GENETIC CHARACTERIZATION OF MAIZE (*Zea mays* L.) INBRED LINES UNDER SUB-TROPICAL CONDITIONS OF JAMMU REGION

By

Surjeet Singh
(J-20-M-748)

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GENETICS AND PLANT BREEDING

Division of Plant Breeding and Genetics

Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu
Main Campus, Chatha, Jammu - 180009
2022

CERTIFICATE - I

This is to certify that the thesis entitled **"Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region"** submitted in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture (Genetics and Plant Breeding)** to the Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, is original work and has similarities with published work not more than minor similarities as per UGC norms of 2018 adopted by the University. Further, the level of minor similarities has been declared after checking the manuscript with **URKUND** software provided by the University.

The work has been carried out by **Mr. Surjeet Singh**, under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma. It is further certified that help and assistance received during the course of thesis investigation have been duly acknowledged.

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We, the members of Advisory committee of **Mr. Surjeet Singh**, Registration No. **J-20-M-748**, a candidate for the degree of **Master of Science in Agriculture (Genetics and Plant Breeding)**, have gone through the manuscript of thesis entitled **"Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region"** and recommend that it may be submitted by the student in partial fulfillment of the requirements for the degree.

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Date : 4/11/2022

ABSTRACT

Title of Thesis : **Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region**
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ABSTRACT

The present study entitled, **"Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region"** was carried out during *kharif* 2021 at Maize Research Station, SKUAST-J, Udhampur, J&K. The objectives of the study were to characterize the maize inbred lines for morpho-agronomical traits as per DUS guidelines and to study genetic divergence among maize inbred lines. Thirty maize inbred lines of diverse origin were evaluated in Randomized Block Design (RBD) in three replications having a plot size of $3.6m^2$ (2 rows of 3m length) with a spacing of 60 cm x 25 cm. Analysis of variance revealed significant differences among the inbred lines for all the traits recorded, while DUS traits were also found to be distinct indicating sufficient variation in the inbred lines. Estimates of genetic parameters revealed that traits like ear height (cm), kernels per row, kernels per cob, 1000 kernel weight (g), and grain yield (q/ha) were found to have high heritability coupled with high genetic advance indicating the effectiveness of these traits in selection. Correlation coefficients were analyzed between all the possible combinations of the traits and it was reported that plant height (cm), ear height (cm), kernels rows per cob, kernels per row, kernels per cob, cob girth (cm), cob length (cm), stem girth (cm), no. of cobs per plant, 1000 kernels weight (g), moisture percentage, and shelling percentage exhibited a significant and positive correlation with grain yield. Kernels per cob having the highest direct effect were significantly and positively correlated with grain yield (q/ha) due to an indirect positive effect via no. of days to 50 per cent silking, plant height (cm), cob length (cm), stem girth (cm), no. of cobs per plant, no. of plants per plot, 1000 kernel weight (g). Kernels per row having a high direct negative effect on grain yield, also had a significant negative correlation due to indirect negative effects via no. of days to 50 per cent tasseling, no. of days to 75 per cent dry husk, ear height (cm), kernel rows per cob, cob girth (cm), moisture percentage, and shelling percentage. Results of D^2 statistics diversified the inbred lines into 13 clusters. Based on genetic diversity, mean performance, and their DUS traits, WN 2453 ×WN 32296 and PFSR 10109 ×WN 32296 were found to be the most diverse parent, and their combination for grain yield and recommended for superior recombinants. Thus, these combinations can be further validated for utilization in the breeding programs.

Keywords: maize, characterization, morpho-agronomical, DUS traits, heritability, cluster, D^2 statistics.

Signature of Major Advisor

Signature of Student

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CHAPTER-1

INTRODUCTION

Maize (*Zea mays* L.) is the only domesticated member of the tribe Maydeae and genus *Zea*. After wheat and rice, it is the third most significant cereal crop in the world. It is a diploid with 2n=2x =20 chromosomes. It belongs to the Gramineae (Poaceae) family and is known as the "queen of cereals" due to its extremely high yield potential relative to other cereals (Anonymous, 2017). It is the most adaptable cereal crop in terms of adaptability, varieties, and uses. It is the second most frequently farmed crop in the world and is grown in the tropics, subtropics, and temperate regions. There are various varieties of field corn, including quality protein maize (QPM), waxy maize, and high oil maize. As a food, feed, and industrial raw material, maize is a crucial crop for billions of people. Approximately 1147.7 million metric tons (MT) of maize are produced by over 170 nations on 193.7 million hectares with an average yield of 5.75 t/ha (FAOSTAT, 2020). India is the 4th largest producer of maize in area (9.2 million ha) and 7th in production (27.8 million MT), with an average yield of 29.65 q/ha. In India, maize is primarily grown during the rainy (*kharif*) and winter seasons (*rabi*). *Kharif* maize accounts for around 83 per cent of maize area in India, while *Rabi* maize accounts for 17 per cent of maize area. In recent years, spring maize acreage in the north-western regions of the country has also expanded rapidly. Madhya Pradesh and Karnataka have the largest area of maize cultivation (15 %), followed by Maharashtra (10 %), Rajasthan (9 %), Uttar Pradesh (8 %), Jammu and Kashmir (3%), and others. After Karnataka and Madhya Pradesh, Bihar is the third-largest producer of maize in India. Andhra Pradesh has the greatest state output (DACNET, 2020). The region of Jammu produces 436.50 metric tons of maize from an area of 0.19 million hectares with an average yield of 22.96 q/ha (Regional Digest of Statistics, 2020).

In either its native or modified form, maize is a staple dietary ingredient. Maize grain is an excellent source of carbohydrate (72%), ash (17%), protein (10.4%), fiber (2.5%), oil (4.5%), vitamins, and minerals (Farhad *et al*., 2009). The value of maize as a key staple crop and a model organism with enormous genetic diversity is recognized globally (Prasanna, 2012; Patel *et al*., 2017). Assessing the genetic diversity and relatedness of breeding material is the most important aspect of a breeding effort. The primary responsibility of maize breeders is the development of superior inbred lines and the identification of optimal parental combinations to produce high-performing hybrids (Semagn *et al*., 2012). Morphological features are the functional manifestation of an organism's underlying genetic makeup; hence, they comprise an essential set of genetic diversity markers. In hybrid maize breeding, therefore, the characterization of the genetic diversity of maize germplasm or inbred lines is of utmost importance (Xia *et al*., 2005). For effective management of genetic diversity, well-characterized germplasm and genetic pools clustered according to genetic diversity are required (Wende *et al*., 2013). Thus, the genetic diversity of crop species impacts their potential for enhanced efficiency and their use in breeding, resulting in an increase in food output. Using morphological, biochemical, and molecular markers, it is possible to estimate the genetic diversity of individuals/populations. Different maize inbred lines of various origins and genetic backgrounds serve as a useful source of material and offer the opportunity to increase genetic variation.

DUS testing, on the other hand, is one approach used to assess inbred lines for distinctness (D), uniformity (U), and stability (S) (Dass *et al*., 2006). Distinctiveness implies that a variety can be distinguished from all other varieties whose existence is common knowledge by at least one basic trait. Uniformity denotes that the variety should be sufficiently uniform in its essential qualities, with variations as expected from its propagation characteristics. Stability necessitates that the key traits endure recurrent propagation (Dhillon *et al*., 2006). Morphological characterization plays an important role in the management of ex-situ gene bank-preserved genetic resources. The fundamental objective of all maize breeding initiatives is to create new open-pollinated varieties (OPVs), inbred lines, hybrids, and synthetics that outperform existing cultivars in a variety of characteristics. The most significant agronomic characteristic to consider when pursuing this objective is grain yield. The understanding of genetic diversity and variability of inbred lines aids the breeder in designing ideal crossings for the generation of superior hybrids. In the seed production program, morphological characteristics are the most important markers for determining the off types. Thus, morphometric characterization aids in maintaining genetic purity in the seed field by identifying and eliminating deviant plants, which facilitates directly meeting the required standards for genetic purity, physical purity, and seed certification (Madhukeshwara and Sajjan, 2015). In India, the Plant Variety Protection and Farmer's Right Act of 2001 encourages the classification and registration of existing, farmer, and novel varieties as a component of the national and botanical property. Inbred lines are employed as seed parents to test the profitability of commercial maize genotypes (Pinnisch *et al*., 2012). Therefore, maize inbred lines must be characterized in order to bring them under IPR protection.

The study of genetic characterization of maize (*Zea mays* L.) inbred lines under sub-tropical conditions in the Jammu region would help determine the genuine potential value of the genotypes and their significance for the agricultural economy and food security. It is crucial for a crop improvement program to preserve the genetic diversity that enables the discovery of prospective genotypes in the germplasm collection, which may then be utilized in the breeding program to generate promising cultivars. The existence of resistance to biotic and abiotic factors and a high degree of adaptability in the genotypes is contingent upon genetic diversity. Selection is successful when there is genetic diversity among a population's individuals. Understanding the level of genetic diversity present in a population is, therefore, crucial for a plant breeder to develop a prudent breeding program. Knowledge of heritability and the genetic advancement of traits suggests the potential for agricultural development via selection. Studies of correlation are an efficient method for identifying the relationship between the agronomic qualities of populations with a wide range of genetic diversity. Moreover, correlations among important qualities will pave the road for appropriate choices in breeding programs, and correlation coefficient analysis is the most commonly used method for determining the relationship between the characters (Yagdi and Sozen, 2009). There is a need for High Yielding Maize Varieties in this region since maize productivity is lower than the national average. As genetic divergence is a precondition for any crop improvement program, the available germplasm must be used for its genetic diversity in order to generate High Yielding Varieties. The selection of varied parents will yield superior recombinants.

Therefore, the current investigation titled "**Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region** " was conducted to examine the genetic characterization and divergence of maize inbred lines with the following objectives:

1. To characterize the maize inbred lines for morpho-agronomical traits as per DUS guidelines
2. To study genetic divergence among maize inbred lines

CHAPTER-2

REVIEW OF LITERATURE

Distinctness, Uniformity, and Stability (DUS) is an intellectual property system introduced in 1961 by the International Union for the Protection of New Varieties of Plants (UPOV) for the purpose of protecting investments and rewarding innovation in the development of new plant varieties. In India, the Protection of Plant Varieties and Farmers' Right authority (PPV & FRA) has acknowledged 31 characters as a prerequisite for the characterization of maize genotypes for DUS (Anonymous, 2007).

Crop improvement programs would benefit from a comprehensive understanding of the genetic diversity, the extent of variation, and heritability of characters among genotypes. Genetic variability is a gift from nature, and its productive use in any crop species necessitates systematic collection, evaluation, description, and grouping according to economic descriptors. Variability is essential to the success of a breeding program for the genetic improvement of any crop. Estimates of various genetic parameters are essential for gaining a better understanding of the nature and magnitude of genetic variability present in breeding material, as well as the association between yield and yield-contributing traits.

A brief review of available information on the above aspects in maize is presented in this section under the following headings:

2.1 DUS Characterization

2.2 Genetic Variability

2.3 Correlation Analysis

2.4 Path Analysis

2.5 Genetic Diversity

2.1 DUS Characterization

Selvi *et al*. (2013) initiated a DUS characterization study based on cluster analysis in 17 maize inbred lines, including 16 domestic inbreds and 1 exotic inbred, for 22 morphological characters, including 6 plant characteristics, 7 tassel, and silk characteristics, and 5 cob characteristics. Maximum numbers of inbreds were found in clusters II, IV, and V, each with four inbreds, while the smallest numbers were found in clusters I, III, and VII, each with one inbred. Among the 17 inbreds, the results revealed that UMI 1200, UMI 1230, and UMI 551 were distinct from the others.

Subbarao *et al*. (2013) carried out characterization for farmer varieties of rice in order to investigate the uniqueness of 65 landraces by employing 43 agro-morphological parameters and the Distinctiveness, Uniformity, and Stability test (DUS). Based on 22 key and 24 supplementary characteristics, 32 out of 65 investigated variants were determined to be unique. According to them, their findings will aid breeders, researchers, and farmers in identifying and selecting the restoration and conservation of valuable genes for crop development, as well as in obtaining legal protection under the Protection of Plant Varieties and Farmer's Rights Act.

Chanda *et al*. (2014) analyzed DUS data to discriminate Southern African Maize (*Zea mays* L.) inbred lines. In this study, 18 maize inbred lines were tested for 25 agronomic and 12 DUS traits. The maize inbred lines were grouped by quality, quantity, or combination. Both qualitative and quantitative similarity matrices were highly correlated (r=0.82 and r=0.61) to mixed data ($p < 0.001$). The Shannon diversity index showed inbred lines were diverse in silking, ear diameter, maturity, shelling percentage, and leaf color. For effective discrimination of maize inbred lines, both agro-morphological and DUS traits should be used.

Madhukeshwara and Sajjan (2015) used DUS guidelines to study two hybrids, GH-0727 and Arjun, and their five parents, CI-4, CI-5, KDMI-15, KDMI-16, and CI-4XCI-5, to look for morphological traits. The analysis of thirteen morphometric characteristics for seven genotypes showed that plant height, tassel attitude, tassel angle, ear shape, and thousand seed weight varied more than the traits being studied.

Nayak *et al*. (2015) examined the Maize Distinctness, Uniformity, and Stability (DUS) characteristics. Using DUS guidelines and 27 morphological characteristics, the objective of the study was to determine the genetic relatedness of 55 early maturity maize inbred lines. Among inbred lines, significant differences were observed in anthocyanin coloration of brace roots, glumes in tassel, and silks; leaf angle and leaf width; tassel characteristics such as density of spikelets and angle between the main axis and lateral branches; and ear characteristics such as ear length, number of rows of grain, kernel arrangement, and thousand kernel weight.

Gull *et al*. (2020) investigated the DUS Characterization of sweet corn inbred lines under temperate conditions and discovered substantial differences in a number of traits between diverse sweet corn inbred lines. When 35 genotypes were evaluated for 31 traits, it was determined that each trait was relevant for trait expression and characterization. Testing for

Distinctness, Uniformity, and Stability (DUS) of novel plant varieties is difficult by the need to compare them to all existing 'common knowledge types. The Protection of Plant Varieties and Farmers' Rights Act (2001) stipulates that new varieties must possess DUS (distinctness, uniformity, and stability) to be registered. The Act also advises that varieties be registered for any one novel trait that is not already registered.

Bayisa *et al*. (2022) evaluated morphological variability and seed quality contributing traits for mid-altitude maize inbred lines in Western Ethiopia, Bako. Distinctness, uniformity, and stability (DUS) are essential for quality seed production and developing new varieties. This study examined 14 inbred line phenotypes. Inbred line characteristics varied greatly. CML161 and CML165 had yellow kernels, while 142-1-e had anthocyanin-tasseled glumes. Knowing the DUS characteristics of these parents is important for developing a new maize hybrid for this trait, as it will help with registration and guide seed producers.

2.2 Genetic Variability

Turi *et al*. (2007) investigated the extent of genetic variability in maize genotypes for yield and yield components in the Peshawar valley. Cob length, grain rows per cob, fresh cob weight, grain moisture content, 300-grain weight, and grain yield exhibited considerable variation. Sarhad White had the longest cobs, while PESV-3-1 and EV-2 Pahari had the shortest. Based on the results of the study, the Sarhad White genotype could be recommended for general cultivation in Peshawar valley's agroclimatic conditions.

Shanthi *et al*. (2011) assessed genetic variability characteristics applied to QPM genotypes for numerous economic traits, including grain yield, growth, maturity, and quality parameters. Grain yield and its component characters, including total anthers dehiscence period, the total period of silk appearance, active pollination period, number of seeds per cob, cob weight, protein yield, and oil yield, had high estimates of GCV and PCV, as well as high heritability (more than 85%) and high genetic advance, out of 26 studied characters. Therefore, it was determined that direct selection had a greater possibility of enhancing these characteristics.

Lal and Singh (2014) conducted a study to quantify the genetic variability in QPM for morphological and quality traits. Seed yield per plot, plant height, ear girth, ear height, ear length, 1000 grain weight, and number of grains per row had high estimates of the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Heritability and genetic advance were low for days to 50% silking, protein concentration, tryptophan concentration, lysine concentration, the number of rows per plant, and the number of grains per row, indicating that non-additive gene action predominated. Therefore, environment plays a significant role in governing these characters, and the improvement of these characters is challenging.

