB
4	V2198-4	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*4/CML582//(CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*5)-B-1-B*4
5	V2198-5	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*5/(LaPostaSeqC7-F64-2-7-2-1-B*4/LaPostaSeqC7-F55-2-2-2-1-B*5)-18-BBB-#-B//(CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*5/PHG39-BB)-B-12-B1-B-1
6	V2198-9	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*7/((CA34505xCA00302)-B-2-1-B-1-BB-B1<20r>-HS4<20r>)-B1-16-B*6)-B-1-3-BB
7	V2198-10	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*7/((CA34505xCA00302)-B-2-1-B-1-BB-B1<20r>-HS4<20r>)-B1-16-B*6)-B-2-1-BB
8	V2198-13	((CML444/VL111354)-42-B-1-BBB-1-BBB/(CML451/LH82//CML451)-B-27-1-1-1-BB-B1)-B-4-1-BB

9	V2198-15	((CML451-B*4//CML451-BBB/LaPostaSeqC7-F18-3-2-2-3-B*7///CML451-B*4//CML451-BBB/DRB-F2-60-1-1-1-BBB-3-B)-BB/(ATZTRLBA905-3-3P-1P-4P-2P-1-1-1-B/G9BC0RL23-1P-2P-3-2P-3-2P-1P-BBB)-B-57TL-2-1-1-B*5)-B-3-B-B1-1
10	V2198-22	(AMDROUT1(DT-Tester)c1F2-36-B*5/(CML451/LH82//CML451)-B-8-1-1-1-B)-B-4-BB-2
11	V2198-23	(CML581-B-B1/(CML581/PHG35-B)-B-1-B-1-B1)-B-4-6-BB
12	V2198-24	(SynB(Cateto|CML226))F2(B2)-4-1-BB
13	V2198-25	(SynB(Cateto|CML226))F2(B3)-9-1-BB
14	V2198-27	(SynB(CML451|LH82|CML444/5*|SW1))F2(GTF)-4-2-BB
15	V2199-1	((CL02450Q/3[SSS]XX//CL02450Q)-B-16-2-1-1-B-#-BB-B1/(CL02450Q/3[SSS]XX//CL02450Q)-B-20-2-1-1-B-#-BB)-B-5-1-BB
16	V2199-5	(SynA(TropA/Temp[SS]))F2(B2)-6-1-BB
17	V2199-8	((AIZTVCPR93A-1-1-4-1-2-BB/AIZTVCPR93A-17-1-3-1-1-BB)-B-30TL-1-1-B*5/CML449-B*7)-B-5-4-BB
18	V2199-9	((AIZTVCPR93A-1-1-4-1-2-BB/AIZTVCPR93A-17-1-3-1-1-BB)-B-30TL-1-2-B*6/(CML474/S92145-2EV-7-3-B*5)-F2-58-1-B*12)-B-3-B-B1-B
19	V2199-11	((AIZTVCPR93A-1-1-4-1-2-BB/AIZTVCPR93A-17-1-3-1-1-BB)-B-34TL-1-4-B*6/(CML474/S92145-2EV-7-3-B*5)-F2-58-1-B*12)-B-4-B-B1-B
20	V2199-12	((AIZTVCPR93A-1-1-4-1-2-BB/AIZTVCPR93A-17-1-3-1-1-BB)-B-34TL-1-4-B*6/(CML474/S92145-2EV-7-3-B*5)-F2-58-1-B*12)-B-5-B-B1-B
21	V2199-13	((AIZTVCPR93A-1-1-4-1-2-BB/AIZTVCPR93A-17-1-3-1-1-BB)-B-34TL-1-4-B*6/(CML474/S92145-2EV-7-3-B*5)-F2-58-1-B*12)-B-8-B-B1-B
22	V2200-5	((CML165/OFP9//CML165)-7-B*5-3-BBB/Composite18-B(Fat)-BB-3-BBB)-B-17-B-1
23	V2200-6	((CML165/OFP9//CML165)-7-B*5-3-BBB/Composite18-B(Fat)-BB-3-BBB)-B-17-B-2
24	V2200-8	((CLQRCYQ28/P390AM//CMLC4F218-B-1-B)-B-43-1-BB-2-B*9)-2-2-3-1-B
25	V2201-1	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*4/CML582//CML582)-B-1

26	V2201-3	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*4/CML582//CML582)-B-12
27	V2201-11	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*4/CML582//(CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*5)-B-10-2
28	V2201-17	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*4/CML582//(CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*5)-B-7-B-5
29	V2201-18	((CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*5/(LaPostaSeqC7-F64-2-7-2-1-B*4/LaPostaSeqC7-F55-2-2-2-1-B*5)-18-BBB-#-B//(CA34505xCA00302)-B-2-1-B-1-BB(T)-B5-#17-3-B-2-B*5/PHG39-BB)-B-14-B-1
30	V2201-19	((CML444/VL111354)-42-B-1-BBB-1-BBB/(CML451/LH82//CML451)-B-27-1-1-1-BB-B1)-B-10-BB
31	V2201-22	((CML451-B*7/(CML395/CML547)DH-3023-B*4)-B-3-B-B1/(CML451-B*7/(CML395/MBRC5BcF114-1-2-3-B-4-2-B)DH-3018-B*4)-B-4-B-B1)-B-14-BB
32	V2201-25	((HYSyn123-#)-B2<20r>-11-2-BB-#-B-B1/SW1-75-2-B-l-BBB-1-B*7)-B-10(Dent)-BB
33	V2201-35	(HYSyn20(20r))F2-26(B3)-B-3
34	V2201-48	((CML444/VL111354)-42-B-1-BBB-1-BBB/(CML451/LH82//CML451)-B-27-1-1-1-BB-B1//(CML444/VL111354)-42-B-1-BBB-1-BBB)-B-5-B-1
35	V2201-51	((HYSyn123-#)-B1-28-BBB-#-BB-B1/SW1-75-2-B-l-BBB-1-B*7)-B-1-BB
36	V2201-52	((HYSyn123-#)-B1-28-BBB-#-BB-B1/SW1-75-2-B-l-BBB-1-B*7)-B-6-BB
37	V2201-55	((HYSyn123-#)-B2<20r>-11-2-BB-#-B-B1/(HYSyn123-#)-B1-28-BBB-#-BB-B1)-B-3-BB
38	V2202-5	(CA14517/P145C4MH7-1-B-1-1-B-1-1-B*17-1-BB-B1-#/(CTS013008/AMATLC0HS71-1-1-2-1-1-1-B*5/Nei402020)-B*16)-B-3-B
39	V2202-7	(CA14517/P145C4MH7-1-B-1-1-B-1-1-B*17-1-BB-B1-#/(POP351C0-HS274-1-1-B*4-2-B*6/Composite14-BBB-1-B-2-B)-B-3-B-2-1-B1-B)-B-9-B

40	V2202-13	(CML563-B-#/(POP351C0-HS274-1-1-B*4-2-B*6/Composite14-BBB-1-B-2-B)-B-3-B-2-1-B1-B)-B-16-B
41	V2202-21	(CML580/POB45c9F22-18-3-1-B*4-1-B*8-#-B)-B-4-B
42	V2202-26	(Composite23-BB-B1-B*6-B2-#/(CTS013008/AMATLC0HS71-1-1-2-1-1-1-B*5/Nei402020)-B*16)-B-17-B
43	V2202-29	(Composite23-BB-B1-B*6-B2-#/(CTS013008/AMATLC0HS71-1-1-2-1-1-1-B*5/Nei402020)-B*16)-B-5-B
44	V2202-42	(Composite23-BB-B1-B*6-B2-#/(POP351C0-HS274-1-1-B*4-2-B*6/Composite14-BBB-1-B-2-B)-B-3-B-2-1-B1-B//(POP351C0-HS274-1-1-B*4-2-B*6/Composite14-BBB-1-B-2-B)-B-3-B-2-1-B1-2(DM)-B1-B)-3
45	V2202-44	(Composite23-BB-B1-B*6-B2-#/(POP351C0-HS274-1-1-B*4-2-B*6/Composite14-BBB-1-B-2-B)-B-3-B-2-1-B1-B//(POP351C0-HS274-1-1-B*4-2-B*6/Composite14-BBB-1-B-2-B)-B-3-B-2-1-B1-2(DM)-B1-B)-9
46	V2202-52	(MPS_OPT195)F3-11-BB
47	V2202-54	(MPS_OPT195)F3-32-B
48	V2202-55	(MPS_OPT195)F3-35-B
49	V2203-23	(CML452=Ac8328BNC6-166-1-1-1-B*15-#-BB/PHG39-BB)-B-10-B
50	V2203-37	(CML563-B/(CL02450Q/3[SSS]XX//CL02450Q)-B-16-2-1-1-B-#-BB-B1)-B-23-B
51	PDKV Arambh	CHECK
52	Phule Champion	CHECK
53	Phule Maharshi	CHECK

3.3 CHARACTERS STUDIED:

Five competitive plants were randomly selected from each entry of each replication in field experiment for recording the observation on grain yield and other character. The phenological characters viz., Days to 50 % tasseling and Days to 50 % silking were recorded on plot basis. Morphological traits:

3.3.1 Days to 50% tasseling:

Days to 50% tasseling was recorded as the number of days from the date of sowing till the 50% of plants have pollen shed.

3.3.2 Days to 50% silking:

Days to 50% silking was recorded as the number of days from the date of sowing to the emergence of silks from 50% of plants.

3.3.3 Anthesis silking interval:

Anthesis silking interval is the difference between the days to 50% anthesis and days to 50% silking.

3.3.4 Plant height (cm):

Plant height was measured in cm from soil surface (ground level) to the tip of main spike excluding the awns.

3.3.5 Ear height (cm):

The plant's height from ground level to the base of the uppermost cob bearing internode is recorded as ear height in centimetres.

3.3.6 Ear length (cm):

Length of cobs from base to the tip of cob measured in centimetres.

3.3.7 Ear girth (cm):

Cob girth in centimetres at the middle of the cob.

3.3.8 Number of grains per ear:

Total number of grains per ear was computed by multiplying number of grains/rows with number of kernel rows.

3.3.9 Hundred seed weight (g):

Weight of 100 grains taken at random adjusted to 15% moisture content expressed in grams.

3.3.10 Grain yield per plant (g):

Grain weight obtained per plant was adjusted to 15% moisture and expressed in grams.

3.3.11 Number of cobs per plant:

The number of cobs per plant has been counted and recorded.

3.3.12 Shelling %:

It was measured in percentage by (grain weight/ear weight) x 100. Used for calculating grain yield.

3.4 STATISTICAL ANALYSIS:

The replication wise mean values for all the characters were subjected to statistical analysis.

1. Analysis of variance
2. Estimation of mean and range
3. Estimation of genetic variability parameters
4. Heritability and genetic advance
5. Correlation
6. Path analysis

3.4.1 Analysis of Variance:

The analysis of variance for all the studied characters was carried out as per the procedure described by Panse and Sukhatme (1985) was followed to test the significance of differences among the genotypes for all the characters under study. The form of analysis of variance as given in Table 3.2 provides a comparison by partitioning of variance due to various sources.

The statistical model used for this analysis is as under

$$Y_{ij} = m + G_j + E_{ij}$$

Where,

Y_{ij} = Observed value of j^{th} genotype in i^{th} replication.

m = average mean

G_i = effect of j^{th} genotypes

E_{ij} = Uncontrolled variation associated with j^{th} genotype in i^{th} replication

Table 3.2 Analysis of variance and expectation of mean squares

Source of variation	**DF**	**Mean square**	**Expected mean square**	**Variance rato 'F' observed**	**Table 'F'**
Replication	(r-1)	RMSS	$\sigma^2 e + \sigma^2$ r	RMSS/EMSS	
Treatment	(t-1)	TMSS	σ2e + r σ^2 g	TMSS/EMSS	
Error	(r-1) (t-1)	EMSS	$\sigma^2 e$		
Total	(rt-1)				

Where,

RMSS	=	Replication mean sum of squares
TRMSS	=	Treatment mean sum of squares
EMSS	=	Error mean sum of squares
r	=	Number of replications
t	=	Number of genotypes

The standard error of mean differences (S.Em.) for treatment means was calculated by using the following formula.

$$\text{Standard Error (S.E)} = \frac{\sqrt{EMSS}}{r}$$

Where,

EMSS	=	error mean sum squares
r	=	number of replications

The critical difference (C.D.) to compare the means of various genotypes was calculated by using the following formula:

$$\text{CD} = \text{S.Em. x } \sqrt{2} \text{ x t}$$

Where,

t = Table value of ‘t’ as error d.f at 5 or 1 per cent level of significance

3.4.2 Estimation of mean and range

The mean values of all the treatments for various traits of genotypes where worked out by dividing the total value of the observations by number of observations

$$\text{Mean} = \frac{\text{Sum of all observations}}{\text{Number of observations}}$$

OR

$$X = \frac{1}{n}\left(\sum_{i=1}^{n} X\, i\right)$$

Where,

$\bar{X}$ = mean of characters

X_i = i^{th} observation of population

n = number of observations per replication

The maximum and minimum values or a highest and lowest value of mean of each trait is nothing but the range.

3.4.3 Estimation of genetic variability parameters

The given below are the different formulae for calculating genetic variability parameters among the germplasm under investigation.

3.4.3.1. Estimate of genotypic and phenotypic variances

The mean square from variance table (Burton 1952) was used to calculate genotypic and phenotypic variance

a) Genotypic variance ($\sigma^2{}_g$) $= \frac{TRMSS-EMSS}{r}$

b) Error variance ($\sigma^2{}_e$) = EMSS

c) Phenotypic variance ($\sigma^2 p$) $= \sigma^2 g + \sigma^2 e$

Where,

r = number of replications

T = number of treatments

$\sigma^2 e$ = error variance

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

3.4.3.2 Estimation of phenotypic and genotypic coefficient of variation

The calculation of genotypic and phenotypic coefficient of variation (PCV and GCV) was estimated by the method suggested by the Burton (1952).