Sharma *et al*. (2014) evaluated the genetic variability, heritability, and genetic advance of twenty diverse maize genotypes for yield and kernel quality traits. Genetic variability parameters indicated that the phenotypic coefficient of variation (PCV) was greater than the corresponding genotypic coefficient of variation (GCV) and that heritability was high for the majority of the traits under investigation. In the maize yield improvement selection program, test weight, grain yield per plant, grains per cob, cob length, grains per row, and harvest index were found to be crucial.

Kapoor and Batra (2015) investigated genetic variability, correlation coefficients, and path coefficients. All the characters' genotypes were significantly different. Invariably, the phenotypic coefficients of variation (PCV) were greater than their corresponding genotypic coefficients of variation (GCV), indicating environmental influences. High GCV and PCV estimates were found for plant height, leaf length, stem girth, number of cobs, number of seeds, dry matter yield, and green fodder yield, indicating that selection based on these traits would facilitate the successful isolation of desirable types.

Rahman *et al*. (2015) evaluated the genetic diversity of nine maize genotypes. On seven morphological characteristics, data was collected. According to statistical analysis, maize genotypes differ significantly. For yield/plant, the phenotypic and genotypic coefficients of variation were found to be the highest among all traits. The genetic advancement was greatest for 1000-kernel weight, followed by number of kernels per ear.

Bhusal *et al*. (2017) determined the degree of genetic variability and trait association in fifty-five maize genotypes. The analysis of variance identified significant differences between the genotypes for 18 of the analyzed characteristics. For grain yield per plant, biological yield per plant, and cob weight, a high genotypic and phenotypic coefficient of variation was observed, along with high heritability and genetic advance.

Kharel *et al*. (2017) analyzed maize genotypes for genetic and yield parameters. High Genotypic coefficient of variation for row-1 kernels and ear height, moderate for plant height, 100-kernel weight, days to 50% silking, ear length, SPAD chlorophyll, and leaf angle. High genetic advance in number of kernels row^{-1}, ear height, plant height, days to 50% silking, SPAD chlorophyll, and 100-kernel weight; moderate in ear length, leaf angle, days to 50% tasseling, and ear girth. Days to 50% tasseling, plant height, SPAD chlorophyll, days to 50% silking, number of kernels row^{-1}, leaf angle, and ear length had high heritability. Ear girth, 100-kernel weight, leaf number, and kernel rows ear^{-1} were moderately heritable.

Sharma *et al*. (2017) tested 13 maize inbred lines in a randomized complete block design with three replications for agro-morphological performance. Plant height, ear height, tasseling days, silking days, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, test weight, and grain yield were all calculated. For grain yield and other agro-morphological parameters, genotypes significantly differed, indicating high genetic variability.

Sravanti *et al*. (2017) studied the variability, heritability, and genetic advance of 42 maize genotypes for 12 yield and contributing traits. The ANOVA revealed significant variability among the maize genotypes. Ear height had the highest PCV and GCV, while days to maturity had the lowest. Ear height and grain yield per plant had high heritability and genetic advance, indicating additive gene action. Directly selecting such characters would increase yield. When selecting for crop yield, prioritize these traits.

Najar *et al*. (2018) found significant variability and high heritability (broad sense) for all traits studied, indicating they are amenable to genetic improvement. Grain yield per plant correlated positively and significantly with plant height, ear height, ear width, number of kernels per row, number of kernel rows, and 100 seed weight at both levels, indicating that selecting for these traits could improve grain yield per plant.

Singh *et al*. (2019) found a wide range of genetic variation among maize genotypes for morpho-physiological parameter studies. A few parameters had high heritability and genetic advance as a percentage of the mean. The 196 genotypes were clustered by D^2 values. D^2 value was highest in Cluster IV. The second was Cluster VIII, and the third was Cluster III. The largest inter-cluster distance was between clusters IV and VI, and the smallest was between clusters I and VII.

2.3 Correlation Analysis

Ilker (2011) generated plant breeder selection criteria using correlation and path coefficient analysis on 8 sweet corn varieties. Due to negligible genotype x year interactions, two years were pooled. In conclusion, fresh ear weight can be utilized as a selection criterion due to its beneficial direct effects on fresh grain yield and indirect effects on all other features. Rows per ear and ear length can be selected in sweet corn breeding.

Jawaharlal *et al*. (2011) found a significant and positive correlation between grain yield and plant height, ear height, ear circumference, number of seed rows per ear, number of seeds per row, number of seeds per ear, and 100-seed weight. The number of seeds per ear showed the most positive link with grain yield, followed by plant height, number of seeds per row, ear height, 100 seed weight, ear circumference, and number of seed rows per ear. The traits like days to 50% tasselling and days to 50% silking demonstrated a negative genotypic connection with grain yield.

Selvaraj and Nagarajan (2011) revealed that plant height, ear height, ear length, ear girth, number of grains per row, number of grains per ear, starch content, hundred-grain weight, and carotene content had significant positive associations with grain yield, whereas days to tasseling and days to silking had positive but non-significant positive associations with grain yield. The correlation between grain yield and the number of rows per ear and crude protein content was negative and insignificant. The association between ear length and grain yield was the strongest, followed by the number of grains per row.

Pinnisch *et al*. (2012) evaluated the yield component characteristics and kernel morphology of 27 inbred lines of maize (*Zea mays* L.) The grain yield, thousand-kernel weight, and ear length were measured for inbred line evaluations. Grain yield, thousand-kernel weight, ear length, and kernel morphology differed significantly amongst inbred lines. According to correlation analysis, a significantly negative association exists between kernel morphology types categorized as "large rounds" and "medium flats," with the latter group being more preferred. Before initiating a breeding, project or selecting an inbred to serve as the seed parent in a production field, plant breeders may have to evaluate the kernel morphology of their inbred parents.

Sumalini and Manjulatha (2012) observed that grain yield was significantly and positively correlated with all of the examined traits, with the exception of days to 50% silk emergence. The genotypic correlation between ear girth and grain yield was the highest, followed by the number of kernels per row and ear length.

Ali *et al*. (2013) investigated the genetic variability and correlation between twenty morphological characters of maize (*Zea mays* L.) seedlings. Both genotypic and phenotypic correlation analyses were performed. For fresh shoot weight, fresh and dry biomass of seedlings, the highest levels of heritability and genetic advance were observed. There were significant genotypic and phenotypic correlations between seedling root and shoot length, fresh and dry biomass. It was proposed that parameters such as fresh and dry biomass of seedlings, root and shoot length might be utilized as selection criteria to acquire maize genotypes with high yields under normal and drought stress environments.

Natraj *et al*. (2014) studied maize (*Zea mays* L.) correlation and path analysis. Grain yield was positively and significantly correlated with ear diameter, number of kernel rows per ear, ear height, ear weight with husk, ear weight without husk, plant height, 100-grain weight, and ear length, both genotypically and phenotypically. Path analysis showed that ear weight with husk, number of kernel rows per ear, and number of kernels per row had the most direct effect on grain yield per plant. The impacts of plant height, ear height, and ear diameter were similarly significant. While the remaining traits reduced grain output per plant.

Sharma *et al*. (2014) found a correlation between grain yield and other major agronomic parameters in 20 maize (*Zea mays* L.) inbred lines grown in a randomized complete block design (RCBD) with two replications. Range, mean, standard error, variance, standard deviation, and correlation coefficient were evaluated for seven agronomic traits. Grain yield was positively correlated with plant height, ear height, leaf length, leaves per plant, and kernels per row. Each morphological attribute can be used to improve maize grain output.

Ghimire and Timsina (2015) studied genetic variability, yield, and yield-attributing traits in 14 maize genotypes. Plant height, ear height, ear length, ear girth, ear weight, kernel rows per ear, and kernels per row were positively correlated with grain yield per hectare. The analysis found a negative and highly significant correlation between days to 50% tasseling and days to 50% silking with grain yield per hectare. Also, days to maturity and grain yield per hectare were negative and non-significantly correlated. Selecting for plant height, ear length, ear girth, number of kernels per row, and ear weight increased grain yield.

Dar *et al*. (2015) correlated fifty temperate maize (*Zea mays* L.) inbred lines using eleven quantitative parameters: days to 50% tasseling, days to 50% silking, days to maturity, plant height, ear height, ear length, ear girth, number of kernel rows ear^{-1}, number of kernels row^{-1}, 100-grain weight, and grain yield plant^{-1}. Plant height, ear height, ear girth, number of kernel rows ear^{-1}, number of kernels row^{-1}, and 100-grain weight correlated positively with grain yield plant^{-1} at the genotypic level. Other traits, such as days to 50% tasseling, days to 50% silking, and days to maturity, had negative and significant associations with grain yield, suggesting early maturity lines. Grain yield plant^{-1} was positively correlated with ear girth.

Prasad and Shivani (2017) examined correlation and path analysis in 18 inbred lines of maize (*Zea mays* L.). At both genotypic and phenotypic levels, days to 50% tasseling and days to 50% silking were found to be negatively correlated with ear length, ear girth, number of kernel rows, number of kernels per row, test weight, and seed yield per plant. The association between plant height and ear height, ear length, ear girth, number of kernel rows, number of kernels per row, test weight, and seed yield per plant was positively significant. Days to 50% tasselling had a negative direct effect and a negative significant association with seed yield per plant, whereas days to 50% silking had a positive direct effect. The positive direct and indirect effects of ear height and ear length on seed yield per plant were mediated by ear circumference, number of kernel rows, number of kernels per row, and test weight. For the improvement of seed yield, traits such as ear length, ear girth, number of kernel rows, and number of kernels per row with high positive correlation coefficients and a significant direct and indirect effect on seed yield should be prioritized.

Khan *et al*. (2018) analyzed the heritability and correlation of morphological and yield traits in sixty maize (*Zea mays* L.) germplasm and three check cultivars using an Augmented Design with three blocks. The majority of the traits revealed significant differences between genotypes via analysis of variance. The GCV and PCV were extremely low for the number of ears plant^{-1}, whereas they were very high for the number of grains cob^{-1}. The majority of the traits under study had broad-sense heritability estimates with maximum values between 0.88 and 1.00. In contrast, days to 90% maturity and number of rows cob^{-1} displayed heritabilities of 0.37 and 0.58, respectively. ACC-15276 yielded the greatest number of grains cob^{-1} (490.00), followed by ACC-14980 (400.60).

Bartaula *et al*. (2019) assessed the genetic variability, heritability, and genetic advance for growth, yield, and yield contributing traits in ten maize genotypes. The variance analysis revealed significant differences between all traits. Positive and significant phenotypic correlations were observed between grain yield and test weight, kernel per row, kernels rows per cob, and cob length, respectively.

Musundire *et al*. (2019) analyzed the genetic variation and path coefficients of 122 introgressed maize inbred lines for economic traits, including sets of introgressed lines from three selection environments, parental inbred lines, and two common checks. Analysis of grain yield and ear prolificacy using Spearman's rank correlation revealed a correlation between selection environments. Grain yield exhibited a significant (< 0.05) positive correlation with plant and ear characteristics, plant height, root and stalk lodging, ear prolificacy, and harvest grain moisture content.

Aruna *et al*. (2020) estimated correlation analysis between 290 maize inbred lines (*Zea mays* L.). The analysis of variance revealed statistically significant differences between inbred lines, indicating the presence of diversity among inbred lines. The most important trait, grain yield plant^{-1}, was found to be positively and highly correlated with kernels row^{-1} (0.81), cob diameter (0.813), cob length (0.811), and 100 seed weight (0.80). (0.706). The highly significant correlation between these traits suggests that selecting for them in a breeding program will increase grain yield per plant^{-1}.

Khalid *et al*. (2020) analyzed 10 maize inbred lines under water stress for morpho-physiological traits. Seed yield at genotypic and phenotypic levels correlated positively with a survival rate at 25% field capacity moisture, root/shoot ratio, and photosynthetically active radiations, while stomatal frequency correlated positively with genotypic seed yield and phenotypic net photosynthesis. Selection based on survival rate at 25% field capacity moisture and photosynthetically active radiations will improve maize yield per plant under drought conditions

Olawamide and Fayeun (2020) conducted research to estimate the character association and path coefficient of maize grain yield and its component characters in order to identify the characters whose selection could be used to increase maize grain yield. At the phenotypic and genotypic levels, plant stands per plot, the number of ears harvested, and field weight was positively and significantly correlated with grain yield.

Yahaya *et al*. (2021) estimated the direct and indirect effects of four agronomic traits on maize (*Zea mays* L.) grain yield in two experimental fields (Kafanchan and Kadawa). Both locations had a strong positive correlation between plant height, cob length, cob diameter, and 1000-grain weight and maize grain yield. In Kadawa, plant height contributed most directly to grain yield (0.653%), followed by 1000-grain weight (0.429%). According to correlation and path coefficient analyses, cob diameter is a less reliable agronomic trait than the three others in maize yield component analysis.

Yadesa *et al*. (2022) studied genetic variability, heritability, correlation analysis, genetic advance, and principal component analysis of grain yield and yield-related traits of 36 inbred lines adapted to Ethiopia's mid-altitude agroecology, along with four controls. Except for days to maturity, genotypes significantly affected all other parameters. High heritability and genetic advance indicate additive gene action controls grain yield. Days to maturity, plant and ear height, ear diameter, number of ears per plant, and kernel weight were all highly correlated with grain yield.

2.4 Path Analysis

Bello *et al*. (2010) examined the correlation between grain yield and other agronomic parameters using 10 maize varieties. They observed that days to 50 percent silking, 100-grain weight and number of grains per ear had the greatest direct effect on grain yield, whereas number of grains per ear had the greatest moderate indirect negative effect on grain yield via ear height. Days to flowering, plant and ear height, number of grains per ear, and 100-grain weight may be crucial selection criteria for obtaining open-pollinated maize varieties and hybrids with a high grain yield.

Hefny (2011) performed genetic parameters and path analysis of yield in corn inbred lines (*Zea mays* L.) at different sowing dates. In 2009, 13 inbred corn lines were evaluated at two sowing dates to estimate genetic parameters and path analysis of plant characters. A split plot design with three replications was used. Under optimal sowing conditions, ear diameter, ear weight plant^{-1}, number of rows ear^{-1}, and number of grains row^{-1} correlated positively with yield plant^{-1}. Ear diameter, grains per row, 100-grain weight, and grain yield are negatively correlated with days to 50 percent tasseling and silking. Genotypic correlations between grain yield plant^{-1} and days to 50 percent tasseling, days to 50 percent silking, ear length, ear weight plant^{-1}, and number of rows ear^{-1} were positive and significant.

Selvaraj and Nagarajan (2011) found that ear length had the most positive direct effect on grain yield, followed by ear height, number of rows per ear, days to silking, crude protein, and carotene content. They contributed primarily to yield and could be used to select genotypes to improve the genetic yield potential of corn. Plant height, days to tasseling, ear girth, number of grains per row, number of grains per ear, 100-grain weight, and starch content affect grain yield.

Bharathiveeramani *et al*. (2012) found that the number of kernels per row and the weight of 100 seeds had a significant direct effect on grain yield. The number of kernel rows had a high direct effect on grain yield, while the number of leaves had a moderate direct effect. The number of kernels per row, the weight of 100 seeds, and the number of leaves had a significant positive direct effect on grain yield, whereas the other characteristics had a negative direct effect on grain yield.

Zarei *et al*. (2012) found that length of the ear, length of the kernel, weight of 100 grains, total number of kernels per ear, and percentage of the ear that is a cob all had a direct positive effect on grain yield. The number of total kernels per ear had the biggest direct effect, while the weight of 100 grains came in second. On the other hand, the number of kernels per ear and the weight of 100 grains had the largest indirect effect on ear length and grain weight. The number of rows per ear and the number of kernels per row had a negative effect on grain yield, which partially canceled out the positive direct effect of 100-grain weight on grain yield.

Hepziba *et al*. (2013) found that the number of kernels rows per cob had the greatest direct positive effect, followed by cob length. The significant relationship between grain yield per plant and hundred kernel weight and number of kernels per row is attributable to positive indirect effects mediated by number of kernels rows per cob, days to 50 percent silking, plant height, and cob length.

Chaudhary *et al*. (2015) studied variability, interrelationships, and path-coefficient in maize (*Zea mays* L.) during the *rabi* season of 2011-12 at the Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P.), India. Almost all characters showed significant variation. Grain yield per plant, kernels per row, and ear height had high genotypic and phenotypic coefficients of variation. Yield per plant, ear height, number of kernels per row, and 100-grain weight is important for direct selection. Number of kernels per row, cob diameter, ear height, and number of kernels rows per cob positively correlated with grain yield per plant. Crop yield was negatively correlated with tasseling and silking days. Number of kernels rows per cob had the greatest direct effect on yield per plant.

Sood *et al*. (2015) analyzed eleven agro-morphometric traits of 40 maize inbred lines (14 QPM lines and 26 non-QPM lines) grown in *kharif* 2011. Correlation analysis found a positive relationship between grain yield and 100-seed weight, indicating that the latter can increase grain yield. Path coefficient analysis divides correlation into direct and indirect effects. Path analysis showed that days to 50 percent silking has the greatest positive direct effect on grain yield, followed by cob girth and 100-seed weight. In this study, the direct and indirect correlation revealed the high positive direct effect of days to 50 percent silking solely; therefore, this trait may be given more weight when selecting high-yield maize genotypes.

Kumar *et al*. (2015) assessed the character association and path analysis for nine characters and discovered that 100 kernel weight had the highest direct effect on grain yield per plant, followed by the number of kernels per row and ear girth. In addition, days to 50 percent tasseling, days to 50 percent silking, and days to maturity had a direct negative effect on grain yield.

Begum *et al*. (2016) analyzed genetic variability, character association, and path analysis in 22 maize genotypes. Character genotypes differed significantly. Ear length and grain yield (t/ha) had moderate GCV and PCV, but low ECV. All characters were inheritable. Height, ear height, and 1000-grain weight showed high heritability and genetic advance. Grain yield was positively correlated with ear length, ear diameter, and kernels per row. The deviations between genotypic and phenotypic correlation and environmental correlation suggested environmental influence on almost all characters. Path coefficient analysis showed that plant height (0.659), ear length (0.934), and kernel rows per ear (0.715) had a significant positive direct effect on grain yield, indicating their importance during selection. Simultaneous restricted selection should be done for number of kernel rows per ear.

Pandey *et al*. (2017) carried out an experiment on grain yield, heritability, correlation, and Path analysis in maize (*Zea mays* L.) Mean performance, genotypic variances, phenotypic variances, genotype-by-environment variances, broad sense heritability, phenotypic and genotypic correlation coefficients, and path analysis were studied. All traits studied showed significant differences, revealing maize genotype diversity. Path analysis was used to separate the genetic correlations between grain yield and related traits. Days to 50 percent silking, physiological maturity, shelling percentage, and 100-seed weight showed a positive effect on grain yield. The days to 50 percent silking had the highest direct effect (0.3032), followed by physiological yield (0.1586)

Jakhar *et al*. (2017) investigated direct and positive effects on yield by days to 75 percent brown husk, tassel length, cob length without husk, days to 50 percent tasseling, leaf width, plant height, 100 seed weight, cob length with husk, cob diameter, indicating the effectiveness of direct selection, whereas days to 50 percent silking and ear height displayed direct and negative effects, indicating the effectiveness of indirect selection.

Shengu (2017) conducted a workout path coefficient analysis of early maize (*Zea mays* L.) inbred lines in Ethiopia's central rift valley. Consequently, fifteen inbred lines were crossed using the diallel mating system. At Melkase Research Center, two standard checks, one candidate variety, and hybrids were evaluated using an Alpha Lattice Design with two replications. Path-coefficient analysis revealed that the majority of traits exerted direct positive effects on grain yield at both the genotypic and phenotypic levels. In general, this study identified inbred lines and hybrid associations whose expression of important traits was desirable.

Goncalves *et al*. (2018) examined the development and selection of super-sweet corn genotypes (sh2) through multivariate approaches to investigate relations among ten traits in super-sweet corn genotypes assessed by simple correlation, path, and canonical variable analyses, and to investigate the relative importance of such traits to the super sweet corn breeding program. In two different environments, 3 × 6 partial diallel of super-sweet (sh2) corn was tested using a randomized block design (RBD) with four repetitions. The correlation study revealed ear diameter and useful ear length contributed most to increasing ear yield (without husk). Canonical variables showed that the genetic backgrounds of sh2-gene donor populations affected recurrent populations, resulting in two divergent groups.

Kandel *et al*. (2018) determined the correlation and path coefficient for 20 inbred maize lines. All lines differed significantly in all characteristics, according to the analysis of variance. Path analysis showed that kernel weight, shelling percentage, kernel ears^{-1}, and silk receptivity impacted a direct positive effect on grain yield. Increasing grain yield under heat stress requires selecting genotypes with the highest thousand kernel weight, shelling percentage, silk receptivity, and number of kernels per ear, as well as a shorter anthesis silking interval, no leaf firing, and tassel blast.

Jilo and Tulu (2019) studied association and path coefficient analysis in Ethiopian maize (*Zea mays* L.). Twenty-four inbred lines developed by the Ethiopian National Maize Breeding Program were evaluated at Jimma Agricultural Research Center in an 8×3 Alpha Lattice (0,1) design with three replications. The goal was to determine phenotypic and genotypic associations between traits in Ethiopian maize inbred lines and compare direct and indirect effects on grain yield. Grain yield per hectare, seed weight, ear height, ear diameter, anthesis-silking interval, and plant aspect had high phenotypic and genotypic variation. Number of kernels per row, number of kernel rows per ear, plant height, and 1000-kernels weight had high direct effects and positive associations with grain yield, indicating they can be used for indirect selection of inbred lines with higher yield potential.

Prakash *et al*. (2019) studied genetic variability, character association, and path analysis for yield and yield component traits in maize (*Zea mays* L.). 100 maize inbred lines and 5 checks were grown in Augmented block design II, and 20 morphological traits were observed. All characters' genotypes showed significant variance in ANOVA. Anthesis silking interval, number of tassel branches, number of kernels per row, grain yield per plant, cob weight, ear height, and number of kernels rows per cob have high PCV, GCV heritability, and genetic advance as a percentage of the mean. Cob girth, number of kernels per row, shelling percentage, days to 50% silking, and ear height actually affect grain yield. These traits can be used to identify elite genotypes in a population.

Chethan *et al*. (2020) worked on correlation and path coefficient analysis for yield and yield component characters of 50 maize (*Zea mays* L.) inbred lines. Grain yield was positively correlated with germination percentage, ear height (cm), cob length (cm), cob width (cm), no. rows per cob, number of grains per row, de-husk cob weight (g), rind weight (g), and test weight (g), but negatively correlated with shelling percentage. Path analysis expressed that de-husk cob weight had the highest positive direct effect on grain yield, followed by shelling percentage, ear height, days to 50 percent tasseling, test weight, number of grains per row, and cob width.

Damtie *et al*. (2021) tested the genetic variability, heritability, trait association, and path coefficient analysis of maize (*Zea mays* L.) to determine the relationship of traits with grain yield and direct and indirect effects. 23 inbred lines were used in RCB design 3 replications. Yield and yield-related traits varied strongly ($p = 0.01$) between inbred lines. Plant height, ear height, and grain yield had moderate to the high genotypic coefficient of variation, heritability, and genetic advance. Plant height, ear height, and number of ears harvested in a plot had positive phenotypic and genotypic associations with grain yield, while days to 50 percent anthesis, silk emergence, and plant and ear aspects had negative phenotypic and genotypic associations with grain yield.

Shahrokhi *et al*. (2021) determined the path analysis of yield and yield components in 24 inbred lines of super-sweet maize (*Zea may*s L. var. Saccarata) grown under drought-stress and normal conditions. The experiment was conducted using a completely randomized block design with four replications. Under normal conditions, path analysis revealed that the number of kernels per row had the greatest positive direct effect (0.717) on grain yield, followed by stem diameter (0.292) and ear diameter (0.193). (0.273). Under conditions of drought stress, ear diameter (0.455) and plant height (0.436) had the most significant positive direct effects on grain yield.

Jagadev *et al*. (2021) studied genetic variability, association, and path coefficients in 50 maize inbred lines. In the present study, all component traits except days to 50 percent tasseling, days to 50 percent silking, days to 75 percent dry husk and shelling percentage had a significant positive association with grain yield. Leaf length, leaf breadth, plant height, ear height, ear size, number of kernels, and 100-kernel weight all positively affect grain yield. Path coefficient analysis showed that 100-kernel weight and number of kernels per ear contributed most directly to grain yield. Number of kernels and 100-kernel weight are important selection criteria for improving grain yield in quality protein maize.

2.5 Genetic Diversity

De Carvalho *et al*. (2008) characterized 43 open-pollinated maize varieties using morphological markers comprising 41 traits. The obtained morphological data were analyzed using multivariate analysis. Based on dissimilarity, four groups were identified. Significant diversity was discovered among the genotypes, which could serve as a valuable resource for worldwide breeding.

Rahman *et al*. (2008) analyzed the genetic variability of morphological and maturity traits in 41 maize populations. All traits within these populations exhibited a significant amount of variation. The cluster analysis of the data revealed a great deal of variation between these populations. Moreover, it was observed that a few genotypes from the tested population reached maturity in fewer days than controls, indicating that they may serve as a useful source for plant breeders to develop new varieties by selecting other desirable traits.

Marker and Krupakar (2009) used Mahalanobis D^2 analysis to assess genetic divergence in exotic maize germplasm. Five genotype clusters were identified. Cluster V had 5 genotypes, and clusters I and IV had 4 each. The highest inter-cluster distance was between cluster II and cluster V, followed by cluster I and V, indicating more genetic variability in these clusters. Cluster II had the highest mean values for 50 percent tasseling, 50 percent silking, plant height, ear height, ear length, grains per row, harvest index, and protein content.

Singh (2009) analyzed 41 maize inbred lines for genetic divergence using Mahalanobis D^2 statistics on 20 characters. The D^2 analysis showed that genotypes were diverse and grouped into nine clusters, with clusters 1 and 5 having the most entries each. Clusters 3 and 8 had the greatest inter-cluster distance, followed by 3 and 8, 2 and 7. 100 kernel weight, dry stover yield, relative water content, proline content, and grain yield contributed the most to genetic diversity.

Ganesan *et al*. (2010) examined the genetic diversity of 105 adapted maize germplasm and classified it into four clusters. Cluster IV had 53 genotypes, followed by cluster II with 32 genotypes. Plant height influenced total divergence, followed by ear length, kernels rows per cob, and ear height. The intra-cluster distance was greatest in cluster II, followed by clusters I and IV. The inter-cluster distance was greatest between clusters III and IV, followed by I and III. Based on inter-cluster distances, genotypes of clusters I, III, and IV are promising as parents in maize hybridization programs to develop heterotic hybrids.

Yadav and Singh (2010) studied various morphometric traits using distinguishability measures of UPOV guidelines and discovered that tassel branching, plant height, number of kernels per row, ear height, ear length, and ear width were the most effective in distinguishing inbred lines from one another. It was confirmed that all inbred lines are morphologically and physiologically distinct. At the morphological level, the maximum and minimum genetic distances were determined.

Ahmad *et al*. (2011) determined the genetic diversity of fourteen distinct maize genotypes. All characteristics, including days to 50 percent pollen shedding, days to 50 percent silking, plant height, ear height, 100-grain weight, harvest index, and grain yield, were significantly affected by the various maize genotypes, according to the results of the analysis.

Gupta and Singh (2011) used 20 maize inbred lines to study genetic diversity. Nine genotype clusters were identified. Supported genetic divergence intra-cluster values ranged from 0.00 to 218.74 (cluster III). In polygenotypic clusters, II, V, VI, VII, VIII, and IX, low intra-cluster values indicate narrow genetic diversity. Uniformity may be due to their similar base material. Cluster IV (HUZM 88, V 994-7) and cluster VII have the highest inter-cluster distance (1528.81). (HKI 1344). The inter-cluster distance was greater than the intra-cluster distance, indicating diversity within clusters and that genotypes within the same cluster are less divergent than genotypes in other clusters.

Kumar *et al*. (2011) assessed the genetic divergence of twenty maize inbred lines utilizing the Mahalanobis D^2 statistic. The inbred lines formed six distinct clusters. The least inter-cluster distance was observed between cluster III and cluster V, while the greatest inter-cluster distance was observed between cluster I and cluster V, indicating that the genotypes of these clusters may be utilized in hybridization programs.

Verma and Kumar (2011) reported that using D^2 analysis, eleven maize genotypes could be grouped into four clusters. The highest inter-cluster D^2 values were found between clusters III and IV and I and IV. Therefore, it is suggested that the genotype of cluster IV could be used in a hybridization program with the genotypes of cluster III and I, respectively, for the development of improved varieties.

Azad *et al.* (2012) studied genetic divergence in thirty maize inbred lines using multivariate analysis and found six clusters. All six clusters had low intra-cluster distances, indicating closely related genotypes. The closest clusters were I and IV, and II and III. Cluster V had 9 and IV had 1 genotype. Cluster VI had the highest kernel yield and yield-related traits except for days to 50 percent tasseling and 50 percent silking. Cluster II had the smallest ears. Days to maturity and ear diameter most affected character divergence. Six inbred lines were chosen based on medium to high inter-cluster distances. High-performing hybrids developed using these genotypes may have higher heterosis.

Reddy *et al.* (2012) evaluated 50 maize genotypes for genetic divergence using the Mahalanobis D^2 statistic. Genotypes were clustered into 8 groups. Cluster III had 20 genotypes, followed by I, II, IV, VIII, V, VI, and VII. The inter-cluster distances were larger than the intra-cluster distances, indicating greater genetic diversity between groups. The inter-cluster distance was highest between clusters II and VI, then II and V, II and VII, I and VI, I and VII, and IV and VI. Cluster VIII had the highest intra-cluster distance, while V, VI, and VII had the least. Grain yield per plant was highest in cluster VII, followed by VI and V. Based on inter-cluster distances, genotypes in clusters I, II, IV, V, VI, and VII can be used as parents for hybridization.

Alam *et al.* (2013) examined the genetic divergence of 17 inbred maize lines using Mahalanobis D^2 statistics. The genotypes were clustered into four groups. Cluster II contained the most lines, whereas cluster I only contained a single genotype. The greatest distance between clusters was observed between clusters I and IV, and the smallest between clusters I and II. The intra-cluster distance was greatest within cluster IV and smallest within cluster I. The genotypes in cluster III exhibited superior performance characteristics, including a shorter growth duration, a shorter stature, a shorter ear height, a higher shelling percentage, and an adequate yielding capacity.

Aliu *et al*. (2013) conducted an experiment to measure the genetic diversity of twelve local maize genotypes. Characteristics of morphology, physiology, and chemical characters were used to estimate the variations. All characteristics exhibited significant variation between these local genotypes. On the basis of their similarity, cluster analysis classified these genotypes into three clusters. As a result, these genotypes were regarded as a good source for developing productive maize hybrids, as they contained a great deal of genetic diversity in traits that are necessary for increased yield.

Kage *et al*. (2013) studied the genetic diversity of new maize inbred lines and found significant differences. 14 clusters of inbred lines indicate genetic diversity. Cluster I have the highest genotypes (67). The maximum inter-cluster distance was between clusters II and XII (22.41), and the maximum intra-cluster distance was in cluster XII (5.46). Cluster mean character performance varied significantly. These genetically diverse inbred lines can be used to create superior hybrids, synthetics, and composites.

Maruthi *et al*. (2013) analyzed morphological characterization of 62 late maturing maize genotypes for genetic relationships. Eight principal components contributed 73.46 percent of genetic diversity through Principal component analysis. The most important morphological traits are ear diameter, ear length, and plant height. Cluster analysis separated genotypes into three groups. Each had subgroups. The morphological display is the final product of genetic makeup, and diversity in morphological traits can be used to improve cultivars and conserve germplasm.

Sharma *et al*. (2013) attempted to describe the genetic diversity and similarity of 20 inbred maize lines using morphological markers. The dendrogram classified the 20 lines into five clusters based on their similarity: A, B, C, D, and E. The researchers concluded that crosses involving genotypes from clusters A and E will be more fruitful.