Following were the formulae for calculating GCV &PCV:

1. Genotypic coefficient of variance (GCV)

$$\text{GCV}(\%) = \frac{\sqrt{\sigma^2 g}}{x} \text{X } 100$$

2. Phenotypic coefficient of variance (PCV)

$$\text{PCV}(\%) = \frac{\sqrt{\sigma^2 p}}{x} \text{X } 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

X = General or grand mean of character

Falconer (1964) suggested the classification of GCV & PCV.

Low = 0-10%

moderate = 10-20%

High 20% and above = 20% and above

3.4.4 Heritability and genetic advance

1. Heritability (h^2) (b.s) (%)

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the population.

Heritability (h^2) in the broad sense was calculated according to the formula given by Johnson *et al.* (1955).

$$h^2 (bs)\ \% = \sigma^2 g / \sigma^2 p \text{ x } 100$$

Where,

h^2 (bs) = heritability in broad sense

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

($\sigma^2 g + \sigma^2 e$) $\sigma^2 e$ = environmental variance

The heritability was classified as recommended by Johnson *et al.,* (1955):

Low	=	0-30%
Medium	=	31-60%
High 61% and above	=	61% and above

2. Genetic advance = h^2 x K x σp

Where,

h^2 = Heritability (broad sense)

k = Selection difference at 5 per cent selection intensity (the value of K = 2.06)

σp = Phenotypic standard deviation

At 5% selection intensity, genetic advance for each character was calculated by using formula given by Johnson *et al.* (1955).

$$\text{GA (m)} = \frac{\text{GA}}{\bar{\text{X}}} \times 100$$

Johnson *et al.* (1955) categorized genetic advance as per cent of mean as

Low	= (≤10%)
Moderate	= (10-20%)
High	= (≥20%)

3.4.5 Estimation of correlation coefficient

To understand the degree of relationship between different characters the genotypic and phenotypic correlation coefficients were carried out from their respective variances and co-variances. Johnson *et al.* (1955) suggested the formulae for calculation of correlation which are given below:

3.4.5.1 Genotypic correlation coefficient (rg_{xy})

$$(rg_{xy}) = \frac{\text{Cov}\ (g_x \times g_y)}{\sqrt{\sigma^2 g_x + \sigma^2 g_y}}$$

Where,

Cov ($g_x.g_y$) = Genotypic covariance between character x and y

$\sigma^2 g_x$ and $\sigma^2 g_y$ = Genotypic variance of character x and y, respectively.

3.4.5.2 Phenotypic correlation coefficient (rp_{xy})

$$(rg_{xy}) = \frac{\mathrm{Cov}\ (p_x\ x p_y)}{\sqrt{\sigma^2 P_x + \sigma^2 P_y}}$$

Where,

Cov ($p_x.p_y$) = Phenotypic covariance between character x and y
$\sigma^2 p_x$ and $\sigma^2 p_y$ = Phenotypic variance of character x and y, respectively.

From the table of Fisher and Yates significance of correlation coefficient at 5 and 1 per cent level of significance was carried out. The 'r' values were compared against (n-2) degrees of freedom.

3.5 Path analysis

The genotypic correlation coefficient among seed yield and its attributes were classified into direct and indirect effects with the path coefficient analysis as outlined by Wright (1921) and Dewey and Lu (1959).

The first stage in path analysis is to construct the path diagram from the source of cause and effect relationship. In the present study, path diagram was arranged by taking yield (Y) as the effect *i.e.* the function of various components like X_1, X_2, X_3 and these components and some other indeterminate factors selected as 'r' show following type of correlation with each other.

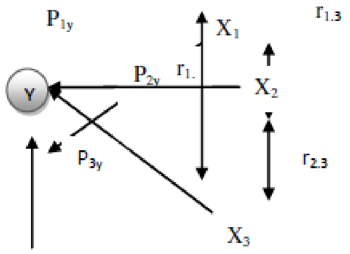

Fig .3.1: Path Diagram

In the diagram double arrowed lines shows the existence of mutual relationship between the yield and attributing traits, while single arrowed lines show the undeviating influence of factors on the yield. Correlation coefficient (r_{ij}) used to calculate mutual relationship while path coefficient (P_{ij}) used to calculate direct effect of traits

By solving a set of simultaneous equations, direct and indirect effects of variables on yield can be measured as recommended by Dewey and Lu (1959).

$$r_{ny} = p_{ny} + r_{n2}\, p_{2y} + r_{n3}\, p_{3y} + \ldots\ldots\ldots\ldots + r_{nx}\, p_{xy}$$

Where,

r_{ny} = Represents correlation coefficient between one component and seed yield.

r_{n2} = Represents correlation coefficient between that character and each of other components

p_{ny} = Represents path coefficient between that characters and seed yield.

Matrix- A Matrix- B

$$\begin{bmatrix} r_1 y \\ r_2 y \\ \downarrow \\ r_n y \end{bmatrix} \qquad \begin{bmatrix} P_1 \\ P_2 \\ \downarrow \\ P_n \end{bmatrix} \qquad \begin{bmatrix} r_1,1 & r_1,2 \ldots\ldots & r_1,n \\ r_2,1 & r_2,2 & r_2,n \\ & \downarrow & \\ r_n,1 & r_n,2 & r_n,n \end{bmatrix}$$

Matrix-B was inverted (B^{-1}) and following formula used to calculate path coefficient (P_{ij})

$$(P_{ij}) = A \times (B^{-1})$$

Where,

$P_1, P_2, \ldots, P_n$ are estimates of direct effects of character

$r_{ij}p_{ij}$ - are indirect effects of i^{th} character on seed yield character through j^{th} character

Residual factor which was uncounted by the above associations was calculated by using the following formula:

$$\text{Residual factor (Rx)} = \sqrt{1 - R^2}$$

Here,

$R^2 = (P_{ly}, r_{1y} + p_{2y}, r_{2y} + \ldots\ldots\ldots\ldots + P_{ny}, r_{ny})$

Where,

$r_{ly}, r_{2y}, \ldots\ldots\, r_{ny},$ = Correlation coefficient

$P_{ly}, P_{2y}, \ldots\ldots\ldots P_{ny},$ = Path values

Plate No. 3.1 General view of experimental trial (*rabi 2024*-25)

RESULTS AND DISCUSSION

CHAPTER-IV

RESULT AND DISCUSSION

In the present study titled "Genetic Variability, Correlation and Path analysis studies in Maize (*Zea mays* L.)" a total of 50 maize genotypes along with three check varieties were evaluated to estimate parameters such as heritability, variability, genetic advance as a percentage of the mean, correlation coefficients and path coefficients. The genotypes were assessed based on twelve traits viz., days to 50% tasseling, days to 50% silking, anthesis silking interval, plant height (cm), ear height (cm), ear length (cm), ear girth (cm), number of grains per ear, hundred seed weight (g), grain yield per plant (g), number of cobs per plant and shelling percentage. The result obtained from the experiment presented in this chapter under the following headings:

4.1 Analysis of variance

4.2 Mean performance

4.3 Variability studies

4.4 Correlation coefficient

4.5 Path coefficient analysis for grain yield

4.1 Analysis of variance

Analysis of variance for 12 characters furnished in the table 4.1. The analysis of variance revealed a significant difference among the genotypes for all the 12 characters.

4.2 Mean performance

The mean performances of fifty-three maize genotypes for twelve characters studied are presented in Table 4.2.

4.2.1 Days for 50% tasseling

The average number of days to reach 50 percent tasseling was 75.61 days, with the observed range spanning from 61.50 to 90.00 days. Genotype V2199-5 and V2199-9 were the earliest to reach 50 percent tasseling at 61.50 days followed by genotypes V2201-1 (62.00 days), V2199-11 (65.00 days) and V2199-12 (66.00 days). On the other hand, genotypes V2202-13 was the late requiring 90.00 days.

4.2.2 Days for 50% silking

The mean number of days to 50% silking ranged from 63 days in genotype V2199-5 to 93 days in the genotypes V2202-13 and V2202-42, with an overall average of 78.72 days. Genotype V2199-5 exhibited the earliest flowering at 63 days followed by genotypes V2199-9 (64.00 days), V2201-1 (64.50 days) and V2199-11 (66.00 days).

4.2.3 Anther silking interval

The anthesis-silking interval varied from 1 to 5.25 days, with an average duration of 3.09 days. Genotypes V2198-9 and V2199-11 recorded the shortest interval at 1 day, while V2202-44 exhibited the longest interval at 5.5 days.

4.2.4 Plant height (cm)

Plant height varied from 215.5 cm in check variety Phule Maharshi to 89.8 cm in the genotype V2201-51. The overall average plant height was133.42 cm. Phule Maharshi was the tallest genotype at 215.50 cm followed by another check varieties Phule Champion at 204.40 cm and PDKV Arambh at 204.25 cm.

4.2.5 Ear height (cm)

Among the 53 genotypes, ear height ranged from 29.2 cm to 112.4 cm, with an overall mean of 66.11 cm. The lowest ear height was observed in genotype V2198-23 (29.2 cm), while the highest was recorded in check variety Phule Maharshi (112.4 cm).

4.2.6 Ear length (cm)

Ear length varied from 14.90 cm to 24.50 cm, with an overall average of 19.16 cm. The longest ear was observed in genotype V2201-19 (24.50 cm), while the shortest was recorded in check variety PDKV Arambh ZH19525 (14.90 cm).

4.2.7 Ear girth (cm)

Ear girth ranged from 11.90 cm to 19.80 cm, with a general average of 14.98 cm. The highest ear girth was recorded in genotype V2202-42 (19.80 cm), while the lowest was observed in V2199-13 (11.90 cm).

4.2.8 Number of grains per ear

The data on the number of grains per ear showed a range from 129.95 to 459.20, with an average of 271.44. The highest grain count per ear was recorded in genotype V2201-25 (459.20) followed by V2201-52 (381.10), V2202-52 (378.45) and V2199-5 (377). On the other hand, the lowest grain count was observed in V2201-18 (129.90) followed by V2201-17 (135.50), V2202-42 (138.20) and V2202-55 (140.85). The check varieties PDKV Arambh, Phule champion and Phule Maharshi recorded mean grain counts of 373.00, 360.70 and 329.35, respectively.

4.2.9 Hundred seed weight (g)

In the study, the 100-grain weight across 53 genotypes ranged from 20.10 g to 52.35 g, with an average of 34.37 g. The highest hundred seed weight was observed in check variety Phule Maharshi (52.35 g), while the lowest was recorded in V2202-29 (20.10 g).

4.2.10 Grain yield per plant (g)

Significant variation in yield per plant was observed among the genotypes. The yield ranged from 35.33 g to 124.49 g, with an overall mean of 72.84 g. The highest grain yield per plant was recorded in genotype V2201-51 (124.49 g) followed by V2202-52 (121.49 g), V2201-48 (121.35 g) and V2201-55 (119.32g). On the lower end, genotypes V2202-44 (35.33 g), V2202-55 (39.15 g) and V2202-7 (40.48 g) recorded the lowest yields. The check varieties PDKV Arambh, Phule champion and Phule Maharshi had yields of 110.95 g, 112.60 and 107.53 g per plant, respectively.

4.2.11 Number of cobs per plant

The mean values of number of cobs per plant range from 1.4 to 2.2, with an average mean of 1.87. The highest number of cobs per plant was observed in genotype V2202-44 (2.2), while the lowest number of cobs per plant was observed in V2198-1 and check variety Phule Champion (1.4).

4.2.12 Shelling%

The data on the shelling% showed a range from 55.67% to 84.65%, with an average of 70.26%. The highest shelling% was recorded in genotype V2201-25 (84.64%) followed by V2198-1 (82.95%), V2201-48 (82.50%) and V2198-10 (81.94%). On the lower end, the lowest shelling% was observed in V2203-37 (55.66%) followed by V2203-23 (56.67%), V2202-7 (57.01%) and V2201-3 (61.36%). The check varieties PDKV Arambh, Phule champion and Phule Maharshi had mean shelling% of 73.94%, 69.89% and 71.32% respectively.

Table 4.1: Analysis of variance for yield and yield contributing characters in fifty-three genotypes of maize

Source	Df	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
Replication	1	0.462	0.235	0.058	31.4	97.28	8.434	46.75	49.86	5.662	0.097	0.15	29.142
Genotype	52	121.4**	140.93**	1.975**	1160.47**	465.22**	8**	6.186**	12754.32**	86.75**	1279.05**	0.053**	104.595**
Error	52	2.404	2.88	0.321	3.76	3.64	2.722	2.184	7.965	2.783	9.73	0.022	3.579

Where * and ** Significant at 0.005 and 0.001 levels of probability, respectively.

DT- Days to 50 % tasseling, **DS**- Days to 50% silking, **ASI** - Anthesis silking interval, **PH** - Plant height, **EH** - Ear height, **EL** - Ear length, **EG** - Ear girth, **NGPE** - Number of grains per ear, **HSW** - Hundred seed weight, **NCPP** - Number of cobs per plant, **SP**-Shelling percentage, **GYPP**- Grain yield per plant.

Table 4.2: Mean values of fifty-three genotypes for different yield attributing characters in maize under field conditions

Sr. No	Genotypes	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
1	V2197-23	77.00	79.50	2.50	132.70	68.20	22.50	14.70	171.80	26.00	1.60	63.64	65.80
2	V2198-1	71.00	73.00	2.00	157.20	85.50	22.50	18.40	174.10	28.60	1.40	82.96	62.70
3	V2198-3	66.00	69.50	3.00	133.10	60.20	17.65	14.65	147.20	26.10	1.80	67.46	52.70
4	V2198-4	74.50	77.50	2.50	130.90	59.20	18.15	14.80	149.55	37.55	1.70	71.08	60.95
5	V2198-5	75.50	79.00	3.50	99.40	41.60	20.90	16.80	320.90	31.00	2.00	78.63	106.15
6	V2198-9	71.00	73.00	1.00	142.00	74.35	19.05	17.20	307.50	35.75	1.70	76.84	99.43
7	V2198-10	69.50	72.00	2.50	124.40	53.90	20.60	13.95	266.65	40.15	1.90	81.95	104.80
8	V2198-13	68.50	70.50	2.00	125.40	56.80	21.05	14.10	304.65	41.30	1.80	75.94	83.03
9	V2198-15	71.50	75.00	3.50	137.60	63.70	21.25	16.90	257.50	40.35	1.70	62.00	79.13
10	V2198-22	69.00	71.50	2.50	138.00	51.40	17.70	17.10	372.85	45.80	1.70	67.21	66.78
11	V2198-23	72.00	73.50	1.50	97.60	29.20	17.75	14.15	254.20	26.85	1.90	66.32	55.72
12	V2198-24	73.50	75.00	3.50	122.90	68.10	20.70	17.70	326.35	35.30	1.90	77.41	93.79
13	V2198-25	73.50	76.50	2.50	131.80	72.40	18.75	16.90	223.65	38.10	1.90	64.27	84.03
14	V2198-27	67.50	70.00	2.00	140.20	82.05	22.50	13.15	214.15	37.20	1.80	73.08	63.63
15	V2199-1	72.50	75.50	2.00	103.70	41.60	21.50	12.05	314.25	27.80	1.90	65.29	48.71
16	V2199-5	61.50	63.00	1.50	133.80	68.40	17.40	13.40	377.00	46.00	1.90	65.54	43.83
17	V2199-8	70.00	73.00	3.00	124.00	54.95	18.40	12.85	298.70	31.75	1.70	67.20	40.58
18	V2199-9	61.50	64.00	2.50	107.30	64.60	18.05	12.90	322.70	37.45	1.90	71.44	79.58
19	V2199-11	65.00	66.00	1.00	109.50	51.20	19.50	13.30	324.40	23.15	1.80	65.44	71.46
20	V2199-12	66.00	68.00	2.00	126.30	59.55	16.85	15.70	260.60	25.70	1.90	64.44	85.38

Sr. No	Genotypes	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
21	V2199-13	69	72.5	2.5	116.8	63.05	17.1	11.9	282.5	33.15	1.7	77.4	60.29
22	V2200-5	70.5	72.5	2	123.1	62.15	19	15.45	182.9	28.5	2.1	79.4	53.38
23	V2200-6	72.5	75	2.5	103.8	41.5	21.3	17.25	313.8	23.6	2	70.84	49.88
24	V2200-8	73.5	75	1.5	110.8	57.4	20.75	14.7	177.8	38.2	2	72.73	54.23
25	V2201-1	62	64.5	2.5	129.3	59.1	20.2	16.25	193.2	42.25	1.9	67.77	53.37
26	V2201-3	81.5	86	5.15	138.3	61	18.4	13.3	149.5	42	2.1	61.36	49.08
27	V2201-11	86.5	91	4.75	137.1	57.1	19.8	16.6	360.8	32	1.9	80.18	53.47
28	V2201-17	79	83	3.75	120.2	59.3	18.7	15.7	135.5	35.65	1.9	61.48	64.95
29	V2201-18	79.5	83	3.3	134.4	61.6	18.8	13.15	129.95	33.75	1.8	68.93	77.74
30	V2201-19	76	79	3.5	123.9	63.88	24.5	16.9	326.75	31.3	1.9	61.56	70.95
31	V2201-22	70.5	73.5	3.05	130	67.05	21.9	15.2	243.5	36.8	2.1	79.49	65.1
32	V2201-25	80.5	84	3.75	136.1	73.5	17.75	14.75	459.2	40.75	2	84.65	115.21
33	V2201-35	83.5	87	3.9	136.4	68.75	17.3	17.7	265.4	30.8	1.9	66.63	54.12
34	V2201-48	74	77.5	3.85	132.25	68.8	18.9	16	347.45	39.5	1.9	82.51	121.35
35	V2201-51	84.5	88	3.75	89.8	50.5	21.15	14.8	257.15	44	1.8	73.83	124.49
36	V2201-52	86.5	90.5	3.9	147.1	69.7	19.9	14.95	381.1	41.5	2	79.59	72.16
37	V2201-55	86	89.5	3.5	148.3	77.45	18.1	12.7	303.7	41.4	1.8	76.8	119.33
38	V2202-5	87.5	91	3.75	136.9	61	20.95	13.75	353.5	31.5	1.9	64.6	102.86
39	V2202-7	82.5	86.5	3.9	103.2	52.8	15.9	12.2	277.7	25.55	1.8	57.02	40.48
40	V2202-13	90	93	2.9	123.7	63.5	16.7	15	315	29.45	2	63.01	41.14
41	V2202-21	81.5	84.5	3.05	134.3	71.7	18.2	14.6	223.05	33	2	70.385	75.31

Sr. No	Genotypes	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
42	V2202-26	80.5	84	3.5	158.8	70.35	21.5	13.9	270	33.4	2	70.625	68.245
43	V2202-29	83.5	87	3.5	141.5	75.3	17.8	15.25	232.8	20.1	1.9	69.155	52.01
44	V2202-42	89	93	3.9	137.7	76.3	19.9	19.8	138.2	34.7	2.1	61.36	51.355
45	V2202-44	79.5	84	5.25	148.05	91.5	16.4	17	312.4	27.05	2.2	77.43	35.33
46	V2202-52	84	88	3.75	145	80.2	18.4	14.8	378.45	28.7	2	66.96	121.5
47	V2202-54	85	89	3.9	152	73.7	18.9	15.8	317.15	31.6	1.9	75.07	81.98
48	V2202-55	86.5	91	4.25	108.6	53.4	18.2	14.5	140.85	36.95	2	67.91	39.15
49	V2203-23	77.5	82.5	4.75	146.8	73.2	19.8	12.3	292	37.55	1.9	56.67	62.62
50	V2203-37	85	89	3.9	135.3	74.7	18.5	14.9	173.2	35.75	1.9	55.67	50.25
51	PDKV Arambh	66.5	70.5	3.8	204.25	103.25	14.9	14.7	373	33.8	1.5	73.94	110.95
52	Phule Champion	67	70.5	3.75	204.4	102.2	15.1	13.9	360.7	32.85	1.4	69.89	112.6
53	Phule Maharshi	70	72.5	2.75	215.5	112.4	17.9	13.7	329.35	52.35	2	71.32	107.53
Range Lowest		61.5	63	1	89.8	29.2	14.9	11.9	129.95	20.1	1.4	55.67	35.33
Range Highest		90	93	5.25	215.5	112.4	24.5	19.8	459.2	52.35	2.2	84.65	124.49
Mean		75.61	78.73	3.1	133.42	66.12	19.16	14.98	271.44	34.37	1.87	70.27	72.84
C.V. (%)		2.05	2.16	18.33	1.57	3.55	8.87	11.72	1.1	4.95	8.51	2.9	4.28
C.D. at 5%		3.12	3.41	1.14	4.2	4.71	3.41	3.52	5.99	3.41	0.32	4.08	6.26

DT- Days to 50 % tasseling, **DS**- Days to 50% silking, **ASI** - Anthesis silking interval, **PH** - Plant height, **EH** - Ear height, **EL** – Ear length, **EG** - Ear girth, **NGPE** - Number of grains per ear, **HSW** - Hundred seed weight, **NCPP** - Number of cobs per plant, **SP**-Shelling percentage, **GYPP**- Grain yield per plant.

4.3 Variability studies

An attempt has been made in present study to estimate various genetical parameters which help in farming an effective breeding programme for making a improvement in desirable direction.

The characters under investigation were analysed for various parameters such as genotypic variance ($\sigma^2 g$), phenotypic variance ($\sigma^2 p$), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense), genetic advance (GA) and expected genetic advance as percentage mean (EGA). In population improvement, for improvement of a character, determination of extent of genetic variability is very important. Presence of wide range of variability in the experimental material will increase the chance of selecting desired genotype. The results are presented in table 4.3 and figure 4.1.

Total variability can be divided into heritable and non-heritable components by estimating genotypic and phenotypic coefficients of variation along with genetic advance. Effective genetic improvement of quantitative traits typically depends on a clear understanding of the nature and magnitude of variability present in the material, as well as the degree to which the desirable traits are inherited.

In the current study, 53 distinct maize genotypes were evaluated to assess their genotypic potential. All genotypes exhibited notable differences in their average performance across the various traits analysed. The findings from the variability analysis, which involved estimating parameters such as genotypic and phenotypic variance, phenotypic and genotypic coefficients of variation, heritability percentage and genetic advance as a percentage of the mean, are summarized in Table 4.3. The results have been organized and presented trait-wise.

These findings are consistent with the results reported by Antony et al. (2024), who observed high heritability (>90%) and low genetic advance for tasseling traits in maize inbred lines, suggesting limited scope for selection. Similarly, Bhusal *et al.* (2017) and Kharel *et al.* (2017) also reported high heritability with low genetic gain for days to tasseling, attributing it to non-additive gene effects. Additionally, Ghimire and Timsina (2015) emphasized that such traits are more effectively improved through hybrid breeding rather than direct selection. Magar *et al*. (2021) also supported this view by reporting very high heritability but low GA, reinforcing that direct phenotypic selection would be inefficient.

Collectively, this evidence suggests that while days to 50% tasseling is heritable, its improvement via selection might not yield substantial genetic gain. Instead, exploiting heterosis through hybridization or using recurrent selection methods might be more suitable for enhancing this trait.

4.3.1 Days to 50 % tasseling

For the trait days to 50% tasseling the genotypic and phenotypic variances were recorded as 59.50 and 60.70 respectively. The genotypic coefficient of variation (GCV) was lower at 10.20% compared to the phenotypic coefficient of variation (PCV) which is about 10.30%. The heritability of this trait was estimated at 98%, accompanied by a high genetic advance as a percentage of the mean, recorded at 20.80%.

Similar findings have been reported by various researchers, reinforcing the interpretation that days to 50% tasseling is a trait with high heritability but moderate to low genetic advance by Antony *et al.* (2024), Bhusal *et al.* (2017), Ghimire & Timsina (2015), Kharel *et al.* (2017) and Magar *et al.* (2021)

4.3.2 Days to 50% silking

The findings of the present study showed a low magnitude of both GCV (10.55) and PCV (10.66), suggesting limited variability for this trait. Although the trait exhibited high broad-sense heritability (97.90%), the genetic gain as a percentage of the mean was high (21.51%). This indicates that the high heritability is likely attributed to additive genetic effects and as a result, selection for improvement of this trait may be less effective.

These findings are consistent with the reports of Bisen *et al.* (2018), Jakhar *et al.* and (2017) who also observed high heritability coupled with low to moderate genetic advance for flowering traits, suggesting that selection alone may not be highly effective for yield improvement via this trait.

4.3.3 Anthesis silking interval

The Anthesis-Silking interval showed a high genotypic coefficient of variation (GCV) of 29.34% and a high phenotypic coefficient of variation (PCV) of 32.07%.

This trait exhibited high heritability (83%) and a high genetic advance as a percentage of the mean (55.31%).

These findings are in accordance with the results of Bello *et al.* (2010) found that ASI exhibited high heritability and genetic advance, indicating its effectiveness for selection under moisture stress conditions, Zaidi *et al.* (2004) highlighted the importance of ASI as a key trait for drought tolerance, showing significant variability and heritability, making it a reliable trait in stress breeding programs and Sahoo *et al.* (2020) also reported high heritability and genetic advance for ASI in maize, suggesting it is governed by additive genes and is suitable for selection in breeding.

4.3.4 Plant height

For plant height, the phenotypic and genotypic variances were 580.24 and 578.35 respectively. The genotypic coefficient of variation (GCV) was 18.02%, which was slightly lower than the phenotypic coefficient of variation (PCV) at 18.05%. This trait exhibited high heritability (99.70%) along with a notable genetic advance as a percentage of the mean, recorded at 37.07%.

These findings are consistent with those reported by Bisen *et al.* (2018) and Jakhar *et al.* (2017), who also observed high heritability and genetic advance for plant height, reinforcing the potential of this trait in contributing to maize improvement programs through selection.

4.3.5 Ear height

For ear height, the genotypic and phenotypic variances were 230.78 and 232.61 respectively. The genotypic coefficient of variation (GCV) was 22.97%, slightly lower than the phenotypic coefficient of variation (PCV) of 23.06%. This trait showed high heritability at 99.20% and a genetic advance as a percentage of the mean of 47.14%.

These findings are in agreement with Bisen *et al.* (2018) and Jakhar *et al.* (2017), who reported high heritability and genetic advance for ear height, highlighting its potential role in indirect selection for improving grain yield.

4.3.6 Ear length

The phenotypic and genotypic variances for ear length were 4.00 and 2.64 respectively. The genotypic coefficient of variation (GCV) for ear length was 8.48%, which was lower than the phenotypic coefficient of variation (PCV) at 10.44%. This trait exhibited high heritability of 66% along with moderate genetic advance as a percentage of the mean of 14.20%.

These findings align with the results of Chauhan et al. (2023), who reported moderate heritability and low genetic advance for ear length in maize, suggesting complex inheritance patterns and the potential role of dominance or epistasis.

4.3.7 Ear girth

Ear girth showed genotypic and phenotypic variances of 2.00 and 3.09 respectively. The genotypic coefficient of variation (GCV) was 9.44%, which was lower than the phenotypic coefficient of variation (PCV) at 11.73%. This trait demonstrated moderate heritability at 64.00% and a genetic advance as a percentage of the mean of 15.64%.

These results are in agreement with the findings of Kumar *et al.* (2018) and Yadav *et al.* (2023), who also observed moderate heritability and low genetic advance for ear girth in maize, suggesting complex genetic inheritance and a lower potential for direct selection gain.

4.3.8 Number of grains per ear

The number of grains per ear exhibited genotypic and phenotypic variances of 6373.18 and 6377.16 respectively. The genotypic coefficient of variation (GCV) was 29.41%, slightly lower than the phenotypic coefficient of variation (PCV) at 29.42%. This trait demonstrated high heritability at 99.90% and a substantial genetic advance as a percentage of the mean, recorded at 60.56%.

Similar trends were observed by Bello *et al.* (2012) and Patel *et al.* (2014), who reported high heritability and genetic advance for the number of grains per ear, concluding that this trait could be reliably selected for improving yield potential in maize.