Shrestha (2013) characterized 60 maize inbred lines morphologically. These inbred lines had high genetic diversity, according to descriptive statistics and cluster analysis. During cluster analysis, 5 inbred lines were grouped together because of their close resemblance and differences in plant height, tassel branching, ear height, tassel length, days to silking, days to anthesis, and anthesis-silking interval. Diverse inbred lines were deemed suitable for hybrid and variety development.

Zaman and Alam (2013) analyzed genetic divergence in 39 maize genotypes using Mahalanobis D^2 statistics. Seven genotype clusters were identified. Cluster VI had the most genotypes. Cluster IV had the highest yield per hectare with medium plant height, days to maturity, and tasseling, silking, and shelling percentages. The highest inter-cluster distance was observed between clusters V and III, followed by clusters I and III and cluster III and VII, indicating that the genotypes in these clusters could be used in hybridization programs.

Natraj *et al.* (2014) examined genetic divergence in 39 inbred maize lines using Mahalanobis D^2 statistics analysis. Twelve clusters were made from the accessions. Intra-cluster genetic divergence ranged from 0.00 to 9.25. The closest clusters were VI and VIII, then III and V. Clusters III and XI had the maximum intra-cluster distance, followed by III and XII. Grain yield per plant (31.71%), days to 50% tasseling (22.81%), and 100-grain weight (18.62%) contributed most to genetic diversity.

Seshu *et al.* (2014) examined 63 genotypes of sweet corn utilizing the Mahalanobis D^2 statistic for eleven traits. The genotypes were clustered into eight distinct groups. Cluster III, containing 14 genotypes, was the largest, followed by clusters IV and V, I and II, and VI, VII, and VIII. Inter-cluster distances were larger than intra-cluster distances. Between clusters VI and VIII, the maximum inter-cluster distance was observed. Cluster VII had the highest mean grain yield per plant, followed by clusters VI and V.

Shukla *et al.* (2014) conducted a diversity analysis on 64 maize genotypes using Mahalanobis's generalized distance D^2 analysis and discovered that biological yield per plant contributed the most to genetic divergence. A total of sixty-four genotypes were categorized into five clusters, with a maximum of sixty genotypes belonging to a single cluster having the highest intra-cluster D^2 value. They suggested that the selection of parents from diverse clusters would be advantageous for crop improvement via single cross hybrid production.

Singh *et al.* (2014) studied genetic divergence in 46 maize inbred lines using Tocher's canonical and Euclidean methods. Both divergence methods grouped genotypes into seven clusters. This showed diversity in the studied inbred lines. Canonical (vector) analysis suggested that plant height, stem girth, and number of leaves per plant contributed most to total variability in the lines. PMS134 was the most diverse inbred with CML324, followed by M8-3, CML158, 6152, and CML399. These inbred lines can be used to breed maize for yield and component traits.

Gonsiorkiewicz *et al.* (2015) explored genetic divergence and relative trait contributors among hybrids for extraction of inbred lines. Combined analysis of variance and multivariate analysis were performed on the data. The multivariate methods were consistent with one another, and the trait that contributed the most to the divergence was the weight of 100 grains, which exhibited similar grain yield behavior between hybrids in both years.

Iqbal *et al*. (2015) determined that grain yield per plant displayed the maximum variance at 3,394.8, followed by plant height at 1,243.3. According to the multivariate analysis, the Euclidean distance was maximum between 15329 and 14909, 15329 and 14959, and 24690. Cluster analysis classified the complete genotypes into five groups, indicating their extensive genetic background.

Nyaligwa (2015) attempted to investigate the genetic diversity of 79 elite maize inbred lines and to identify breeding-specific genotypes. Using cluster analysis, the inbred lines were divided into three main genetic groups. The principal component analysis separated the inbred lines into two main clusters and explained 67 percent of the total genetic variation detected among them. The study identified six elite maize inbred lines from Cluster I, four from Cluster II, and four from Cluster III with significant genetic differences for exploiting heterosis through hybrid breeding.

Rohman *et al*. (2015) used Mahalanobis's statistic (D^2) and principal component analysis to characterize maize inbred lines under salinity stress. All the characters had significant variance. Twenty-five inbred lines formed five clusters at 8 dS salinity, according to multivariate analysis. Cluster III, with eight genotypes, had the highest intra-cluster distance, while cluster II had the lowest. The closest clusters were II and V, and I and III. Cluster II had the highest plant height, cob height, above-ground dry mass, cob per plant, and grain yield per plant. Considering cluster distance, inter-genotypic distance, and other agronomic performances, genotypes CZ12, CZ19, CZ26, CZ29, CZ31, CZ32, CZ33 & CML470 from cluster III and CZ27, CZ37, CML251 and CML456 from cluster V may be better parents for future hybridization programs to obtain desirable segregates of different yield and yield contributing characters under salinity stress.

Pandit *et al*. (2016) assessed genetic diversity in 20 maize genotypes for 21 morphometric traits. Plant height, ear height, days to tasseling, days to silking, and kernel yield per plant varied widely among the 20 maize genotypes. Green-glume base, conico-cylindrical, and white stones predominated. Qualitative and quantitative traits had poor and no correlations. Different clustering methods showed wide variation among and within cluster genotypes.

Thakur *et al*. (2016) observed considerable variation and categorized various test genotypes into two groups. LM-19-07 and HKI-1348 outperformed all other genotypes in terms of grain yield per plant, cob length, cob girth, and kernels per row, based on their average performance. Among all genotypes, LM-02-08 had the highest protein content. Based on a pooled analysis of morphological genotypes, LM-19-07 was determined to be superior and the most divergent of all the accessions examined.

Kumari *et al*. (2017) used 12 quantitative variables to evaluate 75 maize accessions. The accessions varied morphologically. Cluster analysis grouped genotypes based on phenotypic traits into five clusters. Principal component analysis was used to group accessions and study trait contribution to phenotypic variation. The first two principal components explained 50 percent of phenotypic variation. Height, ear width, number of kernel rows, and number of kernels per row contributed to phenotypic diversity. The different groups can be used to create diverse inbred lines and diversify heterotic pools.

Kandel *et al*. (2017) analyzed the genetic diversity of inbred lines of maize (*Zea mays* L.) under heat stress conditions. Twenty maize inbred lines were evaluated for days to 50 percent anthesis and silking, anthesis–silking interval, leaf firing, tassel blast, SPAD reading, and leaf senescence, plant and ear height, leaf area index, ear per plant, cob length and diameter, number of kernels/ears, number of kernel rows/ear, number of kernel rows, silk receptivity, shelling percentage, and grain yield to identify superior heat stress tolerant lines. The analysis of variance revealed significant differences between all characteristics. A multivariable analysis revealed that twenty inbred lines clustered into four groups. Inbred lines belonging to a superior cluster could be viewed as extremely beneficial for developing heat-tolerant varieties and other breeding endeavors.

Matin *et al*. (2017) studied genetic diversity in maize inbred lines. Cluster III had the most similar genotypes. Cluster V had the minimum genotype. The highest inter-cluster distance was observed between clusters VI and III, followed by clusters VI and V and clusters V and I, indicating greater diversity between them. Genotypes in these clusters could be used as donor parents for new maize hybrid development. Cluster V had the greatest intra-cluster distance, and II had the least. Cluster VI had the highest thousand seed weight and yield (t/ha) contributed most to genetic divergence. Negative values for days to 50 percent tasseling, ear length, and thousand seed weight indicated less primary and secondary differentiation.

Shazia *et al*. (2017) evaluated genetic diversity in 47 maize inbred lines using morphological traits. Seven clusters were used to organize the inbreds. Cluster IV contained the most inbred individuals, while clusters III and VI contained the fewest inbred lines. Clusters II and V, V and VI, and VI and VII had the greatest distance between them, indicating a greater likelihood of heterotic hybrids if parents are selected from these clusters. The highest contribution to total divergence was made by days to tasseling and days to maturity. This study illuminated the variability pattern of inbred lines, which will be useful for their future application.

Hassan *et al*. (2018) studied genetic diversity in maize inbred lines. Genotypes were grouped into four clusters. Cluster II had 16 maize genotypes, followed by I and III. Inter-cluster divergence was greatest between II and IV and smallest between I and III. Maximum inter-cluster distances show cluster II genotypes are far from cluster IV. Cluster II genotypes have a high intra-cluster distance, indicating a high degree of divergence, and their mean height and yield per plant are higher. Cluster II genotypes with high plant height, thousand kernel weight, and yield per plant are suitable for future hybridization.

Kumar *et al*. (2018) used D^2 statistics to study the genetic diversity of maize inbred lines. 18 inbred maize lines from different populations were used. ANOVA for the mean sum of squares due to inbred lines was significant for ten characters except for days to flowering, days to brown husk, and ear girth, indicating the selection of promising genotypes for yield improvement. All the genotypes were grouped into five clusters. Cluster V had the most intra-cluster distance. Cluster I and V had the highest inter-cluster distance, followed by Cluster I and IV, Cluster I and II, Cluster III and V, and Cluster III and IV.

Singh *et al*. (2019) found genetic variation and diversity among the studied genotypes for morpho-physiological traits. Few parameters had high heritability and genetic advance as a percent of the mean. 196 genotypes were clustered based on D^2 values. Cluster VIII had the highest D^2 value, followed by Cluster III. The highest inter-cluster D^2 distance was between cluster IV and cluster VI, and the lowest was between cluster I and cluster VII.

Joshi *et al*. (2021) studied genetic diversity in interspecific hybridized advanced maize lines. To improve maize germplasm, 169 teosinte-derived maize inbred lines were developed and studied to assess genetic diversity in 14 morphological traits and cluster the lines. All traits showed significant variation among genotypes in ANOVA. High heritability and genetic advance were observed for anthesis silking interval, flag leaf length, plant height, ear per plant, ear length, ear diameter, number of kernel rows/ear, number of kernels/rows, and thousand kernel weight. High heritability and moderate genetic advance were observed for days to anthesis and days to silking. Flag leaf width, node bearing cob, and grain yield/plant had moderate heritability and high genetic advance.

Shankar *et al*. (2021) assessed the genetic diversity of maize (*Zea mays* L.) inbred lines based on 21 agro-morphological characteristics. Mahalanobis D^2 statistics divided 48 maize inbred lines into 11 clusters. Cluster I had 15 inbred lines, followed by III and V (9). Chlorophyll content contributed most to genetic divergence, followed by an anthesis-to-silking interval, cob girth, cob weight, hundred-grain weight, number of kernels per row, days 75 percent brown husk, plant height at 90 DAS, cob length, and number of kernels rows per cob. Crossing between cluster VIII and cluster X genotypes is possible, and hybrids in these clusters could be used as donor parents for new single cross maize hybrid development to improve yield.

Aman (2021) studied genetic variability, heritability, and association of quantitative maize traits. He concluded that the success of a crop improvement program depends on the population's genetic variability and heritability, which determines how far selection can go. Heritability doesn't prove genotype selection improves genetics. Genetic advance and heritability are helpful. High heritability isn't always linked to genetic advance, so both should be considered. Genetic variability for a given trait is required for systematic breeding. Variability in a crop's germplasm collection is key to breeding better varieties. Maize breeding programs use correlation and path coefficient analysis.

CHAPTER 3

MATERIAL AND METHODS

The experiment entitled "**Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu**" was conducted during *Kharif* 2021. The details regarding the material used, experimental procedures followed and techniques adopted have been mentioned in this chapter.

3.1 Location of the Experiment

The research work was carried out at the Maize Research Station, SKUAST-J, Udhampur, UT-J&K during *Kharif* season 2021.

3.2 Plant Material

A total of 30 maize inbred lines of diverse origin were procured from four different institutes, namely W.N.C. Hyderabad, HAU Karnal, VPKAS Almora, and Maize Research Station Udhampur and evaluated for various traits, at Research Farm of Maize Research Station, SKUAST-J, Udhampur, J&K. The details of experimental material are given in table 3.1.

3.3 Field Experiment Layout:

The material underwent testing using a Randomized Block Design. The experiment was carried out in three replications, each of which included a total of 30 different maize inbred lines. Each treatment was sown in two rows, measuring three meters in length each and a planting geometry of 60×25 cm. The experiment was carried out using standard package of practices for raising the maize crop.

Table 3.1: Origin pedigree and source of the maize inbred lines studied for morpho-agronomical traits

S. No.	Inbred lines	Pedigree	Institute maintaining the line
1	WN 1207	P31C4S5B-33- #- #-11-BBBB-B-B-3	W.N.C. Hyderabad
2	WN 9071-2	CML 116	W.N.C. Hyderabad
3	WN 2453	CM 137	W.N.C. Hyderabad
4	WN 129	CM 152	W.N.C. Hyderabad
5	WN 24249-1	WNCDMR 10RYF W8375	W.N.C. Hyderabad
6	WN 2538	CM 115	W.N.C. Hyderabad
7	WN 2489	DMR QPM 03-118- # -38	W.N.C. Hyderabad
8	WN 33153	HKIPC5	W.N.C. Hyderabad
9	WN 52362	BPT 11	W.N.C. Hyderabad
10	WN 5279	HEY POOL-2011-38-2-1-1-1-1-1	W.N.C. Hyderabad
11	WN 31984	E57B	W.N.C. Hyderabad
12	WN 52188	G18SEQC5F76-2-1-2-1-1B*8	W.N.C. Hyderabad
13	SMSF 7752	CM 123	W.N.C. Hyderabad
14	EV 1439	EV 1439	W.N.C. Hyderabad
15	HKI-193-1	CML 193	HAU Karnal
16	PFSR-10109	PFSR-10109	W.N.C. Hyderabad
17	EV 1465	NC 392	W.N.C. Hyderabad
18	EV 1463	NC 390	W. N.C. Hyderabad
19	UDMI-128-1-5	CML 114	MRS, SKUAST-J, Udhampur
20	V-351	V -351	VPKAS Almora
21	WN 32296	WNCDMR 10RYWS 8384(B)	W.N.C Hyderabad
22	HKI-536	HKI-536	HAU Karnal
23	HKI-323-4-1	HKI-323	HAU Karnal
24	WN 4614-1	DMR N14	W.N.C. Hyderabad
25	WN 2199	CML 427	W.N.C. Hyderabad
26	WN 1079	P31C4S5B-85-##-1-4-5-BBB-B-B-3	W.N.C. Hyderabad
27	WN 554	CML 259	W.N.C. Hyderabad
28	Z-490-26	CA14502-BBB-BB/ (DT/LN/EM-46-3-1x CML311-2-1-3)-B-F153-1-1-1-B)-BBB-1-B	W.N.C. Hyderabad
29	HKI-1105-2-1	HKI-1105	HAU Karnal
30	WN 2402-2	LM 14	W.N.C. Hyderabad

3.4 Recording of Experimental Data

Table 3.2: DUS characters recorded

S. No.	Characteristics
1	Leaf: angle between blade and stem
2	Leaf: attitude of blade
3	Stem: anthocyanin colouration of brace roots
4	Tassel: time of anthesis
5	Tassel: anthocyanin colouration at base of glume
6	Tassel: anthocyanin colouration of glumes excluding base
7	Tassel: anthocyanin colouration of anthers
8	Tassel: density of spikelets
9	Tassel: angle between main axis and lateral branches
10	Tassel: attitude of lateral branches
11	Ear: time of silk emergence
12	Ear: anthocyanin colouration of silks
13	Leaf: anthocyanin colouration of sheath
14	Tassel: length of main axis above lowest side branch
15	Plant: length
16	Plant: ear placement
17	Leaf: width of blade
18	Ear: length without husk
19	Ear: diameter without husk
20	Ear: shape
21	Ear: number of rows of grains
22	Ear: type of grain
23	Ear: colour of top of grain
24	Ear: anthocyanin colouration of glumes of cob
25	Kernel: row arrangement
26	Kernel: poppiness
27	Kernel: sweetness
28	Kernel: waxiness
29	Kernel: opaqueness
30	Kernel: shape
31	Kernel: 1000 Kernel weight (g)

DUS Trait Observation:

3.4.1 Leaf: Angle Between Blade and Stem

It is the angle between the leaf blade just above the upper ear and the stem. It has two states i.e, small (<45°) and wide (>45°).

3.4.2 Leaf: Attitude of Blade

It is the attitude of the leaf blade present just above the upper ear. Drooping and straight are the two states of the attitude of the leaf blade.

3.4.3 Stem: Anthocyanin Colouration of Brace Roots

Anthocyanin colouration of brace roots on the stem is the presence of anthocyanin pigment which is responsible for the purple colour of brace roots.

3.4.4 Tassel: Time of Anthesis

It is the time interval in days, during which 50 per cent of plant's anthesis occurs on the middle third of the main axis.

3.4.5 Tassel: Anthocyanin Colouration at Base of Glume

It is the presence of purple colour due to anthocyanin pigment at the base of the glume in the middle third of the main axis of the tassel.

3.4.6 Tassel: Anthocyanin Colouration of Glumes Excluding Base

It is the presence of purple colour due to anthocyanin pigment at the glume excluding the base in the middle third of the main axis of the tassel.

3.4.7 Tassel: Anthocyanin Colouration of Anthers

It is the presence of anthocyanin colouration of tassel which is observed in the middle third of the main axis of fresh anthers.

3.4.8 Tassel: Density of Spikelets

It is the density of spikelets that is observed in the middle third of the main axis of the tassel.

3.4.9 Tassel: Angle Between Main Axis and Lateral Branches

It is the angle between the main axis and lateral which is observed in the lower third of the tassel.

3.4.10 Tassel: Attitude of Lateral Branches

It is the attitude of lateral branches which is observed in the lower third of the tassel.

3.4.11 Ear: Time of Silk Emergence

It is the time interval in days taken for silk emergence on 50 per cent of plants.

3.4.12 Ear: Anthocyanin Colouration of Silks

It is the presence of anthocyanin colouration which is observed on the day of silk emergence.

3.4.13 Leaf: Anthocyanin Colouration of Sheath

It is the presence of anthocyanin colour on the leaf sheath just below the ear.

3.4.14 Tassel: Length of Main Axis Above Lowest Side Branch

It is the length of the main axis above the side branch of the tassel. It can be short, medium and long.

3.4.15 Plant: Length

It is the total height of the plant from the base of the stem up to the flag leaf of the plant.

3.4.16 Plant: Ear Placement

It is the placement of an ear on the plant which can be low, medium or high.

3.4.17 Leaf: Width of Blade

It is the width of the leaf blade that is observed on the leaf of the upper ear.

3.4.18 Ear: Length Without Husk

It is the total length of the ear without a husk. It can be short, medium, and long.

3.4.19 Ear: Diameter Without Husk

It is the diameter of the ear without a husk which is observed in the middle of the ear.

3.4.20 Ear: Shape

It is the configuration of the ear which have several states like conical, conico-cylindrical, and cylindrical.

3.4.21 Ear: Number of Rows of Grains

It is the total count of kernels present on each ear.

3.4.22 Ear: Type of Grain

It is the type of grain that is observed in the middle third of the ear.

3.4.23 Ear: colour of top of grain

It is the presence or absence of colouration at the top of grains on the ear.

3.4.24 Ear: Anthocyanin Colouration of Glumes of Cob

It is the presence of anthocyanin colouration in the glumes of each cob.

3.4.25 Kernel: Row Arrangement

It is the arrangement of kernel row which is observed in the middle of each ear.

3.4.26 Kernel: Poppiness

It is the presence or absence of poppiness in the kernels which is observed by heating of kernels and can be utilized as popcorn.

3.4.27 Kernel: Sweetness

It is the presence of sweetness in kernels that are observed at the time of physiological maturity of the crop by using a refractometer.

3.4.28 Kernel: Waxiness

It is the presence or absence of waxiness on kernels.

3.4.29 Kernel: Opaqueness

It is the presence or absence of opaqueness in kernels.

3.4.30 Kernel: Shape

It is the shape of kernels that can be observed as shrunken, round, indented, toothed, and pointed.

3.4.31 Kernel: 1000 Kernel weight (g)

It is the weight of thousand kernels which is calculated in grams.

Agro-morphological Trait Observation:

All observations were based on five plants randomly selected from each plot, except for no. of days to 50 percent tasseling, no. of days to 50 percent silking, and days to 75 percent dry husk, number of plants per plot, and grain yield, which were all recorded per plot (Table

3.2). Observations were made on the following morpho-agronomical traits:

3.4.32 No. of Days to 50% Tasseling

The number of days from the date of sowing until fifty percent of the flowers, also known as tassels, had fully opened and become functional was recorded as the number of days to 50% tasseling.

3.4.33 No. of Days to 50 % Silking

The number of days from the date of sowing until the plants produced 50 percent of their silk was counted and recorded as the number of days to 50% of silking.

3.4.34 No. of Days to 75 % Dry Husk

The number of days that passed from the date that the seeds were sown until the date that 75 percent of the plants showed browning of the husk was counted as the number of days to 75% dry husk.

3.4.35 Plant Height (cm)

At the dry silk stage, it was measured from the base of the plant at ground level all the way up to the node tip of the tassel.

3.4.36 Ear Height (cm)

The length of the ear was measured from the bottom of the stem to the beginning of the first attachment of the cob.

3.4.37 Kernels rows per cob

Each plant was evaluated based on the number of rows of kernels in its cob.

3.4.38 Kernels Per Row

The number of kernels in each cob was counted in a row that had been chosen at random, and the average was calculated from those counts.

3.4.39 Kernels Per Cob

The sum of all of the kernels that comes be found and was counted in each individual cob.

3.4.40 Cob Girth (cm)

The circumference of the cob was determined and recorded in centimeters as the thickness of the ear, specifically in the middle of the cob's ear.

3.4.41 Cob Length (cm)

The length from the base of the ear to the tip was measured as cob length and it is expressed in centimeters.

3.4.42 Stem Girth (cm)

The diameter of stem on the main tiller was recorded using a vernier caliper.

The vernier caliper was used to measure the diameter of the stem on the main tiller.

3.4.43 Number of Cobs Per Plant

The number of cobs per plant was recorded as the total cobs present in the plant.

3.4.44 Number of Plants Per Plot

The total number of cobs present on the plant was recorded as the number of cobs per plant.

3.4.45 1000 Kernel Weight (g)

With the aid of an electronic balance, this was determined by weighing a random sample of 1000 kernels from bulk production of the **s**elected plot.

3.4.46 Moisture Percentage (%)

At harvest, the grain's moisture content was measured using a digital moisture meter (DRAMINSKI MOISTURE METER).

3.4.47 Shelling Percentage (%)

The weight of five cobs chosen at random was recorded. The kernels were then removed by hand from the cobs, and the grain was weighed. Calculating the shelling percentage (%) required:

$$\text{Shelling percentage} = \frac{\text{grain weight}}{\text{cob weight}} \times 100$$

3.4.48 Grain Yield Per Plot (g)

The ears of plants of each plot were harvested by hand. The dried ears were shulled and weighed to determine the seed yield per plot.

3.5 Statistical Analysis

In order to achieve the aims of this investigation, the collected data were analyzed using the following statistical and biometrical methods.

3.5.1 Assessment of Variability

a) Analysis of Variance for the Design of the Experiment:

Randomized Block Design was used to analyze data concerning field experiments through OPSTAT, TNAUSTAT, and R software.

The data for all different traits were statistically analyzed on the basis model disclosed below:

Analysis of variance model for RBD is

$$Yij = \mu + ti + rj + eij$$

Where,

μ = the overall mean

ti = the ith treatment effect

rj = the jth replication effect

eij = the error term

Analysis of RBD

The results of RBD can be arranged in a two-way table according to the replications (blocks) and treatments.

There will be r x t observations in total where r stands for the number of replications and t for the number of treatments (Table 3.3).

Table 3.3 The data are arranged in a two-way table form by representing treatments in rows and replications in columns

Treatment	Replication					Total
	1	2	3	…………	r	
1	Y11	Y12	Y13	…………	Y1r	T1
2	Y21	Y22	Y23	…………	Y2r	T2
3	Y31	Y32	Y33	…………	Y3r	T3
t	Yt1	Yt2	Yt3	………….	Ytr	Tt
Total	R1	R2	R3		Rr	G. T

In this design the total variance is divided into three sources of variation viz., between replications, between treatments and error

$$\mathrm{C.F} = \frac{(\mathrm{GT})^2}{\mathrm{rt}}$$

$$\text{Total SS} = \Sigma\Sigma \mathrm{Yij}^2 - \mathrm{C.F}$$

$$\text{Replication SS} = \frac{1}{t}\sum \mathrm{Rj}^2 - \mathrm{C.F}$$

$$\text{Treatment SS} = \frac{1}{r}\sum \mathrm{Ti}^2 - \mathrm{C.F}$$

$$\text{Error SS} = \text{Total SS} - \text{Replication SS} - \text{Treatment SS}$$

$$\mathrm{C.D.} = \mathrm{S.E.(d)} \times \mathrm{t}$$

$$\text{Where, S.E (d)} = \sqrt{\frac{2\mathrm{EMS}}{\mathrm{r}}}$$

t = critical value of t for a specified level of significance and error degrees of freedom

Based on the C.D. value the bar chart can be drawn.

From the bar, the chart conclusion can be written.

Based on the model given above the expectations of various mean squares were derived as follows (Table 3.4):

Table 3.4: The skeleton ANOVA table for RBD with t treatments and r replications

Sources of variation	d-f	SS	MS	F Value
Replication	$r - 1$	RSS	RMS	$\frac{\mathrm{RMS}}{\mathrm{EMS}}$
Genotype	$t - 1$	GSS	GMS	$\frac{\mathrm{GMS}}{\mathrm{EMS}}$
Error	$(r - 1)(t - 1)$	ESS	EMS	
Total	$Rt - 1$	TSS		

Estimation of S. E., C.V., and C. D.

They were calculated using the following formulae:

$$\mathrm{S.E.\ of\ mean\ (S.E.m)} = \sqrt{\frac{\sigma^2\mathrm{e}}{\mathrm{r}}}$$

$$\mathrm{C.V.} = \sqrt{\frac{\mathrm{EMS}}{\mathrm{Mean}}} \times 100$$

$$\mathrm{C.D.} = \mathrm{t\ at\ error\ d.f.} \times \mathrm{S.E.m} \times \sqrt{2}$$

b) Estimation of Mean and Range

The mean values for each character were worked out by dividing the total by a corresponding number of observations:

$$\overline{X} = \frac{\sum_{i=1}^{n} x_i}{n} = \frac{x_1 + x_2 + x_3 + \cdots + x_n}{n}$$

Where,

$\overline{X}$	=	Mean of character
$\sum X_i$	=	Total of all the observations for character
N	=	Number of observations

The lowest and highest values of the mean of each character represented the range.

c) Estimation of Components of Variation

The variances were estimated using the respective mean squares from the variance Table as per Johnson *et al*. 1955 as below.

$$\mathrm{Environmental\ variance}\ (\sigma^2{}_\mathrm{e}) = \mathrm{EMS}$$

$$\mathrm{Genotypic\ variance}\ \left(\sigma^2{}_\mathrm{g}\right) = \frac{\mathrm{GMS} - \mathrm{EMS}}{\mathrm{R}}$$

$$\mathrm{Phenotypic\ variance}\ \left(\sigma^2{}_p\right) = \sigma^2{}_\mathrm{g} + \sigma^2{}_\mathrm{e}$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of squares

r = Number of replications

d) Estimation of Coefficient of Variation

The genotypic and phenotypic coefficients of variation were calculated as per Burton, (1952).

i. Genotypic Coefficient of Variation

$$\mathrm{GCV}(\%) = \frac{\sigma^2{}_{\mathrm{g}}}{\overline{\overline{\mathrm{X}}}} \times 100$$

Where,

$\sigma^2{}_{\mathrm{g}}$ = Genotypic variance and,

$\overline{X}$ = Mean of character

ii. Phenotypic Coefficient of Variation

$$\mathrm{PCV}(\%) = \frac{\sigma^2{}_{p}}{\overline{\overline{\mathrm{X}}}} \times 100$$

Where,

$\sigma^2{}_{p}$ = Phenotypic variance and,

$\overline{X}$ = Mean of character

The high, medium, and low GCV and PCV estimates were classified as

Low : up to 10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

e) Estimation of Heritability (h^2)

Heritability in a broad sense was estimated as suggested by Hanson *et al.* (1956).

$$\mathrm{h}^2(\mathrm{b.s.}) = \frac{\sigma^2{}_{\mathrm{g}}}{\sigma^2{}_{p}}$$

Where,

h^2 = Heritability

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_p$ = Phenotypic variance

The high, medium, and low heritability estimates were classified on the basis of values are given by Johnson *et al*. (1955).

Low heritability	= < 10 %
Moderate heritability	= 10-30 %
High heritability	= > 30 %

f) Genetic Advance (G.A.)

Genetic advance (at 5 % selection intensity) was calculated using the formula given by Allard (1960).

i. Genetic advance (G.A.)

$$\mathrm{G.A} = \frac{\sigma^2{}_g}{\sigma^2{}_p} \times \sigma_p \times \mathrm{K}$$

Where,

$\sigma^2{}_g$ = Genotypic variance

$\sigma^2{}_p$ = Phenotypic variance

K = Selection differential (at 5 % selection = 2.06)

Σ_p = Phenotypic standard deviation

ii. G.A. as a percentage of means (GAM)

$$\mathrm{GAM} = \frac{\mathrm{GA}}{\overline{\mathrm{X}}} \times 100$$

Where,

G. A. = Genetic advance

$\overline{\mathrm{X}}$ = Character mean

GA (As a percentage of mean) was classified as

Low : 10 per cent

Medium : 10 to 20 per cent

High : > 20 per cent

3.5.2 Correlation Coefficient:

To calculate the correlation coefficient between any two traits, estimates of variances and covariances were substituted according to the formula proposed by Al-Jibouri *et al.* (1958). The significance of the correlation coefficient was evaluated using the following form:

$$\mathrm{t} = \frac{\mathrm{r}.(\mathrm{n}-2)^{0.5}}{(1-\mathrm{r}^2)^{0.5}}$$

Where,

n = Number of treatments, and,

r= Correlation coefficient

3.5.3 Path Analysis

Path analysis, which was developed by Wright (1921) and suggested by Dewey and Lu (1959)., was the first step that was used to establish a cause-and-effect relationship. This step involved partitioning the correlation coefficient into direct and indirect effects

Path coefficients were obtained by solving a set of the simultaneous equation of the form as per Dewey and Lu (1959).

$$\mathrm{r}_{\mathrm{ny}} = \mathrm{P}_{\mathrm{ny}} + \mathrm{r}_{\mathrm{n2}}\mathrm{P}_{\mathrm{2y}} + \mathrm{r}_{\mathrm{n3}}\mathrm{P}_{\mathrm{3y}} + \cdots$$

Where,

r_{ny} = represents the correlation between one component and yield

P_{ny} = represents the path coefficient between that character and yield

R_{n2}= represents the correlation between that character and each of the other components in turn.

$$\begin{array}{ccc} \text{Matrix A} & \text{Matrix B} & \text{Matrix C} \\ \begin{matrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{matrix} & \begin{matrix} r_{11} & r_{12} & r_{13}\ldots\ldots\ldots\ r_{1n} \\ r_{21} & r_{22} & r_{23}\ldots\ldots\ldots\ r_{2n} \\ r_{n1} & r_{n2} & r_{n3}\ldots\ldots\ldots\ 1 \end{matrix} & \begin{matrix} P_{1y} \\ P_{2y} \\ P_{3y} \end{matrix} \end{array}$$

Where,

r_{12}= r_{21} and so on

r_{1y}= Correlation between one component character and seed yield

The, B' matrix was inverted $[B]^{-1}$ and path coefficients (P_{ij}) were obtained as,

i.e. $P_{ij} = (B)^{-1}.A$

The indirect effects of a specific character through other characters were calculated by multiplying the direct paths and specific correlations between these characters individually.

$$\text{Indirect effects} = r_{ij} \times p_{iy}$$

Where,

i = 1 to 9

j = 1 to 9

P_{iy} = P_{1y}, P_{2y}, ... , P_{ny}

Path coefficient (Pij), correlation coefficient (rij), and residual factors (R) were depicted using a diagram. Using the following formula, the residual factor, or yield variation not accounted for by these associations, was determined.