4.3.9 Hundred seed weight

For 100-seed weight, the phenotypic and genotypic variances were 43.37 and 41.98 respectively. The genotypic coefficient of variation (GCV) was 18.85%, which was slightly lower than the phenotypic coefficient of variation (PCV) at 19.16%. This trait showed high heritability at 96.80% and high genetic advance as a percentage of the mean of 38.21%.

Similar findings were reported by Abdulmalik *et al.* (2015) and Singh *et al.* (2017), who noted high heritability and genetic advance for 100-seed weight, indicating the reliability of this trait for yield enhancement through selection.

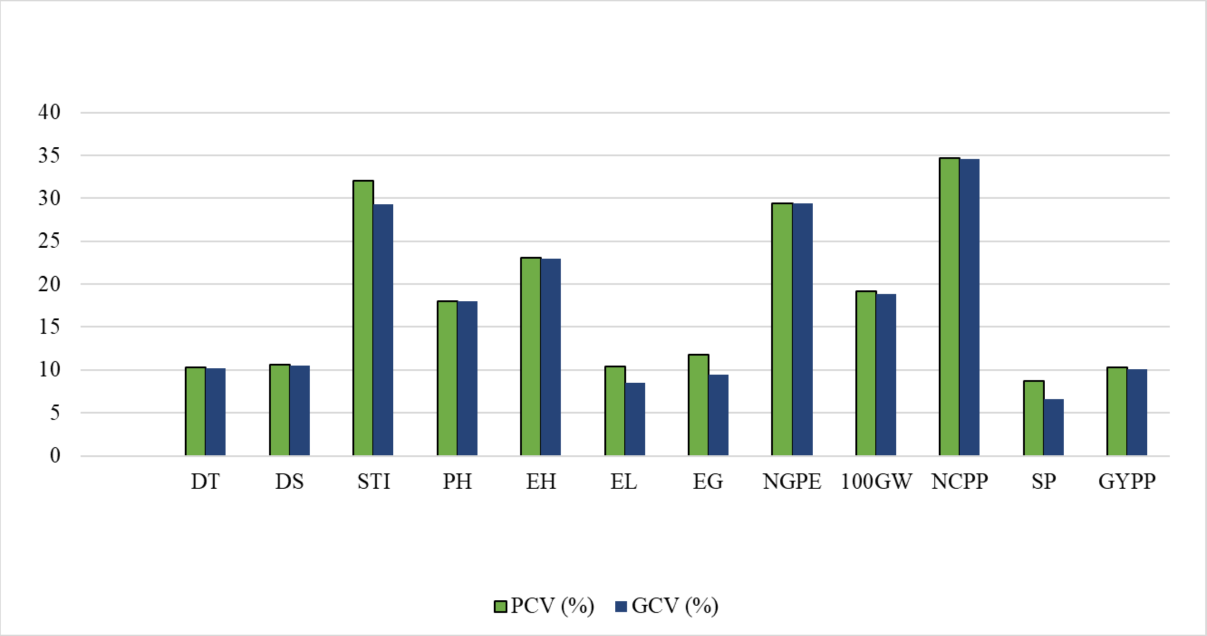

Fig.4.1. Genotypic and Phenotypic coefficient of variation for twelve characters in maize

DT- Days to 50 % tasseling**, DS**- Days to 50% silking**, ASI -** Anthesis silking interval**, PH -** Plant height**, EH -** Ear height**, EL -** Ear length**, EG -** Ear girth**, NGPE -** Number of grains per ear**, HSW -** Hundred seed weight**, NCPP -** Number of cobs per plant, **SP**-Shelling percentage, **GYPP**- Grain yield per plant.

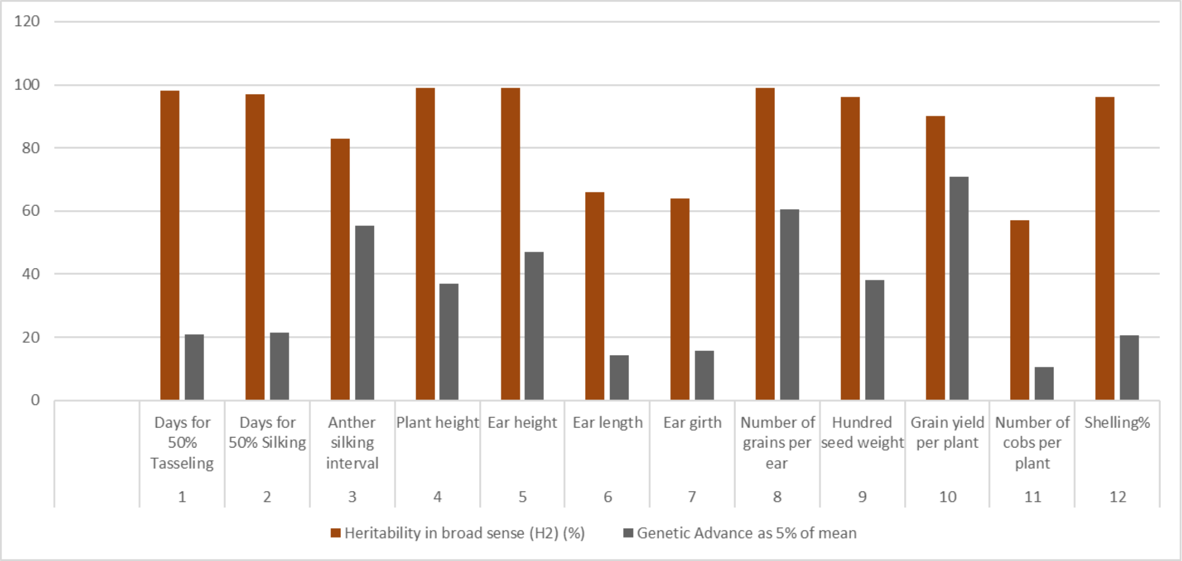

Fig.4.2. Heritability and Genetic advance as per cent of mean for twelve characters in maize

4.3.10 Grain yield per plant

Grain yield per plant showed genotypic and phenotypic variances of 634.66 and 639.53 respectively. The genotypic coefficient of variation (GCV) was 34.58%, which was slightly lower than the phenotypic coefficient of variation (PCV) at 34.71%. This trait exhibited high heritability at 99.20% and a notable genetic advance as a percentage of the mean, recorded at 70.97%.

Similar trends were reported by Meena *et al.* (2018) and Ganesan *et al.* (2017), who found high heritability and high genetic advance for grain yield per plant in maize, supporting the use of this trait in selection strategies for genetic improvement.

4.3.11 Number of cobs per plant

The number of cobs per plant exhibited genotypic and phenotypic variances of 0.01 and 0.02 respectively. The genotypic coefficient of variation (GCV) was 6.63%, which was lower than the phenotypic coefficient of variation (PCV) at 8.72%. This trait showed moderate heritability at 57.90% and a genetic advance as a percentage of the mean of 10.40%.

Similar results were reported by Patel *et al.* (2014) and Ravindra *et al*. (2019), who observed moderate heritability and low genetic advance for the number of cobs per plant in maize, indicating that this trait is more influenced by environment and is governed by non-additive gene action.

4.3.12 Shelling percentage

Shelling per cent exhibited genotypic and phenotypic variances of 50.50 and 52.29 respectively. The genotypic coefficient of variation (GCV) was 10.11%, slightly lower than the phenotypic coefficient of variation (PCV) at 10.29%. This trait demonstrated high heritability at 96.60% along with a genetic advance as a percentage of the mean of 20.47%.

Similar observations were made by Gurbuz *et al.* (2020) and Ramesh *et al.* (2018), who also reported high heritability and moderate genetic advance for shelling percentage in maize. These findings reinforce the idea that this trait is largely governed by additive genes, making it a suitable candidate for selection-based improvement.

Table 4.3: Estimates of variability parameters for twelve characters for yield and yield contributing characters in fifty-three genotypes of maize

Sr. No	Characters	Mean	Range		Phenotypic Variance	Genotypic Variance	PCV (%)	GCV (%)	Heritability in broad sense (H^2) (%)	Genetic Advance as 5% of mean
			Min	Max						
1	Days for 50% Tasseling	75.61	61.50	90	60.70	59.50	10.30	10.20	98.00	20.80
2	Days for 50% Silking	78.72	63.00	93	70.46	69.02	10.66	10.55	97.70	21.51
3	Anther silking interval	3.09	1.00	5.25	0.98	0.82	32.07	29.34	83.70	55.31
4	Plant height	133.42	89.80	215.5	580.24	578.35	18.05	18.02	99.70	37.07
5	Ear height	66.11	29.20	112.4	232.61	230.78	23.06	22.97	99.20	47.14
6	Ear length	19.15	14.90	24.5	4.00	2.64	10.44	8.48	66.00	14.20
7	Ear girth	14.98	11.90	19.8	3.09	2.00	11.73	9.44	64.70	15.64
8	Number of grains per ear	271.43	129.95	459.2	6377.16	6373.18	29.42	29.41	99.90	60.56
9	Hundred seed weight	34.36	20.10	52.35	43.37	41.98	19.16	18.85	96.80	38.21
10	Grain yield per plant	1.87	1.40	2.2	639.53	634.66	34.71	34.58	99.20	70.97
11	Number of cobs per plant	70.26	55.66	84.645	0.02	0.01	8.72	6.63	57.90	10.40
12	Shelling percentage	70.26	35.33	124.49	52.29	50.50	10.29	10.11	96.60	20.47

GCV = Genotypic coefficient of variation, **PCV** = Phenotypic coefficient of variation.

4.4 Correlation studies

The correlation coefficients among fifty-three genotypes were analyzed to examine the relationships between yield and various traits at both phenotypic and genotypic levels. This investigation was conducted on maize inbred lines, including three check varieties, across fourteen traits to assess the strength and direction of their association with yield per plant. Correlation estimates were tested for significance at the 5%, 1% and 0.1% levels by comparing them with corresponding tabulated values. The genotypic and phenotypic correlation coefficients for the twelve traits across fifty genotypes are summarized in Tables 4.4 and 4.5 and illustrated in Figures 4.2 and 4.3.

4.4.1 Days to 50% tasseling

The trait days to 50% tasseling showed a positive and significant correlation with days to 50% silking (G = 0.9992, P = 0.9936), anthesis silking interval (G = 0.7037, P = 0.5824) and number of cobs per plant (G = 0.4762, P = 0.305), at both genotypic and phenotypic levels. It exhibited positive non-significant association with ear height (G = 0.0077, P = 0.012) and ear girth (G = 0.169, P = 0.1166), at both genotypic and phenotypic levels. Additionally, ear length (P = 0.0064) exhibited a positive association at the phenotypic level only. Conversely, days to 50% tasseling had a non-significant negative correlation with plant height (G = -0.048, P = -0.0468), number of grains per ear (G = -0.0715, P = -0.0708), hundred seed weight (G = -0.1144, P = -0.1142) and Shelling percentage (G = -0.1438, P = -0.125), at both genotypic and phenotypic levels. Additionally, ear length (G = -0.005) exhibited a negatively non-significant association at the genotypic level only.

These findings are in agreement with findings by Ahmed *et al.* (2020), Tejaswini *et al.* (2022) and Gogoi *et al.* (2025), highlighting the role of synchronized flowering in enhancing yield traits. The non-significant positive association with ear height and girth aligns with results from Prakash *et al.* (2019) and Chaurasia *et al.* (2020). The negative correlation with plant height, grain number per ear, 100 seed weight and shelling percentage supports observations by Malik *et al.* (2005) and Zarei *et al.* (2012), indicating potential yield penalties with delayed tasseling. These results emphasize the importance of early tasseling as a desirable trait in maize improvement programs.

4.4.2 Days to 50% silking

Days to 50% silking showed a positive and significant correlation both genotypically and phenotypically with anthesis silking interval (G = 0.7381, P = 0.6496) and number of cobs per plant (G = 0.4682, P = 0.2975).

These findings are in close agreement with those of Ahmed *et al.* (2020), Tejaswini *et al.* (2022) and Gogoi *et al.* (2025), who reported strong associations among flowering traits and yield components. Similar correlations were also noted by Al-Rawi *et al.* (2024) and Amegbor *et al.* (2022), emphasizing the role of timely silking in optimizing reproductive efficiency and cob formation in maize. These results confirm that early and synchronized flowering traits such as tasseling and silking are critical indicators of improved yield performance.

4.4.3 Anthesis silking interval

The anthesis-silking interval exhibited a positive and significant correlation both genotypically and phenotypically with ear height (G = 0.2853, P = 0.2364) and number of cobs per plant (G = 0.3575, P = 0.2098). Additionally, it showed a significant positive correlation with plant height (P = 0.2232) at phenotypic level only.

A similar trend was reported by Ahmed *et al.* (2020), Gogoi *et al.* (2025) and Tejaswini *et al.* (2022), highlighting the interdependence of flowering traits and ear development. The significant phenotypic association of ASI with plant height also aligns with the findings of Al-Rawi *et al.* (2024) and Amegbor *et al.* (2022), suggesting that taller plants may exhibit longer intervals under certain environmental conditions. These results reaffirm ASI as a critical trait influencing reproductive efficiency and yield potential in maize.

4.4.4 Plant height

This trait demonstrated a positive and significant correlation with ear height (G = 0.891, P = 0.8801), grain yield per plant (G = 0.3115, P = 0.3103), at both genotypic and phenotypic levels. Additionally, it showed positive correlation with number of grains per ear (0.2146) and hundred seed weight (0.2432) only at phenotypic level. On the other hand, plant height showed a significant negative correlation with number of cobs per plant (G = -0.3923, P = -0.2407).

These results are consistent with findings by Ahmed *et al.* (2020), Gogoi *et al.* (2025) and Prakash *et al.* (2019), who also reported that taller plants tend to support better ear placement and yield. Its positive association at the phenotypic level with ASI, number of grains per ear and hundred seed weight is in line with results from Al-Rawi *et al.* (2024) and Tejaswini *et al.* (2022), suggesting partial influence on reproductive and grain-filling traits. The significant negative correlation with number of cobs per plant agrees with the findings of Malik *et al.* (2005) and Chaurasia *et al.* (2020), indicating that excessive vegetative growth may limit cob production.