Residual factor (R) = $(1 – R^2)$

Where,

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

P_{1y}, P_{2y}, ..., P_{ny} = Direct path values

r_{1y}, r_{2y}, r_{ny} = Correlation coefficient

3.5.4 Analysis of Genetic Divergence using Mahalanobis D^2 Statistics

Data recorded on characters were used for Mahalanobis D^2 statistics (Mahalanobis, 1936) as explained by Rao (1952) to group the genotypes into different clusters.

Mahalanobis D^2 analysis between two genotypes estimated on the basis of the 'p' characters are given by the equation:

$$\mathrm{D}^2 = \sum_{\mathrm{i=l}}^{\mathrm{p}} \sum_{\mathrm{j=l}}^{\mathrm{p}} \mathrm{wij}\ (\mathrm{Xi1} - \mathrm{Xi2})\ (\mathrm{Xj1} - \mathrm{Xj2})$$

Where,

wij = variance-covariance matrix

wij = reciprocal of (wij), (i, j = 1,2. , p).

$Xi1$ = sample mean for i th character for the first sample

$Xi2$ = sample mean for i th character for the second sample

In the present study, 17 characters (p = 1 to 17) were used to perform the above analysis. For conducting D^2 analysis, the computer program “TNAUSTAT” was used. The D^2 value was calculated for each pair of germplasm lines.

3.5.5 Estimates of Genetic Divergence

Using the method provided forward by Rao (1952) and Singh and Chaudhary (1985), the genetic divergence was calculated. Under the following headings, the specifics of the analysis are described.

1. Calculation of D^2 values
2. Contribution of each character, individually, to the overall divergence, and
3. Constellation in Groups

3.5.5.1 Calculation of D^2 Values

The differences in transformed values for different characters for each pair-wise combination of the varieties were computed, and D^2-values were determined using the formula below:

Where,

$$\mathrm{D}^2 = \sum_{\mathrm{i=l}}^{\mathrm{p}} (\overline{\mathrm{Y}}\mathrm{ij} - \overline{\mathrm{Y}}ik)^{2}$$

p = Number of characters studied

$\overline{\mathrm{Y}}\mathrm{ij} - \overline{\mathrm{Y}}ik$ are transformed variables of the ith character for two populations

3.5.5.2 Contribution of Each Character, Individually, to the Overall Divergence

The ranking of the differences in uncorrelated means between all of the characters for all of the pair-wise combinations of varieties that were carried out, with the highest differences being given first place in the ranking. In the end, the relative contribution of a character towards total divergence was estimated by computing the percentage of the first rank in that character.

3.5.5.3 Constellation in Groups

The Tocher's method was used to assign different varieties to distinct clusters. A third variety with the lowest average D^2 value for the first two varieties was added to the two varieties with the smallest distance between them. The process continued until the average D^2 value increased, at which point the nearest fourth variety was introduced. The remaining varieties were then considered for the subsequent cluster, and the procedure was repeated until all varieties had been included in various clusters. Using the square root of the average intra-cluster D^2 values, the spatial distances between clusters were calculated.

For each combination (pair of genotypes), the mean deviation (d^2i) was computed, i.e., y_1-y_1 with i = 1, 2, 3..., p, and D^2 values were computed as the sum of the squares of these deviations, i.e., (y_i1-yi^2), where y_i is the transformed version of the original variable xi. Consequently, D^2 values were calculated for each combination. The D^2 values thus obtained for each pair of populations were treated as X^2 and compared to the tabulated X^2 values for p degrees of freedom, where p is the number of traits under consideration.

In all possible permutations, each character was ranked according to $d_i = y_{ij}$-y_{ik} values. The highest mean difference was assigned rank 1, while the lowest was assigned rank p. Where p represents the total amount of characters. Each character's contribution to the total divergence was determined in this manner. The Tocher's method was adopted for grouping varieties into various clusters. Rao (1952) and Singh and Chaudhary (1985) provide a simplified description of this method.

CHAPTER-4

RESULTS

The present investigation entitled **"Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu"** was undertaken to observe 31 DUS characters in 30 maize inbred lines and to generate information on the genetic divergence for various morpho-agronomical traits among maize inbred lines viz., no. days to 50% tasseling, no. of days to 50% silking, no. days to 75% dry husk, plant height (cm), ear height (cm), kernels rows per cob, kernels per row, kernels per cob, cob girth (cm), cob length (cm), stem girth (cm), number of cobs per plant, number of plants per plot, 1000 kernel weight (g), moisture percentage (%), shelling percentage (%), grain yield (q/ha). The results obtained and inferences drawn are described in this chapter.

The experimental findings are described in respect of the following aspects:

4.1 Characterization of Morpho-agronomical Traits

4.2 Analysis of Variance

4.3 Mean Performance of Inbred Lines

4.4 Genetic Variability

4.5 Correlation Coefficient Analysis

4.6 Path Coefficient Analysis

4.7 Estimation of Genetic Divergence

4.1 Morpho-agronomical Characterization as Per DUS guidelines

31 DUS characters were evaluated for each of the 30 maize inbred lines. The recorded observations are shown in Table 4.1to 4.31.

4.1.1 Leaf: Angle Between Blade and Stem:

Among thirty inbred lines, twenty-nine had a small leaf angle and only one had a wide leaf angle.

4.1.2 Leaf: Attitude of Bade

In seven inbred lines, the leaf blade angle was upright/straight, whereas it was drooping in twenty-three inbred lines.

4.1.3 Stem: Anthocyanin Colouration of Brace Roots

In two inbred lines, anthocyanin pigmentation was absent, while it was present in twenty-eight inbred lines.

4.1.4 Tassel: Time of Anthesis

In thirty inbred lines, the time of anthesis varied widely, with one, two, seventeen, and ten inbred lines exhibiting very early, early, medium, and late tasseling, respectively.

4.1.5 Tassel: Anthocyanin Colouration at Base of Glume

Tassel anthocyanin colouration at the base of glume was absent in nine inbred lines, whereas it was present in twenty-one inbred lines

4.1.6 Tassel: Anthocyanin Colouration of Glumes Excluding Base

Tassel anthocyanin colouration of the glumes excluding the base was present in all thirty inbred lines.

4.1.7 Tassel: Anthocyanin Colouration of Anthers

In all thirty inbred lines, anther colouration was present.

4.1.8 Tassel: Density of Spikelets

Out of thirty inbred lines, fifteen inbred lines exhibited sparsely and the remaining fifteen inbred lines had the dense type of spikelet intensities.

4.1.9 Tassel: Angle Between Main Axis and Lateral Branches

Narrow and wide type tassel angle between the main axis and lateral branches was exhibited in fourteen and sixteen inbred lines respectively.

4.1.10 Tassel: Attitude of Lateral Branches

The lateral branch tassel attitude was curved in fifteen inbred lines, strongly curved in one inbred line, and straight in fourteen inbred lines.

4.1.11 Ear: Time of Silk Emergence

The time of silking in thirty inbred lines showed a wide range of variation, with one, two, seventeen, and four inbred lines exhibiting very early, early, medium, and late silk emergence, respectively.

4.1.12 Ear: Anthocyanin Colouration of Silks

Silk anthocyanin pigmentation was present in all thirty inbred lines

4.1.13 Leaf: Anthocyanin Colouration of Sheath

Leaf-sheath anthocyanin pigmentation was absent in sixteen inbred lines and present in fourteen inbred lines.

4.1.14 Tassel: Length of Main Axis Above Lowest Side Branch

There were approximately five and twenty-five inbred lines with the medium and long type of tassel length of the main axis above the side branch respectively.

4.1.15 Plant: Length

The height/length of thirty inbred lines was categorized into three groups: short (zero), medium (eight inbred lines), and long (twenty-two).

4.1.16 Plant: Ear Placement

On the plant, two inbred lines exhibited low ear placement and twenty-eight inbred lines exhibited medium ear placement.

4.1.17 Leaf: Width of Blade

In thirty inbred lines, leaf width was also categorized into three groups: narrow, medium, and broad, and was present in fourteen, twelve, and four inbred lines respectively.

4.1.18 Ear: Length Without Husk

In one inbred line, ear length without husk was found short, whereas in twenty inbred lines, it was medium and in nine inbred lines it was long.

4.1.19 Ear: Diameter Without Husk

Ear diameter without husk less than 4 cm was present in twenty-two inbred lines and in eight inbred lines, it was present between 4 and 5 cm.

4.1.20 Ear: Shape

In five inbred lines, the ear shape was conical, while in twenty-two and three inbred lines, the ear shape was conical-cylindrical and cylindrical, respectively.

4.1.21 Ear: Number of Rows of Grains

Five out of thirty inbred lines had less than 10 rows of kernels per cob, while seventeen inbred lines had between 10 and 12 rows and eight inbred lines had more than 12 rows of kernels per cob.

4.1.22 Ear: Type of Grain

Flint and semi-flint/dent kernel types were observed in twenty-six and four inbred lines, respectively.

4.1.23 Ear: colour of top of grain

In thirty inbred lines, three types of kernels colour were observed: eight yellow inbred lines, six orange inbred lines, and sixteen yellow with cap inbred lines.

4.1.24 Ear: Anthocyanin Colouration of Glumes of Cob

In all thirty inbred lines, white ear anthocyanin colouration of glumes of cob was present.

4.1.25 Kernel: Row Arrangement

In three and twenty-seven inbred lines, the arrangement of the kernel rows was irregular and straight, respectively.

4.1.26 Kernel: Poppiness

Out of all thirty inbred lines kernel poppiness was found in seventeen inbred lines and was absent in the remaining.

4.1.27 Kernel: Sweetness

Kernel sweetness was absent in all thirty inbred lines.

4.1.28 Kernel: Waxiness

All inbred lines were found devoid of kernel waxiness.

4.1.29 Kernel: Opaqueness

Opaqueness was absent in all thirty lines

4.1.30 Kernel: Shape

In twenty-one inbred lines, the kernel shape was round, while in three inbred lines, it was shrunken and in six inbred lines it was toothed.

4.1.31 Kernel: 1000 Kernel Weight (g)

Approximately three inbred lines had a small 1000 kernel weight, while twenty-two had a medium 1000 kernel weight and five had a large 1000 kernel weight.

Table 4.1: Leaf: angle between blade and stem

States	**No. of inbred lines**	**Inbred lines**	**Frequency**
Small (<45°)	29	WN1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, WN 33153, WN 52362, WN 5279, WN 31984, WN 52188, SMSF 7752, EV 1439, WN 2402-2, HKI-193-1, EV 1465, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554, Z-490-26, HKI-1105-2-1	**0.97**
Wide (>45°)	01	PFSR-10109	**0.03**

Table 4.2: Leaf: attitude of blade

States	**No. of inbred lines**	**Inbred lines**	**Frequency**
Straight	07	WN 2538, WN 52188, EV 1439, PFSR-10109, WN4614-1, WN 2199, HKI-1105-2-1	**0.23**
Drooping	23	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2489, WN 2402-2, WN 52362, WN 5279, WN 31984, SMSF 7752, HKI-193-1, EV 1465, EV 1463, WN 33153, UDMI-128-1-5, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 1079, WN 554, Z-490-26.	**0.77**

Table 4.3: Stem: anthocyanin colouration of brace roots

States	**No. of inbred lines**	**Inbred lines**	**Frequency**
Absent	02	WN 129, V-351	**0.07**
Present	28	WN 1207, WN 9071-2, WN 2453, WN 24249-1, WN 2538, WN 2489, WN 33153, PFSR-10109, EV 1465, EV 14 63, UDMI-128-1-5, WN 32296, HKI-536, HKI-323-4-1, WN 52362, WN 5279, WN 31984, WN 52188, SMSF 7752, EV 1439, HKI-193-1	**0.93**

Table 4.4: Tassel: time of anthesis

States	No. of inbred lines	Inbred lines	Frequency
Very early (<45 days)	01	EV 1439	**0.03**
Early (45-50days)	02	WN 33153, WN 554	**0.07**
Medium (50-55 days)	17	WN 9071-2, WN 129, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 5279, SMSF 7752, HKI-193-1, EV 1463, V-351, HKI-536, HKI-323-4-1, Z-490-26, HKI-1105-2-1, EV 1465, WN 2402-2	**0.57**
Late (>55 days)	10	WN 1207, WN 2453, WN 31984, WN 52188, PFSR-10109, UDMI-128-1-5, WN 32296, WN 4614-1, WN 2199, WN 1079	**0.33**

Table 4.5: Tassel: anthocyanin colouration at base of glume

States	No. of inbred lines	Inbred lines	Frequency
Absent	**09**	WN 1207, WN 2453, WN 129, WN 24249-1, WN 33153, WN 52362, SMSF 7752, HKI-193-1, HKI-536	**0.30**
Present	**21**	WN 9071-2, Z-490-26, HKI-1105-2-1, WN 2199, WN 1079, WN 554, PFSR-10109, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-323-4-1, WN 4614-1, EV 1465	**0.70**

Table 4.6: Tassel: anthocyanin colouration of glumes excluding base

States	No. of inbred lines	Inbred lines	Frequency
Present	**30**	WN 1207, WN 9071-2, WN 2453, WN 129, WN24249-1, WN 2538, WN 2489, WN 33153, WN 52362, WN 5279, WN 31984, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465, UDMI-128-1-5, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554, Z-490-26, HKI-1105-2-1, WN 2402-2	**1.00**

Layout of field

Sowing

Crop at vegetative stage

Production of Inbred lines

Crop Harvesting

Post-harvest data collection

Plate 4.1: Maize research station, Udhampur, SKUAST- Jammu (J&K)

Table 4.7: Tassel: anthocyanin colouration of anthers

States	No. of inbred lines	Inbred lines	Frequency
Present	**30**	WN 1207, WN 9071-2, WN 2453, WN 129, WN24249-1, WN 2538, WN 2489, WN 33153, WN 52362, WN 5279, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465, UDMI-128-1-5, V-351, WN 32296, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554, Z-490-26, HKI-1105-2-1, WN 2402-2, HKI, WN 31984	**1.00**

Table 4.8: Tassel: density of spikelets

States	No. of inbred lines	Inbred lines	Frequency
Sparse	**15**	WN 9071-2, WN 129, WN 24249-1, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 5279, SMSF 7752, PFSR-10109, EV 1465, EV 1463, WN 32296, HKI-323-4-1, WN 1079	**0.5**
Dense	**15**	WN 1207, WN 2453, WN 33153, WN 31984, WN 52188, EV 1439, HKI-193-1, V-351, UDMI-128-1-5, WN 2402-2, HKI-536, WN 4614-1, WN 2199, Z-490-26, HKI-1105-2-1	**0.5**

Table 4.9: Tassel: angle between main axis and lateral branches

States	No. of inbred lines	Inbred lines	Frequency
Narrow (<45°)	14	WN 1207, WN 2453, WN 33153, WN 31984, WN 52188, EV 1439, HKI-193-1, UDMI-128-1-5, V-351, HKI-536, WN 4614-1, WN 2199, HKI-1105-2-1, WN 2402-2	**0.47**
Wide (>45°)	16	WN 9071-2, WN 129, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 5279, SMSF 7752, PFSR-10109, EV 1465, EV 1463, WN 32296, HKI-323-4-1, WN 1079, WN 554, Z-490-26	**0.53**

Table 4.10: Tassel: attitude of lateral branches

States	No. of inbred lines	Inbred lines	Frequency
Straight	14	WN 1207, WN 2453, WN 33153, WN 52188, HKI-193-1, UDMI-128-1-5, V-351, HKI-536, WN 4614-1, WN 2199, Z-490-26, HKI-1105-2-1, WN 2402-2	**0.47**
Curved	15	WN 9071-2, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 5279, SMSF 7752, EV 1439, PFSR-10109, EV 1465, EV 1463, WN 32296, HKI-323-4-1, WN 1079 WN 554	**0.5**
Strongly curved	01	WN129	**0.03**

Table 4.11: Ear: time of silk emergence

States	No. of inbred lines	Inbred lines	Frequency
Very early (< 48 days)	01	EV 1439	**0.03**
Early (48-53 days)	02	WN 33153, WN 554	**0.07**
Medium (53-58 days)	17	WN 9071-2, WN 129, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 5279, SMSF 7752, HKI-193-1, Z-490-26, HKI-1105-2-1, WN 2402-2, EV 1465, EV 1463, V-351, HKI-536, HKI-323-4-1	**0.57**
Late (>58 days)	04	WN 1207, WN 2453, WN 31984, WN 52188, PFSR-10109, WN 32296, WN 4614-1, WN 2199, UDMI-128-1-5	**0.13**

Table 4.12: Ear: anthocyanin colouration of silks

States	No. of inbred lines	Inbred lines	Frequency
Present	30	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, WN 33153, WN 52362, WN 5279, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554, Z-490-26, HKI-1105-2-1, WN 2402-2, HKI-536, WN 31984	**1.00**

Table 4.13: Leaf: anthocyanin colouration of sheath

States	No. of inbred lines	Inbred lines	Frequency
Absent	16	WN 1207, WN 9071-2, WN 2453, WN 24249-1, WN 33153, HKI-193-1, PFSR-10109, EV 1465, WN 32296, HKI-536, WN 52188, EV 1439, WN 554, HKI-323-4-1, WN 4614-1, WN 1079	**0.53**
Present	14	WN 129, WN 2538, WN 2489, WN 52362, WN 5279, WN 31984, UDMI-128-1-5, V-351, WN 2199, Z-490-26, HKI-1105-2-1, WN 2402-2, UDMI-128-1-5, V-351, WN 2199, Z-490-26, HKI-1105-2-1, WN 2402-2, SMSF 7752, EV 1463	**0.47**

Table 4.14: Tassel: length of main axis above lowest side branch

States	No. of inbred lines	Inbred lines	Frequency
Medium (20-30 cm)	05	WN 33153, WN 5279, V-351, HKI-536, WN 1079, WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489,	**0.17**
Long (>30 cm	25	Z-490-26, HKI-1105-2-1, WN 2402-2, EV 1465, EV 1463, WN 52362, WN 31984, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, UDMI-128-1-5, WN 32296, HKI-323-4-1, WN 4614-1, WN 2199, WN 554	**0.83**

Table 4.15: Plant: length

States	No. of inbred lines	Inbred lines	Frequency
Medium (150-180 cm)	08	WN 1207, WN 2453, WN 129, WN 24249-1, WN 33153, SMSF 7752, EV 1463, V-351	**0.27**
Long (>150 cm)	22	WN 9071-2, WN 2538, WN 2489, WN 52362, WN 5279, WN 31984, WN 52188, EV 1439, HKI-193-1, PFSR-10109, EV 1465, UDMI-128-1-5, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554, Z-490-26, HKI-1105-2-1, WN 2402-2	**0.73**

Table 4.16: Plant: ear placement

States	No. of inbred lines	Inbred lines	Frequency
Low	02	WN 33153, V-351	**0.07**
Medium	28	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 5279, WN 31984, EV 1465, EV 1463, UDMI-128-1-5, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, Z-490-26, HKI-1105-2-1, WN 2402-2	**0.93**

Table 4.17: Leaf: width of blade

States	No. of inbred lines	Inbred lines	Frequency
Narrow (< 8 cm)	14	WN 1207, WN 2453, WN 129, WN 2538, WN 33153, WN 5279, WN 52188, SMSF 7752, EV 1465, EV 1463, V-351, WN 32296, WN 2199, WN 1079	**0.47**
Medium (8-9 cm)	12	WN 24249-1, WN 2489, WN 52362, EV 1439, HKI-193-1, PFSR-10109, UDMI-128-1-5, HKI-536, HKI-323-4-1, WN 4614-1, WN 554, WN 2402-2	**0.40**
Broad (> 9cm)	04	WN 9071-2, WN 31984, Z-490-26, HKI-1105-2-1	**0.13**

Table 4.18: Ear: length without husk

States	No. of inbred lines	Inbred lines	Frequency
Short (<10 cm)	01	V-351	**0.03**
Medium (10-15 cm)	20	WN 1207, WN 24249-1, WN 2538, WN 2489, WN 33153, WN 52362, WN 5279, SMSF 7752, EV 1439, Z-490-26, HKI-193-1, EV 1465, EV 1463, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554	**0.67**
Long (> 15cm)	09	WN 9071-2, WN 2453, WN 129, WN 31984, WN 52188, PFSR-10109, UDMI-128-1-5, HKI-1105-2-1, WN 2402-2	**0.3**

Table 4.19: Ear: diameter without husk

States	No. of inbred lines	Inbred lines	Frequency
Small (<4cm)	22	WN 1207, WN 24249-1, WN 2538, WN 33153, WN 52362, WN 5279, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, WN 1079, WN 554, Z-490-26, WN 31984, WN 52188, SMSF 7752, EV 1439, HKI-193-1, EV 1463, UDMI-128-1-5	**0.73**
Medium (4-5 cm)	08	WN 9071-2, WN 2453, WN 129, WN 2489, PFSR-10109, EV 1465, HKI-1105-2-1, WN 2402-2	**0.27**

Table 4.20: Ear: shape

States	No. of inbred lines	Inbred lines	Frequency
Conical	05	WN 5279, WN 52188, EV 1439, EV 1465, Z-490-26	**0.17**
Conico-cylindrical	22	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, WN 554, SMSF 7752, HKI-193-1, PFSR-10109, EV 1463, UDMI-128-1-5, V-351, WN 2489, WN 31984, HKI-1105-2-1, WN 2402-2	**0.73**
Cylindrical	03	WN 33153, WN 52362, WN 1079	**0.1**

Table 4.21: Ear: number of rows of grains

States	No. of inbred lines	Inbred lines	Frequency
Few (<10)	05	WN 52362, EV 1465, UDMI-128-1-5, V-35, WN 32296	**0.17**
Medium (10-12)	17	WN 2453, WN 2538, WN 33153, WN 5279, WN 31984, WN 52188, SMSF 7752, HKI-193-1, PFSR-10109, EV 1463, HKI-536, HKI-323-4-1, WN 2199, WN 1079, WN 554, HKI-1105-2-1, WN 2402-2	**0.57**
Many	08	WN 1207, WN 9071-2, WN 129, WN 24249-1, WN 2489, EV 1439, WN 4614-1, Z-490-26	**0.27**

Table 4.22: Ear: type of grain

States	No. of inbred lines	Inbred lines	Frequency
Flint	26	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, V-351, WN 32296, HKI-536, WN 1079, WN 554, Z-490-26, V-351, WN 32296, HKI-536, WN 1079, WN 554, Z-490-26, WN 5279, WN 31984, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465, EV 1463, UDMI-128-1-5, WN 33153, WN 52362, HKI-1105-2-1, WN 2402-2, EV 1463, UDMI-128-1-5, WN 33153, WN 52362, HKI-1105-2-1, WN 2402	**0.87**
Semi-flint / semi dent	4	WN 52188, HKI-323-4-1, WN 4614-1, WN 2199	**0.13**

Table 4.23: Ear: colour of top of grain

States	No. of inbred lines	Inbred lines	Frequency
Orange	06	WN 1207, WN 9071-2, WN 24249-1, WN 2489, WN 5279, SMSF 7752	**0.20**
Yellow	08	WN 2453, WN 2538, WN 52362, WN 52188, EV 1439, PFSR-10109, HKI-536, HKI-323-4-1	**0.27**
Yellow with cap	16	WN 129, WN 33153, WN 31984, HKI-193-1, EV 1465 EV 1463, UDMI-128-1-5, V-351, WN 1079, WN 554, HKI-1105-2-1, WN 2402-2, WN 32296, WN 2199, Z-490-26, WN 4614-1	**0.53**

Table 4.24: Ear: anthocyanin colouration of glumes of cob

States	**No. of inbred lines**	**Inbred lines**	Frequency
White	30	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 2199, EV 1463, UDMI-128-1-5, WN 1079, WN 554, WN 33153, WN 2489, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465, Z-490-26, HKI-1105-2-1, WN 2402-2, WN 52362, WN 5279, WN 31984	**1.00**

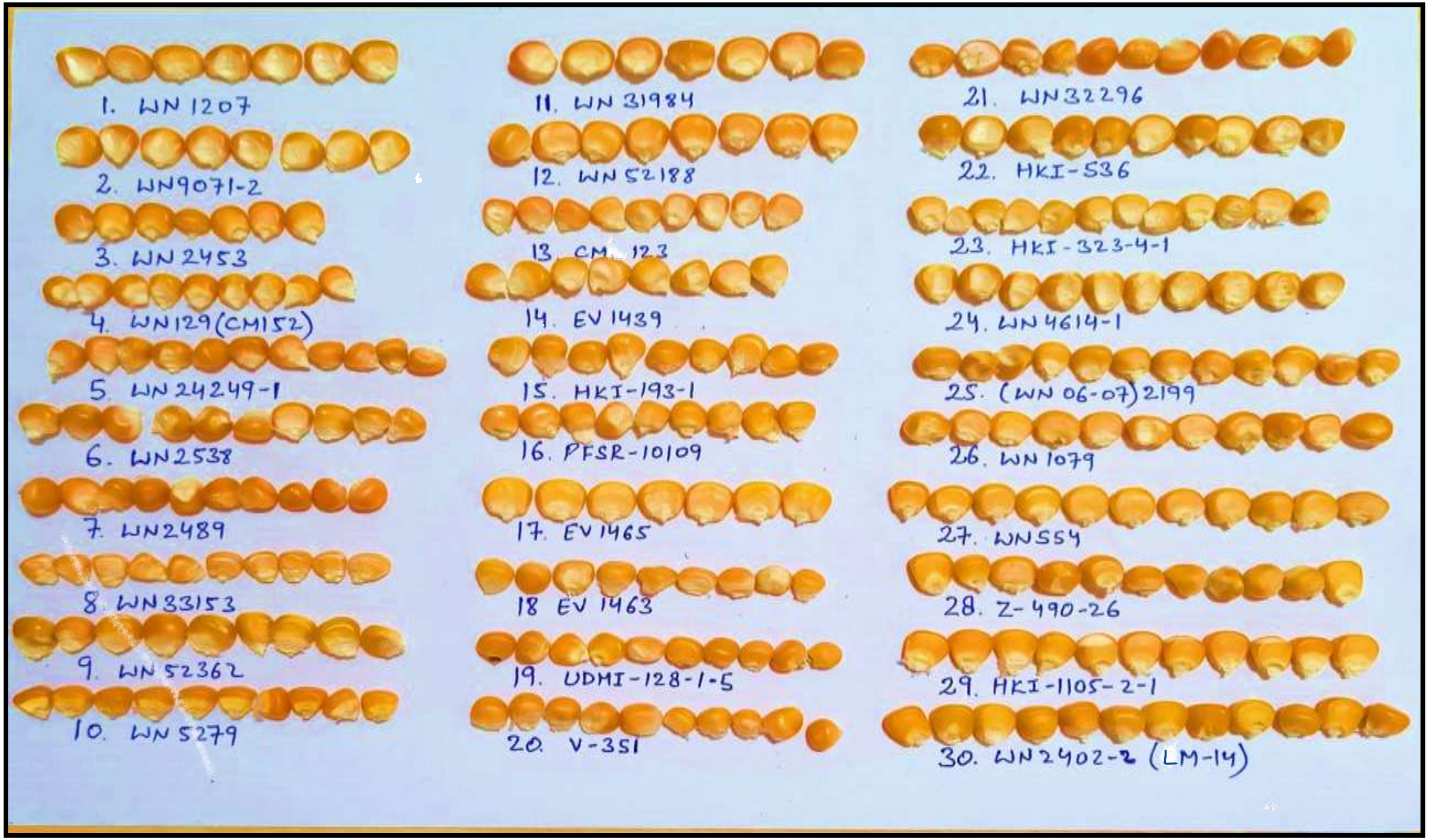

Plate 4.2: Kernels of 30 Maize inbred lines

Table 4.25: Kernel: row arrangement

States	No. of inbred lines	Inbred lines	Frequency
Irregular	03	WN 33153, HKI-323-4-1, WN 2199	**0.1**
Straight	27	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 1079, HKI-193-1, PFSR-10109, EV 1465, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-536, WN 4614-1, WN 5279, WN 31984, WN 52188, SMSF 7752, EV 1439, Z-490-26, HKI-1105-2-1, WN 2402-2, WN 554	**0.9**

Table 4.26: Kernel: Poppiness

States	No. of inbred lines	Inbred lines	Frequency
Absent	13	WN 1207, WN 2453, WN 2489, WN 31984, WN 52188, EV 1465, UDMI-128-1-5, V-351, WN 4614-1, WN 2199, WN1079, WN554, HKI-1105-2-1,	**0.43**
Present	17	WN 9071-2, WN 129, WN 24249-1, WN 2538, WN 33153 WN 52362, WN 5279, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1463, WN 32296, HKI-536, HKI-323-4-1, Z-490-26, WN 2402-2	**0.57**

Table 4.27: Kernel: sweetness

States	No. of inbred lines	Inbred lines	Frequency
Absent	30	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, HKI-1105-2-1, WN 33153, WN 52362, WN 5279, WN 2199, WN 1079, WN 554, WN 2402-2, Z-490-26, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465	**1.00**

Table 4.28: Kernel: waxiness

States	No. of inbred lines	Inbred lines	Frequency
Absent	30	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, HKI-1105-2-1, WN 33153, WN 52362, WN 5279, WN 2199, WN 1079, WN 554, WN 2402-2, Z-490-26, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 31984, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-1010, EV 1465	**1.00**

Table 4.29: Kernel: opaqueness

States	No. of inbred lines	Inbred lines	Frequency
Absent	30	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, HKI-1105-2-1, WN 33153, WN 52362, WN 5279, WN 2199, WN 1079, WN 554, WN 2402-2, Z-490-26, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 33153, WN 52362, WN 5279, WN 2199, WN 1079, WN 554, WN 2402-2, Z-490-26, WN 31984, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465, EV 1463, UDMI-128-1-5, V-351, WN 32296, HKI-536, HKI-323-4-1, WN 4614-1, WN 31984, WN 52188, SMSF 7752, EV 1439, HKI-193-1, PFSR-10109, EV 1465	**1.00**

Table 4.30: Kernel: shape

States	No. of inbred lines	Inbred lines	Frequency
Round	21	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2538, WN 2489, WN 52362, WN 31984, SMSF 7752, WN 554, WN 2402-2, WN 1079, WN 33153, EV 1439, HKI-193-1, PFSR-10109, EV 1465, V-351, WN 32296, HKI-536	**0.7**
Shrunken	3	WN 5279, WN 4614-1, WN 2199	**0.1**
Toothed	6	WN 52188, EV 1463, UDMI-128-1-5, HKI-323-4-1 Z-490-26, HKI-1105-2-1	**0.2**

Table 4.31: Kernel: 1000 kernel weight (g)

States	No. of inbred lines	Inbred lines	Frequency
Small (100-200g)	3	WN 33153, SMSF 7752, WN 2199,	**0.1**
Medium (200-300g)	22	WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2489, WN 52362, WN 2402-2, UDMI-128-1-5, V-351, WN 32296, HKI-536, WN 1079, WN 554, WN 5279, WN 31984, EV 1439, HKI-193-1, PFSR-10109, EV 1465, EV 1463, HKI-1105-2-1	**0.73**
Large (>300g)	5	WN 2538, WN 52188, WN 4614-1, Z-490-26, HKI-323-4-1	**0.17**

4.2 Analysis of Variance

Seventeen distinct morpho-agronomical and yield-contributing traits for thirty genotypes sown in Randomized Block Design were analyzed by means of the analysis of variance (Table 4.32). The data for moisture percentage and shelling percentage were transformed using the binomial distribution prior to variance analysis. The analysis of variance showed that the mean sum of squares for treatments was significant for all traits.

In addition, the experimental material was analyzed in terms of the variance between the treatments. It was evaluated that the mean sum of squares due to treatments was significant for all the traits i.e, no. days to 50% tasseling, no. of days to 50% silking, no. days to 75% dry husk, plant height (cm), ear height (cm), kernels rows per cob, kernels per row, kernels per cob, cob girth (cm), cob length (cm), stem girth (cm), number of cobs per plant, number of plants per plot, 1000 kernel weight (g), moisture percentage (%), shelling percentage (%), grain yield (q/ha).

4.3 Mean Performance of Maize Inbred (*Zea mays* L.) Lines for Various Morpho-Agronomical Traits

The mean values for various morpho-agronomical traits are mentioned in Table 4.33. The results of maize inbred lines for the individual trait have been described as follows:

4.3.1 No. of Days to 50% Tasseling

The trait exemplified a variation between 43.67 and 62.33 days, with a mean of 53.71 days. The inbred line WN 2199 had the highest number of days to 50% tasseling, while EV 1439 had the lowest number of days to 50 % tasseling.