4.4.5 Ear height

Ear height exhibited a significant positive correlation with grain yield per plant (G = 0.3107, P = 0.3078), at both genotypic and phenotypic levels. Additionally, ear height showed a significant positive association with the hundred seed weight (P = 0.2156) only at phenotypic level.

These findings are consistent with the results of Ahmed et al. (2020), Gogoi *et al.* (2025) and Tejaswini *et al.* (2022), who also reported strong interrelations among vegetative growth, flowering traits and yield. The significant phenotypic association with hundred seed weight aligns with observations by Al-Rawi *et al.* (2024) and Prakash *et al.* (2019), suggesting that higher ear placement may indirectly contribute to grain development. These associations indicate the importance of ear height as a contributing factor to overall plant productivity.

4.4.6 Ear length

This trait exhibited a positive and significant correlation with ear girth (G = 0.2776) only at the genotypic level. In contrast, cob length showed a negative and significant association with plant height (G = -0.3666, P = -0.2502) and ear height (G = -0.342, P = -0.2329), at both genotypic and phenotypic levels.

Similar results were observed by Ahmed *et al.* (2020) and Tejaswini *et al.* (2022), who emphasized the contribution of cob girth to cob development. Conversely, its significant negative association with plant height and ear height at both genotypic and phenotypic levels aligns with the observations of Gogoi *et al.* (2025) and Al-Rawi *et al.* (2024), indicating that taller plants with higher ear placement may not necessarily produce longer cobs. These results suggest that cob length may be influenced by compact plant architecture and could serve as a selection trait for improving ear quality.

4.4.7 Ear girth

This trait also demonstrated a positive and significant correlation ear length (G = 0.2776) only at the genotypic level. Additionally, girth showed a negative and non-significant relationship with grain yield per plant (G = -0.0013, P = -0.0075), at both genotypic and phenotypic levels, these results aligning with the findings of Ahmed *et al.* (2020) and Tejaswini *et al.* (2022), who reported similar associations among cob-related traits. However, its negative and non-significant correlation with grain yield per plant is in agreement with Al-Rawi *et al.* (2024) and Gogoi *et al.* (2025), indicating that cob girth alone may not directly influence overall yield performance. These observations suggest that while cob girth is linked with ear development, it may have limited value as a direct selection trait for yield improvement.

4.4.8 Number of grains per ear

The number of grains per ear showed a significant and positive correlation with shelling percentage (G = 0.3063, P = 0.2941) and grain yield per plant (G = 0.4461, P = 0.4444), at both genotypic and phenotypic levels. Additionally, plant height (P = 0.2146) exhibited significant and positive correlation only at the phenotypic level.

Number of grains per ear showed a significant positive correlation with shelling percentage and grain yield per plant at both genotypic and phenotypic levels, supported by Ahmed *et al.* (2020) and Tejaswini *et al.* (2022). A significant phenotypic correlation with plant height was also observed, aligning with results from Gogoi *et al.* (2025), suggesting that taller plants may slightly influence grain development. These results highlight the importance of grain number as a key determinant of yield and shelling efficiency in maize.

4.4.9 Hundred seed weight

The 100-seed weight showed a positive and significant correlation with grain yield per plant (G = 0.3288, P = 0.3231) at both genotypic and phenotypic levels. Additionally, it exhibited a positive and significant association with the plant height (P = 0.2432) and ear height (P = 0.2156), only at phenotypic level.

Similar results were reported by Ahmed *et al.* (2020) and Tejaswini *et al.* (2022), who identified seed weight as a major contributor to yield. Its significant phenotypic association with plant height and ear height also aligns with findings from Gogoi *et al.* (2025), suggesting that taller plants may favor better grain filling. These results emphasize the role of 100-seed weight as a reliable selection trait for improving grain yield in maize.

4.4.10 Number of cobs per plant

The number cobs per plant showed a significant and positive correlation with days to 50% tasseling (G = 0.4762, P = 0.305), days to 50% silking (G = 0.4682, P = 0.2975) and anthesis silking interval (G = 0.3575, P = 0.2098) at both genotypic and phenotypic levels. Number of cobs per plant showed negative and significant association with plant height (G = -0.3923, P = -0.2407), at both genotypic and phenotypic levels. Additionally, this trait had shown a negative and significant association with grain yield per plant at the genotypic level (G = -0.2959) and a negative but non-significant association at the phenotypic level (P =-0.2225).

Similar results were reported by Ahmed *et al.* (2020) and Tejaswini *et al.* (2022). Its significant negative association with plant height aligns with findings from Gogoi *et al.* (2025), suggesting that increased vegetative growth may limit cob formation. Additionally, the negative correlation with grain yield per plant, particularly significant at the genotypic level, reflects observations by Al-Rawi *et al.* (2024), indicating that more cobs per plant do not necessarily translate to higher yield due to possible resource competition. This suggests the need for balanced selection to optimize both cob number and grain productivity.

4.4.11 Shelling percentage

At both the genotypic and phenotypic levels, this trait also demonstrated a positive and significant correlation with number of grains per ear (G = 0.5333, P = 0.2941) and grain yield/plant (G = 0.4068, P = 0.396), indicating that the environment has the least impact on these characters' expression.

These findings are supported by Ahmed *et al.* (2020) and Tejaswini *et al.* (2022), suggesting that shelling percentage is strongly influenced by genetic factors with minimal environmental effect. This highlights its reliability as a stable and important trait for improving grain yield in maize.

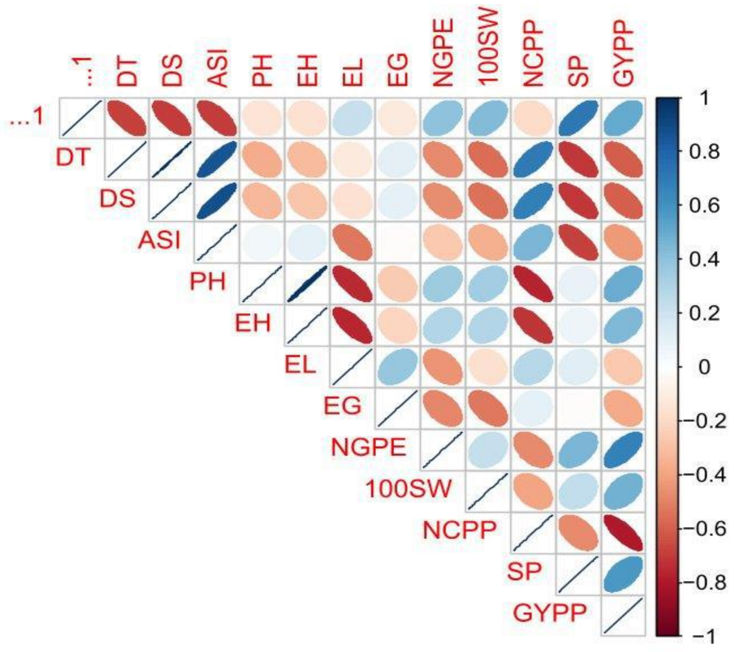

Fig.4.3a. Genotypic correlation plot for twelve characters in maize

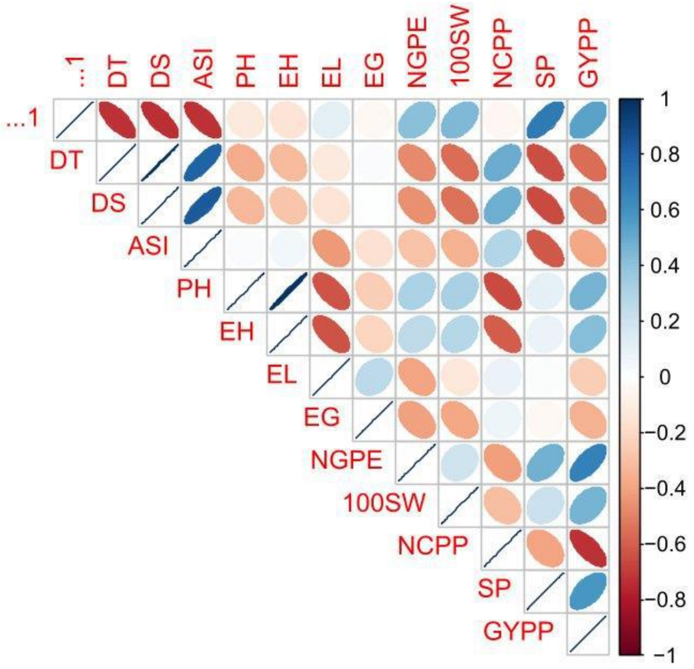

Fig.4.3b. Phenotypic correlation plot for twelve characters in maize

Table 4.4: Genotypic correlation coefficient for different characters in Maize

	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
DT	1 **	0.9992 **	0.7037 **	-0.048	0.0077	-0.005	0.169	-0.0715	-0.1144	0.4762 **	-0.1438	-0.0322
DS		1 **	0.7381 **	-0.0199	0.0321	-0.0335	0.1574	-0.0696	-0.1033	0.4682 **	-0.1496	-0.0335
ASI			1 **	0.2584	0.2853 *	-0.262	0.1608	0.0678	0.0555	0.3575 **	-0.1089	0.0492
PH				1 **	0.891 **	-0.3666 **	0.0419	0.2156	0.2542	-0.3923 **	0.1094	0.3115 *
EH					1 **	-0.342 *	0.0935	0.1561	0.2172	-0.2524	0.1462	0.3107 *
EL						1 **	0.2776 *	-0.1955	0.0327	0.1739	0.1396	0.022
EG							1 **	-0.1009	-0.1174	0.0893	0.1904	-0.0013
NGPE								1 **	0.1162	-0.0448	0.3063 *	0.4461**
HSW									1 **	0.0416	0.1687	0.3288 *
NCPP										1 **	-0.0148	-0.2959*
SP											1 **	0.4068**
GYPP												1 **

**** - Significant at p = 0 .01 * - Significant at p = 0. 05**

DT- Days to 50 % tasseling, **DS-** Days to 50% silking, **ASI -** Anthesis silking interval, **PH -** Plant height, **EH -** Ear height, **EL -** Ear length, **EG -** Ear girth, **NGPE -** Number of grains per ear, **HSW -** Hundred seed weight, **NCPP -** Number of cobs per plant, **SP**-Shelling percentage, **GYPP**- Grain yield per plant.

Table 4.5: Phenotypic correlation coefficient for different characters in maize

	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
DT	1 **	0.9936**	0.5824**	-0.0468	0.012	0.0064	0.1166	-0.0708	-0.1142	0.305 **	-0.125	-0.0356
DS		1 **	0.6496**	-0.0202	0.0346	-0.0166	0.0987	-0.0685	-0.1058	0.2975**	-0.1362	-0.0352
ASI			1 **	0.2232 *	0.2364 *	-0.128	0.0516	0.0586	0.0497	0.2098 *	-0.0838	0.0423
PH				1 **	0.8801**	-0.2502**	0.0287	0.2146 *	0.2432 *	-0.2407*	0.1068	0.3103**
EH					1 **	-0.2329 *	0.0665	0.1545	0.2156 *	-0.1594	0.1382	0.3078**
EL						1 **	0.1791	-0.1424	0.0447	0.0365	0.084	0.0099
EG							1 **	-0.0752	-0.0604	0.0981	0.1386	-0.0075
NGPE								1 **	0.1133	-0.0286	0.2941**	0.4444**
HSW									1 **	0.0567	0.1486	0.3231**
NCPP										1 **	-0.0088	-0.2225
SP											1 **	0.396 **
GYPP												1 **

**** - Significant at p = 0 .01 * - Significant at p = 0. 05**

DT- Days to 50 % tasseling, **DS-** Days to 50% silking, **ASI -** Anthesis silking interval, **PH -** Plant height, **EH -** Ear height, **EL -** Ear length, **EG -** Ear girth, **NGPE -** Number of grains per ear, **HSW -** Hundred seed weight, **NCPP -** Number of cobs per plant, **SP**-Shelling percentage, **GYPP**-Grain yield per plant.

4.5 Path coefficient analysis for grain yield per plant

Since correlation studies by themselves are unable to clearly depict the direct and indirect effects of yield-contributing features on grain production, path analysis was employed to investigate these effects. The degree to which a characteristic can be reliably selected for indirectly to boost grain yield is shown by its direct effect on grain yield. Selecting for a trait is likely to be successful if its direct effect and correlation are both strong and substantial. This is because the correlation reflects the actual relationship between the trait and grain yield. Table 4.6 and Figure 4.3a and 4.3b showed the genotypic and phenotypic correlations between the direct and indirect effects of yield contributing variables and grain production per plant.

The path coefficient analysis, a statistical device developed by Wright (1921), which takes into account the cause and effect relation between the variables is unique in partitioning the association into direct and indirect effect through other independent variables. The comparative significance of the causal elements involved is also measured by the path coefficient analysis. The overall correlation value is subdivided into a causal scheme in this straightforward standardized partial regression analysis.

At the genotypic level, several traits showed a positive direct impact on grain yield per plant. These included days to 50% silking (4.7878), ear height (0.3896), ear length (0.2112), ear girth (0.0085), number of grains per ear (0.4195), hundred seed weight (0.2712) and shelling % (0.2429). On the other hand, traits such as days to 50% tasseling (-4.3659), anthesis silking interval (-0.2268), plant height (-0.3786) and number of cobs per plant (-0.4538) exhibited a negative direct effect on grain yield. These results, in line with findings by Bisen *et al*. (2018) and Ahmed *et al.* (2020), suggest that emphasis should be placed on reproductive efficiency and grain parameters for effective genetic enhancement of yield in maize.

At the phenotypic level, several traits showed a positive direct influence on grain yield per plant. These included days to 50% tasseling (1.2335), anthesis silking interval (0.0882), ear height (0.2137), ear length (0.0816), number of grains per ear (0.3309), hundred seed weight (0.2423) and shelling % (0.2406). In contrast, negative direct effects on grain yield were observed for days to 50% silking (-1.1496), plant height (-0.0746), ear girth (-0.04) and number of cobs per plant (-0.2664). These observations are consistent with the findings of Bisen *et al*. (2018) and Tejaswini *et* *al*. (2022), reinforcing the value of grain and ear traits in enhancing phenotypic grain yield performance. In the present study, the path coefficient analysis carried at genotypic level and the results are discussed as below.

4.5.1 Days to 50% tasseling

The direct effect of days to 50% tasseling on grain yield per plant was negative (-4.366). It also exerted positive indirect effects on grain yield through traits such as plant height (0.2098), ear length (0.022), number of grins per ear (0.3121), hundred seed weight (0.4995) and shelling % (0.6279). In contrast, it showed negative indirect effects via days to 50% silking (-4.3622), anthesis silking interval (-3.0721), ear height (-0.0336), ear girth (-0.7377) and number of cobs per plant (-2.0791).

4.5.2 Days to 50% silking

The direct effect of days to 50% silking on grain yield per plant was positive (4.7878). It also showed positive indirect effects on grain yield through days to 50% tasseling (4.7837), anthesis silking interval (3.5338), ear height (0.1537), ear girth (0.7536) and number of cobs per plant (2.2415). However, negative indirect effects were observed via plant height (0.0951), ear length (0.1603), number of grains per ear (0.3333), hundred seed weight (0.4945) and shelling % (0.7163).

4.5.3 Anthesis silking interval

The direct effect of anthesis silking interval on grain yield per plant was negative (-0.2268). Nevertheless, it exerted positive indirect effects on grain yield through ear length (0.0594) and shelling % (0.0247). In contrast, negative indirect effects were recorded via days to 50% tasseling (-0.1601), days to 50% silking (-0.1674), plant height (-0.0586), ear height (-0.0647), ear girth (-0.0365), number of grains per ear (-0.0154), hundred seed weight (-0.0126) and number of cobs per plant (-0.0811).

4.5.4 Plant height

The direct effect of plant height on grain yield per plant was negative (-0.3786). It also showed positive indirect effects through days to 50% tasseling (0.0182), days to 50% silking (0.0075), ear length (0.1388) and number of cobs per plant (0.1485). However, negative indirect effects were observed via anthesis silking interval (-0.0978), ear height (-0.3374), ear girth (-0.0159), number of grains per ear (-0.0816), hundred seed weight (-0.0963) and shelling % (-0.0414).

4.5.5 Ear height

The direct effect of ear height on grain yield per plant was positive (0.3896). However, it exerted positive indirect effects through days to 50% tasseling (0.003), days to 50% silking (0.0125), anthesis silking interval (0.1112), plant height (0.3471), ear girth (0.0364), number of grains per ear (0.0608), hundred seed weight (0.0846) and shelling % (0.057). In contrast, negative indirect effects were observed via ear length (-0.1332) and number of cobs per plant (-0.0984).

4.5.6 Ear length

The direct effect of ear length on grain yield per plant was positive (0.2112). It showed positive indirect effects through ear girth (0.0587), hundred seed weight (0.0069), number of cobs per plant (0.0367) and shelling % (0.0295). Conversely, negative indirect effects were recorded via days to 50% tasseling (-0.001), days to 50% silking (-0.0071), anthesis silking interval (-0.0554), plant height (-0.0774), ear height (-0.0722) and number of grains per ear (-0.0413).

4.5.7 Ear girth

The direct effect of ear girth on grain yield per plant was positive (0.0085). However, it exerted positive indirect effects through days to 50% tasseling (0.0014), days to 50% silking (0.00.13), anthesis silking interval (0.0014), plant height (0.0004), ear height (0.0008), ear length (0.0024), number of cobs per plant (0.0008) and shelling % (0.0016). In contrast, negative indirect effects were observed via number of grains per ear (-0.0009) and hundred seed weight (-0.001).

4.5.8 Number of grains per ear

The direct effect of number of grains per ear on grain yield per plant was positive (0.4195). However, it exerted positive indirect effects through anthesis silking interval (0.0285), plant height (0.0904), ear height (0.0655), hundred seed weight (0.0487) and shelling % (0.1285). In contrast, negative indirect effects were observed via days to 50% tasseling (-0.030), days to 50% silking (-0.0292), ear length (-0.082), ear girth (-0.0423) and number of cobs per plant (-0.0188).

4.5.9 Hundred seed weight

The direct effect of hundred seed weight on grain yield per plant was positive (0.2712). However, it exerted positive indirect effects through anthesis silking interval (0.015), plant height (0.069), ear height (0.0589), ear length (0.0089), number of grains per ear (0.0315), number of cobs per plant (0.0113) and shelling % (0.0458). In contrast, negative indirect effects were observed via days to 50% tasseling (-0.031), days to 50% silking (-0.028) and ear girth (-0.0318).

4.5.10 Number of cobs per plant

The direct effect of number of cobs per plant on grain yield per plant was negative (-0.4538). However, it exerted positive indirect effects through plant height (0.178), ear height (0.1146), number of grains per ear (0.0203) and shelling % (0.0067). In contrast, negative indirect effects were observed via days to 50% tasseling (-0.216), days to 50% silking (-0.2124), anthesis silking interval (-0.1622), ear length (-0.0789), ear girth (-0.0405) and hundred seed weight (-0.0189).

4.5.11 Shelling %

The direct effect of shelling % on grain yield per plant was positive (0.2429). However, it exerted positive indirect effects through plant height (0.0266), ear height (0.0355), ear length (0.0339), ear girth (0.0463), number of grains per ear (0.0744) and hundred seed weight (0.041). In contrast, negative indirect effects were observed via days to 50% tasseling (-0.035), days to 50% silking (-0.0363), anthesis silking interval (-0.0265) and number of cobs per plant (-0.0036).

These traits contribute to yield enhancement through their strong association with key yield components, as supported by Ahmed *et al.* (2020) and Bisen *et al.* (2018). In contrast, number of cobs per plant showed a significant negative indirect effect, suggesting possible resource competition. These insights underscore the importance of indirect contributors in trait-based yield improvement strategies.

Residual effect

Phenotypic and genotypic residual effects were 0.7591 and 0.7167 respectively indicating that some characters which had due weightage in selection for yield improvement are to be included.

Table 4.6: Genotypic path coefficient analysis showing direct (diagonal) and indirect effects of eleven causal variables on grain yield per plant in fifty-three genotypes of maize

	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
DT	**-4.366**	-4.3622	-3.0721	0.2098	-0.0336	0.022	-0.7377	0.3121	0.4995	-2.0791	0.6279	-0.0322
DS	4.7837	**4.7878**	3.5338	-0.0951	0.1537	-0.1603	0.7536	-0.3333	-0.4945	2.2415	-0.7163	-0.0335
ASI	-0.16	-0.1674	**-0.2268**	-0.0586	-0.0647	0.0594	-0.0365	-0.0154	-0.0126	-0.0811	0.0247	0.0492
PH	0.0182	0.0075	-0.0978	**-0.3786**	-0.3374	0.1388	-0.0159	-0.0816	-0.0963	0.1485	-0.0414	0.3115*
EH	0.003	0.0125	0.1112	0.3471	**0.3896**	-0.1332	0.0364	0.0608	0.0846	-0.0984	0.057	0.3107*
EL	-0.001	-0.0071	-0.0554	-0.0774	-0.0722	**0.2112**	0.0587	-0.0413	0.0069	0.0367	0.0295	0.022
EG	0.0014	0.0013	0.0014	0.0004	0.0008	0.0024	**0.0085**	-0.0009	-0.001	0.0008	0.0016	-0.0013
NGPE	-0.03	-0.0292	0.0285	0.0904	0.0655	-0.082	-0.0423	**0.4195**	0.0487	-0.0188	0.1285	0.4461**
HSW	-0.031	-0.028	0.015	0.069	0.0589	0.0089	-0.0318	0.0315	**0.2712**	0.0113	0.0458	0.3288 *
NCPP	-0.216	-0.2124	-0.1622	0.178	0.1146	-0.0789	-0.0405	0.0203	-0.0189	**-0.4538**	0.0067	-0.2959*
SP	-0.035	-0.0363	-0.0265	0.0266	0.0355	0.0339	0.0463	0.0744	0.041	-0.0036	**0.2429**	0.4068**

**** - Significant at p = 0 .01, * - Significant at p = 0. 05, G-genotypic, P-phenotypic, Residual effect = 0.7167**

DT- Days to 50 % tasseling, **DS**- Days to 50% silking, **ASI** - Anthesis silking interval, **PH** - Plant height, **EH** - Ear height, **EL** - Ear length, **EG** - Ear girth, **NGPE** - Number of grains per ear, **HSW** - Hundred seed weight, **NCPP** - Number of cobs per plant, **SP**-Shelling percentage, **GYPP**-Grain yield per plant.

Table 4.7: Phenotypic path coefficient analysis showing direct (diagonal) and indirect effects of eleven causal variables on grain yield per plot in fifty-three genotypes of maize

	DT	DS	ASI	PH	EH	EL	EG	NGPE	HSW	NCPP	SP	GYPP
DT	**1.2335**	1.229	0.7843	-0.0585	0.0122	0.0021	0.1675	-0.0877	-0.141	0.4477	-0.1655	-0.0356
DS	-1.145	**-1.1496**	-0.7909	0.023	-0.0384	0.0266	-0.1387	0.0794	0.1202	-0.4085	0.1641	-0.0352
ASI	0.0561	0.0607	**0.0882**	0.0211	0.0228	-0.0156	0.0081	0.0055	0.0046	0.0229	-0.0084	0.0423
PH	0.0035	0.0015	-0.0178	**-0.0746**	-0.0661	0.0219	-0.0025	-0.016	-0.0185	0.0218	-0.0081	0.3103 **
EH	0.0021	0.0071	0.0551	0.1893	**0.2137**	-0.0585	0.0163	0.0332	0.0463	-0.0408	0.0304	0.3078 **
EL	0.0001	-0.0019	-0.0145	-0.024	-0.0223	**0.0816**	0.0172	-0.0132	0.0032	0.0064	0.0086	0.0099
EG	-0.005	-0.0048	-0.0037	-0.0013	-0.0031	-0.0085	**-0.04**	0.0034	0.0033	-0.0038	-0.0063	-0.0075
NGPE	-0.024	-0.0228	0.0207	0.0712	0.0514	-0.0536	-0.0279	**0.3309**	0.0379	-0.0113	0.0993	0.4444 **
HSW	-0.028	-0.0253	0.0126	0.0602	0.0524	0.0095	-0.0199	0.0278	**0.2423**	0.0121	0.0384	0.3231 **
NCPP	-0.097	-0.0947	-0.069	0.0779	0.0509	-0.021	-0.0254	0.0091	-0.0133	**-0.2664**	0.0029	-0.2225
SP	-0.032	-0.0343	-0.0228	0.026	0.0342	0.0253	0.0378	0.0722	0.0381	-0.0026	**0.2406**	0.3960 **

**** - Significant at p = 0 .01, * - Significant at p = 0. 05, G-genotypic, P-phenotypic, Residual effect = 0.7591**

DT- Days to 50 % tasseling, **DS-** Days to 50% silking, **ASI -** Anthesis silking interval, **PH -** Plant height, **EH -** Ear height, **EL -** Ear length, **EG -** Ear girth, **NGPE -** Number of grains per ear, **HSW -** Hundred seed weight, **NCPP -** Number of cobs per plant, **SP**-Shelling percentage, **GYPP**-Grain yield per plant.

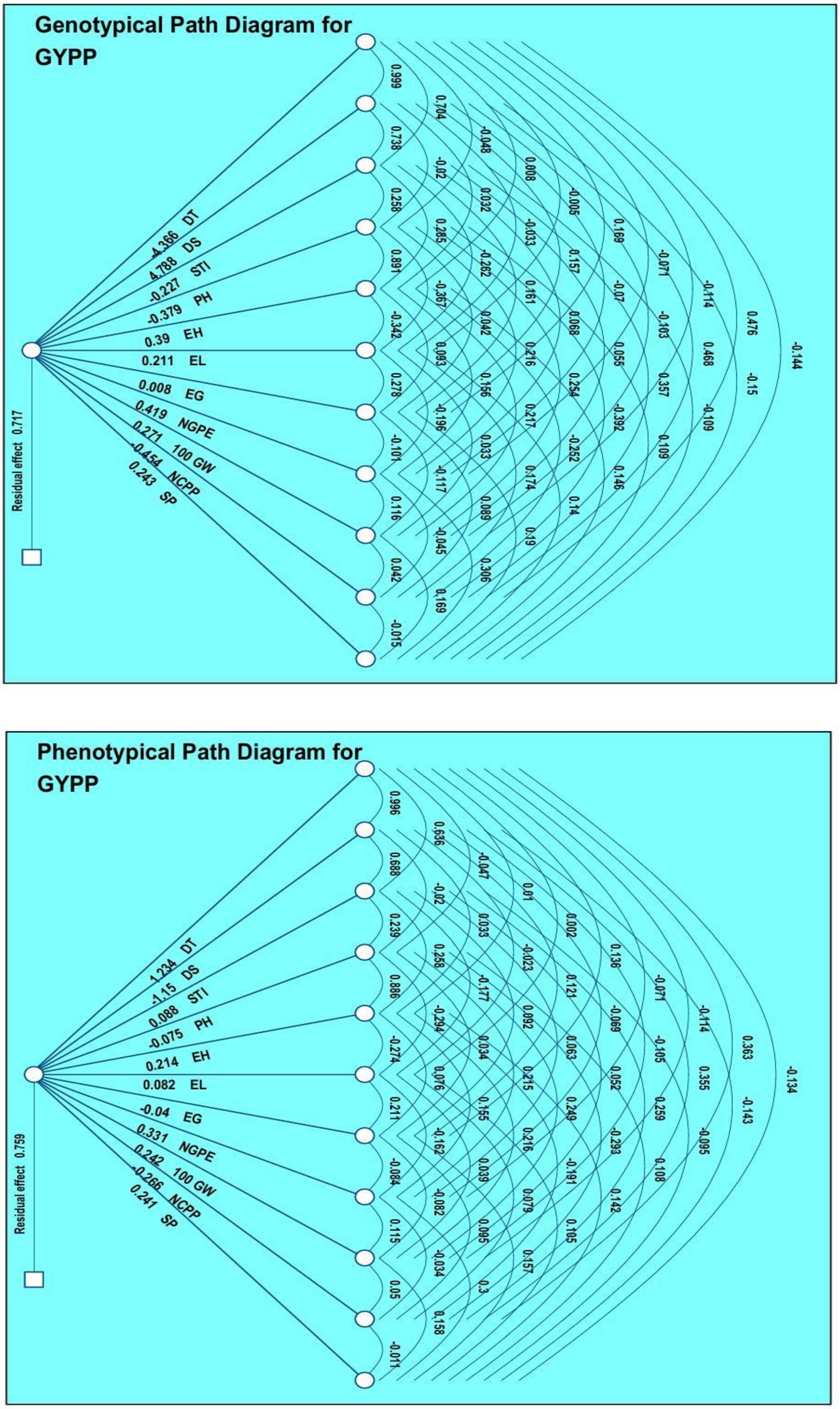

Fig 4.4 Genotypic and phenotypic path diagram for grain yield/plant

SUMMARY AND CONCLUSIONS

CHAPTER-V

SUMMARY AND CONCLUSION

The present investigation entitled “Genetic Variability, Correlation and Path analysis studies in Maize (*Zea mays* L.)” was carried out to obtain information on genetic variability, genotypic and phenotypic correlation coefficient and direct and indirect effects of yield contributing characters on yield through path coefficient analysis in maize undertaken with the following objectives.

- To study genetic variability for yield and yield attributing characters in maize.
- To study correlation of grain yield and yield attributing characters.
- To study the direct and indirect effect of yield contributing characters on grain yield.

The present investigation was carried out at experimental farm of Wheat and Maize Research Scheme, VNMKV, Parbhani during *rabi* (2024-2025). The experimental material was comprised of 50 diverse genotypes of maize along with three checks. The seeds of these genotypes (CIMMYT) were obtained from Wheat and Maize Research scheme, VNMKV Parbhani. The 50 genotypes along with three checks were evaluated in randomized block design (RBD) with two replications. The experimental material was assessed for twelve characters *viz.,* days to 50 % tasseling, days to 50% silking, anthesis silking interval, plant height, ear height, ear length, ear girth, number of grains per ear, hundred seed weight, grain yield per plant, number of cobs per plant and shelling %.

The analysis of variance revealed that the genotypes showed significant differences across all twelve traits studied, indicating substantial genetic variability among the germplasm accessions. This wide range of variation suggests considerable potential for selecting promising genotypes to improve grain yield. Based on performance across two replications, genotype V2201-51 exhibited the highest average grain yield per plant, followed by V2202-52, highlighting their suitability for use in hybridization programs aimed at yield enhancement. Genotypes V2199-5 and V2199-9 showed the earliest anthesis and silking, respectively, making them valuable candidates for developing early-maturing varieties. In terms of plant height, V2201-51 was identified as the shortest genotype, while the check variety Phule Maharshi was the tallest, suggesting their potential use in breeding programs targeting specific plant height preferences. Furthermore, V2202-44, Phule Maharshi, V2201-19, V2202-42, V2201-25, Phule Maharshi, V2202-44 and V2201-25 recorded the highest mean values for anthesis silking interval, ear height, ear length, ear girth, number of grains per ear, hundred seed weight, number of cobs per plant and shelling %, respectively. These traits make these genotypes particularly promising for contributing to grain yield improvement.

For the traits studied such as days to 50% tasseling, days to 50% silking, plant height, ear height, number of grains per ear, grain yield per plant and shelling percentage the small difference between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) suggests minimal environmental influence on their expression. This indicates that observed phenotypic differences likely reflect true genetic variation, making these traits reliable for selection in breeding programs. In contrast, traits like anthesis-silking interval, ear length, ear girth, 100-seed weight and number of cobs per plant exhibited moderate to large differences between PCV and GCV, implying that both genetic and environmental factors influence their expression. Furthermore, anthesis silking interval, ear length, ear girth and number of cobs per plant showed moderate heritability combined with moderate to high genetic advance as a percentage of the mean (at 5%), suggesting that selection for these traits would be effective in achieving genetic improvement. Overall, the study highlights grain yield per plant, plant height and number of grains per ear as traits with the highest values for PCV, GCV, heritability and genetic advance, making them strong candidates for selection to improve yield. On the other hand, traits such as days to 50% anthesis, days to 50% silking, ear length, ear girth and number of cobs per plant showed low PCV and GCV but high heritability along with moderate genetic advance, indicating they are mainly governed by additive genetic variance, though present at a lower magnitude.

The correlation analysis revealed that grain yield per plant was positively associated with several traits, including plant height, ear height, number of grains per ear, 100-seed weight and shelling %. These findings suggest that selecting germplasm lines with higher average values for these traits could effectively enhance maize grain yield. To further understand the relationships, path coefficient analysis was conducted to separate direct and indirect effects. Traits such as, plant height, ear height, number of grains per ear, 100 seed weight and shelling % exhibited strong significant direct effects on grain yield per plant. In contrast, number of cobs per plant showed significant negative indirect effects on grain yield, indicating that a greater number of cobs per plant negatively influence productivity.

In conclusion, the current study revealed important insights into various yield-related traits in maize improvement. Among the genotypes evaluated, V2201-51 and V2202-52 emerged as promising candidates due to their favourable performance in yield and associated traits. These genotypes hold potential as parental lines in hybridization programs aimed at producing hybrids with enhanced heterosis in the F1 generation or generating valuable transgressive segregants in subsequent generations. Additionally, genotypes V2199-5 and V2199-9 exhibited the earliest tasseling and silking, respectively, indicating their suitability for the development of early-maturing maize varieties.

LITERATURE CITED

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Abdulmalik, R. O., Bello, O. B., Azeez, M. A., & Afolabi, M. S. (2015). Genetic variability, heritability and genetic advance of some selected maize (*Zea mays* L.) varieties. *International Journal of Plant & Soil Science*, 8(5), 1–8.

Ahmed, N., Chowdhury, A. K., Uddin, M. S., & Rashad, M. M. I. (2020). Genetic variability, correlation and path analysis of exotic and local hybrid maize (*Zea mays* L.) genotypes. *Asian Journal of Medical and Biological Research*,6(1), 8-15.

Al-Rawi, O. H., Bedn, A. A., & Hamed, M. A. (2024). Genetic variability and path coefficient analysis for three-way cross in maize. SABRAO *J. Breed. Genet.,* 56(1), 204-210.

Amegbor, I. K., van Biljon, A., Shargie, N., Tarekegne, A., & Labuschagne, M. T. (2022). Heritability and associations among grain yield and quality traits in quality protein maize (QPM) and non-QPM hybrids. *Plants*, 11(6), 713.

Amini, Z., Khodambashi, M., & Houshmand, S. (2013). Correlation and path coefficient analysis of seed yield related traits in maize. *International Journal of Agriculture and Crop Sciences*, 5(19): 2217.

Antony, B. J., Kachapur, R. M., Naidu, G. K., Talekar, S. C., Zerka, M., & Harlapur, S. I. (2024). Genetic variability and character association among maize (*Zea mays* L.) Inbred lines. *Bangladesh Journal of Botany*, 53(1), 57-65.

Arsode, P., Krishna, M., Sunil, N., & Sree, S. V. (2018). Correlation studies for grain yield and its components in hybrids of quality protein maize (*Zea mays* L.). *Electronic Journal of Research Professor Jayashankar Telangana State Agricultural University*,46(2-3), 85-88.

Bello, O. B., Abdulmaliq, S. Y., Afolabi, M. S. and Ige, S. A. (2010). Correlation and path coefficient analysis of yield and agronomic characters among open pollinated maize varieties and their F_1 hybrids in a diallel cross. *African Journal of Biotechnology*, 9 (18): 2633-2639.

Bello, O. B., Ige, S. A., Azeez, M. A., Afolabi, M. S., Abdulmaliq, S. Y., & Mahamood, J. (2012). Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). *International Journal of Plant Research*, 2(5): 138-145.

Bello, O. B., Ige, S. A., Azeez, M. A., Afolabi, M. S., Abdulmaliq, S. Y., & Mahamood, J. (2010). Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). *International Journal of Plant Breeding and Genetics*, 4(2), 105–107.

Beulah, G., Marker, S., & Rajasekhar, D. (2018). Assessment of quantitative genetic variability and character association in maize (*Zea mays* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(1): 2813-2816.

Bharathiveeramani, B., Prakash, M. and Seetharam, A. (2012). Variability studies of quantitative characters in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, 3 (4): 995-997.

Bhusal, T., Lal, G. M., Marker, S. and Synrem, G. J. (2017). Genetic variability and traits association in maize (*Zea mays* L.) genotypes. *Annals of Plants and Soil Research*, 19 (1): 59-65.

Bisen, R., Kumar, R., & Mehta, A. K. (2018). Genetic variability, heritability and genetic advance studies in maize (*Zea mays* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, 7(1), 1723–1729.

Burton, G.W. (1952) Quantitative inheritance in grass. *Proceedings of 6th International Grass Land Congress,* 1, 17-23.

Chauhan, S. K., & Mohan, J. (2010). Estimates of variability, heritability and genetic advance in baby corn. *Indian Journal of Horticulture*, 67(4): 238-241.

Chaurasia, N. K., Nirala, R. B. P., Singh, B., & Mandal, S. S. (2020). Trait association and path coefficient analysis in maize (*Zea mays* L.) for grain yield and its attributes. *Journal of Pharmacognosy and Phytochemistry*, 9(6), 527-531.

Dar, I. A., Dar, Z. A., K., Sofi, P. A., Hussan, S., Dar, M. S., & Alie, W. (2018). Genetic variability studies involving drought tolerance related traits in maize genotypes. *Journal of Agriculture and Ecology Research International*, 14(2): 1-13.

Dewey, D.R. & K.H., Lu. (1959). A correlation and path analysis of component of crested wheat grass seed production. *Agronomy Journal*. 51;515-518.

Duvvada, S. K., Malik, G. C., Banerjee, M., & Saren, B. K. (2024). Correlation studies on growth, yield parameters and yield of maize as influenced by conservation tillage practices and site-specific nutrient management in maize (*Zea mays* L.). *Environment and Ecology*, 42(2A), 579-583.

Falconer, D.S. (1964). An introduction to quantitativegenetics. *Second Edition. Oliver and Boyd, Edinburgh. pp*. 312-324.

Ganesan, K. N., Kumar, D., & Rajeswari, S. (2017). Genetic variability and correlation studies for grain yield and its components in maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences*, 6(7), 2693–2700.

Ghimire, B. and Timsina, D. (2015). Analysis of yield and yield attributing traits of Maize Genotypes in Chitwan, Nepal. *World Journal of Agricultural Research*, 3 (5): 153-162.

Gogoi, D., Bordoloi, D., Sarma, A., & Barua, N. S. (2025). Correlation and path analysis of early inbred lines of Maize (*Zea mays* L.) for yield and yield related traits. *Indian Journal of Plant Genetic Resources,* 38(01), 123-130.

Gurbuz, F., Akin, E., & Akar, T. (2020). Genetic variability, heritability and genetic advance studies in maize (*Zea mays* L.). *Journal of Agricultural Sciences*, 26(1), 34–40.

Hepziba, S. J., Geetha, K. and Ibrahim, S. M. (2013). Evaluation of genetic diversity, variability, character association and path analysis in diverse inbreds of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, 4 (1): 1067-1072.

Hemavathy, A. T., Balaji, K., Ibrahim, S. M., Anand, G., & Sankar, D. (2008). Genetic variability and correlation studies in maize (*Zea mays* L.). *Agricultural Science Digest*, *28*(2), 112-114.

Izzam, A., Sohail, H. R. A., Shahzad Ali, M., & Hussain, Q. (2017). Genetic variability and correlation studies for morphological and yield traits in maize (*Zea mays* L.). *Pure and Applied Biology (PAB)*, *6*(4), 1234-1243.

Jakhar, D. S., Singh, R. and Kumar, A. (2017). Studies on path coefficient analysis in maize (*Zea mays* L.) for grain yield and its attributes. *International Journal of Current Microbiology and Applied Sciences*, 6: 2851-2856.

Jawaharlal, J., Reddy, G. L. and Kumar, R. S. (2011). Genetic variability and character association studies in maize. *Agricultural Science Digest*, 31 (3): 173-177.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47, 314-318.

Kandel, B. P., Sharma, B. K., Sharma, S., & Shrestha, J. (2018). Genetic variability, heritability and genetic advance estimates in maize (*Zea mays* L.) genotypes in Nepal. *Agricultura*, 107(3-4), 29-35.

Kapoor, R. and Batra, C. (2015). Genetic variability and association studies in maize (*Zea mays* L.) for green fodder yield and quality traits. *Electronic Journal of Plant Breeding*, 6 (1): 233-240.

Kharel, R., Ghimire, S. K., Ojha, B. R. and Koirala, K. B. (2017). Estimation of genetic parameters, correlation and path coefficient analysis of different genotypes of maize (*Zea mays* L*.). International Journal of Agriculture Innovations and Research*. 6 (1): 2319-1473.

Kumar, V., Singh, S. K., Bhati, P. K., Sharma, A., Sharma, S. K., & Mahajan, V. (2015). Correlation, path and genetic diversity analysis in maize (*Zea mays* L.). *Environment & Ecology,*33(2A), 971-975.

Lal, M. and Singh, D. (2014). Studies of variability using morphological and quality traits in Quality Protein Maize (*Zea mays* L.). *Electronic Journal of Plant Breeding.* 5 (3): 526-530.

Magar, B. T., Acharya, S., Gyawali, B., Timilsena, K., Upadhayaya, J., & Shrestha, J. (2021). Genetic variability and trait association in maize (*Zea mays* L.) varieties for growth and yield traits. *Heliyon*, 7(9).

Malik, H. N., Malik, S. I., Hussain, M. O. Z. A. M. I. L., Chughtai, S. U. R., & Javed, H. I. (2005). Genetic correlation among various quantitative characters in maize (*Zea mays* L.) hybrids. *Journal of Agriculture & Social Sciences*, 3: 262-265.

Meena, H. P., Kumar, B., & Singh, A. K. (2018). Genetic variability, heritability and genetic advance studies in maize (*Zea mays* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(2), 2686–2689.

Muhammad Akbar, Shakoor, M.S., Amerhussain and Muhmmad Sarwar. (2008). Evaluation of maize 3-way crosses through genetic variability, broad sense heritability, character association and path analysis. *J. Agric. Res., Lahore*, 46(1): 39-45.

Nagaraju, K. (2012). Studies on genetic variability for yield and yield attributing characters in maize (*Zea mays* L). Thesis submitted to Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Nataraj, V., Shahi, J. P., & Agarwal, V. (2014). Correlation and path analysis in certain inbred genotypes of maize (*Zea mays* L.) at Varanasi. *International journal of innovative Research and Development*, 3(1): 14-17.

Nemati, A., Sedghi, M., Sharifi, R. S., & Seiedi, M. N. (2009). Investigation of correlation between traits and path analysis of corn (*Zea mays* L.) grain yield at the climate of Ardabil region (Northwest Iran). *Notulae Botanicae Horti Agrobotanici Cluj-Napoca,* 37(1): 194-198.

Nzuve, F., Githiri, S., Mukunya, D. M., & Gethi, J. (2014). Genetic variability and correlation studies of grain yield and related agronomic traits in maize. *Journal of Agricultural Science*, 6(9), 166–176.

Olawamide, O. D. and Fayeun, L. S. 2020. Correlation and path coefficient analysis for yield and yield components in late maturing pro-vitamin a synthetic maize (*Zea mays* L.) breeding line. *Journal of Experimental Agriculture International*, 42 (1): 64-72.

Panse, V. G. and Sukhatme, P. V. (1978). *Statistical methods for agricultural workers.* Indian Council of Agricultural Research, New Delhi, 3, 235-246.

Panwar, L. L., Mahawar, R. K., & Narolia, R. S. (2013). Genetic variability and interrelationships among grain yield and yield components in maize. *Annals of Plant and Soil Research,* 15(1): 15-18.

Patel, D. A., Patel, R. A., Bhatt, R. K., & Pandya, H. M. (2014). Genetic variability, heritability and genetic advance for yield and its components in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding,* 5(4), 802–805.

Patil, S.M., Kumar Kamlesh, Singh Jakhar Dan, Rai Abhijit, Borle, U.M. and Singh Pargat (2016). Studies on variability, heritability, genetic advance and correlation in maize (*Zea mays* L.). *Int. J. Environ. Agric. Biotech.*, 9(6): 1103-11081.

Prakash, R., Ravikesavan, R., Vinodhana, N. K., & Senthil, A. (2019). Genetic variability, character association and path analysis for yield and yield component traits in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*,10(2), 518-524.

Rafique, C., Rafique, M., Hussain, A. and Altaf, M. (2010). Studies on heritability, correlation and path analysis in maize (*Zea mays* L.). *Journal of Agricultural Research* (03681157), 48(1).

Raghu, B., Parimala, K. and Reddy, A. V. (2011). Correlation and path analysis for yield and quality traits in maize (*Zea mays* L.). *Plant Archives*, 11(2), 1045-1047.

Rahim, F., Khan, M.Q., Ashraf, N., Shafi, N., Khawaja, S., Khalid, S., Zahid, G., Ahmad, M. and Ahmed, M.S. (2019). Characterization of *Zea mays* L. through morphological, biochemical and molecular markers. *Appl. Ecol. Environ. Res.*, 17(3): 6445-6456.

Rahman, S., Mia, M. M., Quddus, T., Hassan, L., & Haque, M. A. (2015). Assessing genetic diversity of maize (*Zea mays* L.) genotypes for agronomic traits. *Research in Agriculture Livestock and Fisheries*, 2(1), 53-61.

Rajesh, V., Kumar, S. S., Reddy, V. N. and Sankar, A. S. (2013). Studies on genetic variability, heritability and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.).

Ramesh, K., Rao, Y. V., & Rao, L. V. (2018). Genetic variability and heritability studies in maize (*Zea mays* L.) for grain yield and its components. *International Journal of Current Microbiology and Applied Sciences*, 7(9), 2046–2051.

Rani, G. U., Rao, V. S., Ahmad, M. L., & Rao, K. N. (2017). Character association and path coefficient analysis of grain yield and yield components in maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences*, 6(12): 4044-4050.

Ravindra, L., Hiremath, S. M., & Sajjan, A. S. (2019). Genetic variability studies in maize (*Zea mays* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*, 8(2), 1732–1739.

Reddy, S. G. M., Lal, G. M., Krishna, T. V., Reddy, Y. V. S., & Sandeep, N. (2022). Correlation and path coefficient analysis for grain yield components in maize (*Zea mays* L.). *International Journal of Plant & Soil Science*, 34(23), 24-36.

Reddy, V. R. and Jabeen, F. (2016). Narrow sense heritability, correlation and path analysis in maize (*Zea mays* L.). *Society for Advancement of Breeding Researches and Genetics in Asia and Oceania Journal of Breeding and Genetics,* 48(2), 120-126.

Reddy, V. R., Jabeen, F., Sudarshan, M. R. and Rao, A. S. (2012). Studies on genetic variability, heritability, correlation and path analysis in maize (*Zea mays* L.) over locations. *International Journal of Applied Biology and Pharmaceutical Technology*, 4(1), 196-199.

Sahoo, B. B., Sahu, S. C., Rout, S., & Sahoo, D. (2020). Estimation of genetic variability, heritability and genetic advance for yield and its component traits in maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences*, 9(1), 2666–2673.

Saidaiah, P., Satyanarayana, E., & Kumar, S. S. (2008). Association and path coefficient analysis in maize (*Zea mays* L.). *Agricultural Science Digest,* 28(2): 79-83.

Sandeep, S., Bharathi, M., Reddy, V. N., & Eswari, K. B. (2015). Genetic variability, heritability and genetic advance studies in inbreds of maize (*Zea mays* L.). *Ecology, Environment and Conservation*: 278.

Saritha, A., Umarani, E., Ramanjaneyulu, A. V., & Sridevi, S. (2024). Studies on genetic variability, heritability and genetic advance in maize (*Zea mays* L.) populations for yield and its contributing traits. *International Journal of Advanced Biochemistry Research*, 8(12S), 1550–1553.

Satyanarayana, E., Saidaiah, P. and Kumar, S. S. (2008). Association and path coefficient analysis in maize (*Zea mays* L.). *Agricultural Science Digest*, 28(2), 79-83.

Selvaraj, C. I. and Pothiraj, N. (2011). Interrelationship and path-coefficient studies for qualitative traits, grain yield and other yield attributes among maize (*Zea mays* L.). *International Journal of Plant Breeding and Genetics*, 5(3), 209-223.

Shanthi, P., Satyanarayana, E., Babu, G. S., & Kumar, R. S. (2011). Studies on genetic variability for phenological, yield and quality parameters in quality protein maize (QPM) (*Zea mays* L.). *Crop Research,* 41(1-3): 188-191.

Sharma, R., Maloo, S. R. and Joshi, A. (2014). Genetic variability analysis in diverse maize genotypes (*Zea mays* L.). *Electronic Journal of Plant Breeding.* 5 (3): 545-551.

Singh, N. P., Singh, R. N., & Singh, A. K. (2017). Genetic variability and heritability studies in maize (*Zea mays* L.). *International Journal of Agricultural Sciences,* 9(5), 3853–3855.

Singh, P. K., Sushma, B., & Kumari, N. (2022). Character association and path analysis for yield components and biochemical traits in maize (*Zea mays* L.) Genotypes. *Indian Journal of Agricultural Research*, 56(2).

Sravanti, K., Swarnalatha, I., Sudarshan, M. R. and Supriya, K. (2017). Evaluation of maize genotypes (*Zea mays* L.) for variability, heritability and genetic advance. *International Journal of Current Microbiology and Applied Sciences*. 6 (10): 2227-2232.

Sukumar, K., Hemalatha, V., Reddy, V. N. and Reddy, S. N. (2019). Character association and path analysis for yield and quality traits in quality protein maize (*Zea mays* L.*). International Journal of Current Microbiology and Applied Sciences* 8(8), 3097-3110.

Sumalini, K. and Manjulatha, G. (2012). Heritability, correlation and path coefficient analysis in maize. *Maize Journal*, 1(2): 97 –101.

Tadesse Jilo, Leta Tulu, Techale Birhan and Lemi Beksisa. (2018). Genetic variability, heritability and genetic advance of maize (*Zea mays* L.) inbred lines for yield and yield related traits in southwestern Ethiopia. *J. Pl. Breed. Crop Sci*., 10(10):281-289.

Tejaswini, N., Sukumar, K., Srikanth, T., & Mallaiah, B. (2022). Correlation and path coefficient analysis in maize (*Zea mays* L.). *International Journal of Environment and Climate Change*, 12(10), 780-787.

Teron, R., Neog, S.B., Barua, N.S., Das, K. and Phukan, S.N. (2020). Evaluation of S1 line of maize (*Zea mays* L) for fodder related attributes. *Int. J. Agric. Sci.,*12(7): 9678-9682.

Ubi, G. M., Onabe, M. B., & Kalu, S. E. (2019). Path coefficient analysis, character association and variability studies in selected maize (*Zea mays* L.) Genotypes Grown in Southern Nigeria. *Annual Research & Review in Biology*, 5(2): 1-6.

Vida Ahmadi, Somaye Eslami Fard and Zahra Rabieyan (2014). Correlation and path coefficient analyses of forage yield in corn hybrids as second crop. *Int. J. Biosci.,* 4(4): 170-175.

Wannows, A. A., Azzam, H. K., & Al-Ahmad, S. A. (2010). Genetic variances, heritability, correlation and path coefficient analysis in yellow maize crosses (*Zea mays* L.). *Agriculture and Biology Journal of North America*, 1(4): 630 637.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research*. 20,557-585.

Yadav, P. K., Tripathi, M. K., Tiwari, S., Chauhan, S., Tripathi, N., Sikarwar, R. S., ... & Singh, A. K. (2023). Genetic components and variability assessment for grain yield and its accrediting traits in maize (*Zea mays* L.). *International Journal of Environment and Climate Change*, 13(9), 772-784.

Yahaya, M. S., Bello, I., & Unguwanrimi, A. Y. (2021). Correlation and path-coefficient analysis for grain yield and agronomic traits of maize (*Zea mays* L.*). Science World Journal*, 16(1), 10-13.

Zaidi, P. H., Rafique, S., & Singh, N. N. (2004). Response of maize (*Zea mays* L.) genotypes to drought stress: Comparison of drought tolerance indices and utility for drought tolerance breeding. *Journal of Plant Breeding and Crop Science,* 3(2), 44–55.

Zarei, B., Kahrizi, D., Aboughadareh, A. P. and Sadeghi, F. (2012). Correlation and path coefficient analysis for determining inter-relationships among grain yield and related characters in corn hybrids (*Zea mays* L.). *International journal of agriculture and crop sciences*, 4 (20):1519-1522.

APPENDIX

APPENDIX

Weekly Weather Data 2024-25

SMW	Period	RF	Temperature ºC		Humidity (%)		EVP (mm)	BSS (Hrs.)	WS (Kmph)
			Max	Min	RH1	RH2			
48	25-02 Dec.	0.00	28.1	11.9	79	36	4	6.1	4.5
49	03-09 Dec.	1.20	31	19	89	50	3.2	4.2	2.6
50	10-16 Dec	0.00	17.8	8.1	86	25	4	8.6	2.8
51	17-23 Dec	0.00	25.1	10.4	83	33	3.5	7.1	1.1
52	24-31 Dec	0.00	29.7	16.3	90	43	3.2	5.2	2.5
1	01-07 Jan	0.00	29.64	9.34	88.29	27.00	3.83	8.17	2.04
2	08-14 Jan	0.00	28.17	12.06	86.14	38.00	3.47	5.17	2.66
3	15-21 Jan	0.00	29.40	11.56	89.86	29.43	4.09	5.51	3.13
4	22-28 Jan	0.00	32.71	11.13	86.57	24.00	4.51	9.17	1.16
5	29- 04 Feb	0.00	34.24	13.90	81.57	25.86	4.26	8.39	0.00
6	05-11 Feb	0.00	33.86	15.86	77.43	27.71	5.01	7.57	0.00
7	12-18 Feb	0.00	34.03	12.13	66.86	18.00	6.19	9.13	0.00
8	19-25 Feb	0.00	34.46	13.27	67.43	20.71	6.47	9.71	0.00
9	26-04 Mar	0.00	31.20	13.00	59.00	16.25	6.05	8.05	0.00
10	05-11 Mar	0.00	35.73	13.17	57.43	12.29	7.94	9.59	0.00
11	12-18 Mar	0.00	38.49	18.54	52.86	13.71	7.69	8.86	2.04
12	19-25 Mar	0.00	37.99	18.86	57.57	14.29	8.07	8.81	2.63
13	26-01 Apr	0.00	39.21	20.83	46.86	15.57	8.74	6.80	3.36
14	02-08 Apr	4.20	38.31	21.17	59.86	18.43	8.57	7.33	5.63
15	09-15 Apr	0.00	40.06	20.97	45.71	13.86	9.49	8.73	4.00
	Total	5.40	649.20	291.49	1450.43	502.11	112.28	152.19	40.14
	Mean (X)	0.27	32.46	14.57	72.52	25.11	5.61	7.61	2.01

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SSC	Akshara Talent High School, Ieeja.	Board of Secondary Education, Telangana	2016	88.00	First Division
Intermediate	Sri Chaitanya Junior Kalasala, Hyderabad.	Board of Secondary Education, Andhra Pradesh	2018	98.30	First Division
B.Sc. (Hons.) Agriculture	College of Agriculture, Golegaon.	Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani,	2023	8.34	First Class with Distinction

Place: Parbhani

Date: 22/09/2025

Signature of Student