4.3.2 No. of Days to 50% Silking

The range of the trait was between 46.67 and 64.67 days, with a mean of 56.60 days. The inbred WN2199 had the highest number of days to 50% silking, while EV1439 had the lowest number of days to 50% silking.

4.3.3 No. of Days to 75% Dry husk

The trait displayed a range of 96.67 to 113.33 days with a mean of 103.73 days. The inbred line WN 2199 had the highest number of days to 75% dry husk, whereas EV1439 had the lowest.

4.3.4 Plant Height (cm)

The range for this trait was between 125.47cm and 214.40 cm, with a mean value of 167.08 cm. The WN52188 inbred line produced the tallest plants. The inbred line WN 33153 had the shortest plant height.

4.3.5 Ear Height (cm)

The trait displayed a range of 27.60 cm to 90.80 cm with a mean of 60.49 cm. The inbred line WN52188 produced the longest ears. While inbred line WN 33153 exhibited the shortest ear length.

4.3.6 Kernels Rows Per Cob

The range for this trait was 9.20 to 12.67, with a mean of 11.23. The inbred line WN 9071-2 had the greatest number of kernels rows per cob, while inbred line V-351 had the fewest.

4.3.7 Kernels Per Row

The range of the trait was between 10.18 and 25.06, with a mean of 20.04. The inbred line WN 129 had the highest number of kernels per row, whereas the inbred line V-351 had the lowest number of kernels per row.

4.3.8 Kernels Per Cob

The total number of kernels per cob varied between 139.36 and 314.64, with a mean of 227.43. The WN129 had the highest kernels per cob compared to other inbred lines, V-351 had the lowest kernels per cob.

4.3.9 Cob Girth (cm)

The range for this trait was found between 8.60 cm and 14.35 cm, with an overall mean of 11.42 cm. The inbred line WN 2453 had the maximum cob girth, whereas the inbred line V-351 had the minimum cob girth.

4.3.10 Number of Plants Per Plot

The trait exhibited the range from 18.67 to 24 with a mean of 22.41. The highest number of plants per plot was recorded for the inbred lines WN 554 and Z-490-26, While, the inbred line WN 52188 recorded the lowest number of plants per plot.

4.3.11 Cob Length (cm)

The trait ranged from 9.87 to 17.67 cm, with a mean of 13.89 cm. The inbred line WN 9071-2 produced the longest cob length, whereas the inbred line V-351 produced the shortest cob length.

4.3.12 Stem Girth (cm)

The trait displayed a range of 5.11 cm to 8.61 cm, with a mean of 6.86 cm. The inbred line HKI-323-4-1 had the highest stem girth measurements. Whereas inbred line UDMI-128-1-5 had the lowest measurement for stem girth.

4.3.13 Number of Cobs Per Plant

The trait displayed a range of 1 to 1.73 with a mean of 1.13. The highest number of cobs per plant was recorded by the inbred lines WN 5279 while inbred lines WN 1207, WN 9071-2, WN 2453, WN 129, WN 24249-1, WN 2489, WN 33153, WN 52362, WN 31984, EV 1439, HKI-193-1, PFSR-10109, UDMI-128-1-5, V-351, WN 1079, WN 554, Z-490-26, WN 2402-2 had the lowest number of cobs per plant.

4.3.14 1000 Kernel Weight (g)

The trait ranged between 184.91 and 338.72 g, with a mean value of 261.67 g. The inbred line HKI-323-4-1 recorded the highest 1000 kernel weight, whereas the inbred line WN 33153 recorded the lowest.

4.3.15 Moisture Percentage (%)

The trait displayed a range of 23 to 26.37, with a mean value of 24.48. The WN 2538 inbred line had the highest moisture percentage (%) value. While the inbred line V-351 had the lowest moisture percentage (%) value.

4.3.16 Shelling Percentage (%)

The trait displayed a range of 67.70 to 82.52, with a mean value of 78.14. The Z-490-

26 inbred line had the highest shelling percentage (%). As opposed to the inbred line V-351 had the lowest shelling percentage (%).

4.3.17 Grain Yield (q/ha)

The trait depicted a range of 21.22–56.55 q/ha, with a mean value of 41.93 q/ha. The inbred line Z-490-26 had the greatest grain yield (q/ha), while the inbred line V-351 had the lowest grain yield (q/ha).

Table 4.32: Analysis of variance for seventeen morpho-agronomical and yield contributing traits of maize inbred lines

Source of variation	Degree of Freedom	No. of days to 50% tasseling	No. of days to 50% silking	No. of days to 75% dry husk	Plant height (cm)	Ear height (cm)	Kernels rows per cob	Kernels per row	Kernels per cob	Cob girth (cm)
Replication	2	2.18	2.23	12.40	288.91	24.11	0.01	26.98	26.98	0.08
Treatments	**29**	40.73**	41.94**	50.67**	1720.74**	879.07**	2.78**	4195.57**	4195.57**	6.83**
Error	58	2.64	2.43	5.25	208.45	37.69	0.20	354.36	354.36	0.53

Source of variation	Degree of Freedom	Cob length (cm)	Stem girth (cm)	No. of cobs per plant	No. of plants per plot	1000 kernel weight (g)	Moisture percentage (%)	Shelling percentage (%)	Grain yield (q/ha)
Replication	2	0.45	0.08	0.01	3.38	1222.79	0.28	14.94	49.13
Treatments	**29**	10.07**	3.25**	0.13**	6.32**	5094.99**	2.88**	61.00**	306.97**
Error	58	0.62	0.21	0.01	1.45	453.64	0.60	8.18	19.99

**** denotes significance level at 1 %**

Table 4.33: Mean performance of thirty maize inbred lines for various morpho-agronomical and yield contributing traits

Inbred Lines	No. of days to 50% tasseling	No. of days to 50% silking	No. of days to 75% dry husk	Plant height (cm)	Ear height (cm)	Kernels rows per cob	Kernels per row	Kernels per cob	Cob girth (cm)
WN 1207	57.33	60.00	106.33	149.73	52.73	12.53	19.39	242.04	11.17
WN 9071-2	52.33	55.67	100.67	193.87	69.83	12.67	23.85	304.28	14.00
WN 2453	56.67	60.33	105.33	143.40	45.01	11.60	22.10	256.60	14.35
WN 129	53.67	56.33	103.33	132.93	41.47	12.65	25.06	314.64	13.57
WN 24249-1	51.33	53.67	101.00	148.00	46.53	12.60	19.81	249.44	11.67
WN 2538	52.33	55.33	102.33	186.83	60.17	11.07	21.09	237.44	12.45
WN 2489	53.67	56.67	103.33	180.83	73.00	12.40	18.06	221.39	12.68
WN 33153	47.67	50.33	98.00	125.47	27.60	10.93	17.50	200.50	9.47
WN 52362	53.33	56.00	102.33	192.40	86.53	9.73	22.44	216.00	10.10
WN 5279	53.33	56.00	104.33	170.67	71.40	10.67	19.61	205.29	9.70
WN 31984	56.00	59.00	105.67	181.37	84.73	10.93	23.73	259.35	11.27
WN 52188	57.33	61.00	108.67	214.40	90.80	11.27	22.26	251.64	11.43
SMSF 7752	51.33	54.00	99.00	145.53	43.40	11.73	15.11	180.62	10.30
EV 1439	43.67	46.67	96.67	152.33	57.40	12.07	18.31	225.02	11.13
HKI-193-1	52.67	55.67	102.33	174.73	63.57	10.80	17.56	189.77	10.12
PFSR-10109	56.33	59.33	107.33	153.53	39.53	10.80	24.72	266.98	13.52
EV 1465	52.67	55.67	102.33	162.03	61.07	9.87	19.89	198.14	12.80
EV 1463	51.67	54.00	99.33	145.87	54.27	10.80	20.00	216.38	9.73
UDMI-128-1-5	55.33	58.33	104.67	159.90	52.00	9.87	21.33	206.91	10.08
V-351	51.33	53.33	98.67	125.80	26.00	9.20	10.18	139.36	8.60
WN 32296	59.67	62.67	112.00	212.20	82.43	9.73	17.53	170.78	9.63
HKI-536	54.67	57.67	105.00	158.73	55.40	11.33	20.22	228.58	11.27
HKI-323-4-1	53.67	56.67	103.00	162.20	70.07	11.20	21.06	234.81	11.83
WN 4614-1	56.33	59.33	108.00	159.33	55.20	12.27	19.44	235.98	10.97

WN 2199	62.33	64.67	113.33	185.20	83.60	10.73	17.67	184.40	10.07
WN 1079	56.67	59.67	110.00	213.60	87.40	10.93	20.44	221.96	11.33
WN 554	46.67	49.67	97.33	174.33	56.20	11.73	22.72	265.99	10.98
Z-490-26	52.33	56.33	103.00	163.20	59.60	12.40	20.22	251.89	11.73
HKI-1105-2-1	54.33	57.33	103.67	163.03	64.00	10.93	18.68	204.14	13.10
WN 2402-2	54.67	56.67	105.00	181.07	53.87	11.40	21.32	242.45	13.51
MEAN	53.71	56.60	103.73	167.08	60.49	11.23	20.04	227.43	11.42
C.V	3.02	2.75	2.20	8.64	10.15	4.02	6.36	8.28	6.35
C.D	2.66	2.55	3.73	23.66	10.06	0.74	2.09	30.85	1.19

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Inbred Lines	**Cob length (cm)**	**Stem girth (cm)**	**No. of cobs per plant**	**No. of plants per plot**	**1000 kernel weight (g)**	**Moisture percentage (%)**	**Shelling percentage (%)**	**Grain yield (q/ha)**
WN 1207	12.48	5.53	1.00	23.00	274.55	24.37	80.08	45.54
WN 9071-2	17.67	6.62	1.00	20.00	283.06	25.43	81.64	47.75
WN 2453	16.22	8.41	1.00	23.33	294.13	25.33	81.45	48.93
WN 129	15.53	6.43	1.00	20.33	217.29	24.33	80.06	39.22
WN 24249-1	11.74	6.37	1.00	21.00	246.84	23.87	79.01	36.10
WN 2538	14.20	6.36	1.13	23.33	323.10	26.37	82.30	56.23
WN 2489	14.82	7.43	1.00	21.67	245.57	23.47	74.77	32.39
WN 33153	12.35	6.64	1.00	21.67	184.91	23.20	68.50	23.28
WN 52362	14.37	6.67	1.00	23.33	245.35	23.53	76.14	34.33
WN 5279	12.28	6.92	1.73	23.33	210.28	24.67	81.04	47.90
WN 31984	16.23	6.26	1.00	23.67	270.05	24.47	80.68	47.01
WN 52188	16.53	7.77	1.20	18.67	321.70	25.67	82.14	50.87
SMSF 7752	12.27	7.37	1.40	23.67	196.54	23.47	73.43	33.03

EV 1439	13.97	7.62	1.00	23.00	238.95	23.70	76.46	34.45
HKI-193-1	12.23	7.43	1.00	23.67	262.68	23.43	72.78	32.76
PFSR-10109	15.32	7.48	1.00	19.33	277.85	24.43	80.67	39.78
EV 1465	14.20	7.36	1.60	23.33	270.74	26.00	82.20	55.50
EV 1463	10.73	5.38	1.47	23.00	235.47	24.50	80.69	47.30
UDMI-128-1-5	15.82	5.11	1.00	22.33	249.65	23.40	71.07	32.43
V-351	9.87	5.22	1.00	20.67	261.98	23.00	67.70	21.22
WN 32296	11.92	5.49	1.33	23.67	221.05	23.50	74.96	33.27
HKI-536	13.88	5.53	1.07	23.33	235.24	24.00	77.75	36.91
HKI-323-4-1	14.05	8.61	1.13	21.33	338.72	25.53	81.93	52.60
WN 4614-1	13.43	8.37	1.20	22.67	300.36	25.50	81.84	53.59
WN 2199	12.23	5.65	1.13	23.00	184.95	23.47	69.70	29.26
WN 1079	14.00	8.35	1.00	23.67	274.71	24.30	79.26	40.05
WN 554	13.27	6.43	1.00	24.00	290.15	25.47	81.69	52.51
Z-490-26	14.05	7.28	1.00	24.00	337.32	26.00	82.52	56.55
HKI-1105-2-1	15.40	7.37	1.53	22.67	280.32	25.57	81.95	55.76
WN 2402-2	15.55	8.23	1.00	21.67	276.70	24.30	79.74	41.23
MEAN	13.89	6.86	1.13	22.41	261.67	24.48	78.14	41.93
C.V	5.65	6.66	7.72	5.37	8.14	3.16	3.66	10.66
C.D	1.28	0.75	0.14	1.97	34.90	1.27	4.69	7.33

4.4 Genetic Parameters of Variability Among Inbred Lines

Thirty inbred lines of maize were used to calculate the genetic variability for seventeen morpho-agronomical traits. The results are shown in Table 4.34 for the genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), heritability percentage (h^2), genetic advance (GA), and genetic advance as a percentage of mean. An examination of the table showed that for each of the seventeen traits under investigation, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV). If the value Of PCV > GCV, it means that the apparent variation is not only due to genotypes but also due to the influence of the environment.

If the value of heritability in a broad sense is high, it indicates that though the character is least influenced by the environment, the selection may not be useful, as it includes total genetic variance which includes both fixable and non-fixable components.

If the value of genetic advance is high, it shows that characters are governed by additive genes and selection will be rewarding. High heritability coupled with high genetic advance is effective for selection. To compare genetic advance in two different traits, genetic advance as a percentage of mean is needed how much advancement is there for the traits.

Genetic Advance is the improvement in the mean genotypic value of selected parents over the parent population.

4.4.1 Genotypic Coefficient of Variance

It was found that the genotypic coefficient of variance ranged from 3.57 per cent to 27.69 per cent. The highest genotypic coefficient of variance was observed for ear height (cm) (27.69) followed by grain yield (23.33), number of cobs per plant (18.13), kernels per cob (15.74), kernels per row (15.73), 1000 kernel weight (g) (15.03), stem girth (cm) (14.69), plant height (cm) (13.44), cob length (cm) (12.78), cob girth (cm) (12.70), kernels rows per cob (8.26), no. days to 50% tasseling (6.63), no. of days to 50% silking (6.41), number of plants per plot (5.68), shelling percentage (%) (5.37), no. days to 75% dry husk (3.75), and the lowest was found in moisture percentage (%) (3.57).

4.4.2 Phenotypic Coefficient of Variance

It was found that the phenotypic coefficient of variance ranged from 4.35 per cent to 29.49 per cent. The highest phenotypic coefficient of variance was observed for ear height (cm) (29.49) followed by grain yield (q/ha) (25.65).number of cobs per plant (19.70), kernels per cob (17.78), kernels per row (17.77), 1000 kernel weight (g) (17.10), stem girth (cm) (16.12), plant height (cm) (15.98), cob girth (cm) (14.20), cob length (cm) (13.98), kernels rows per cob (9.18), number of plants per plot (7.82), no. days to 50% tasseling (7.29), no. of days to 50% silking (6.98), shelling percentage (%) (6.00), moisture percentage (%) (4.77) and the lowest was found in no. days to 75% dry husk (4.35).

4.4.3 Heritability

It was found that the heritability ranged from 52.87 per cent to 88.15 per cent. The highest heritability was observed for ear height (cm) (88.15) followed by number of cobs per plant (84.67), no. of days to 50% silking (84.43), cob length (cm) (83.63), stem girth (cm) (83.02), no. days to 50% tasseling (82.80), grain yield (q/ha) (82.72), kernels rows per cob (80.84), cob girth (cm) (79.98), kernels per cob (78.33), kernels per row (78.32), 1000 kernel weight (g) (77.33), no. days to 75% dry husk (74.26), plant height (cm) (70.75), shelling percentage (%) (68.30), moisture percentage (%) (56.06), and the lowest was found in number of plants per plot (52.87).

4.4.4 Genetic Advance

It was found that the genetic advance ranged from 0.39 per cent to 71.25 per cent. The highest genetic advance was observed for 1000 kernel weight (g) (71.25) followed by kernels per cob (65.25), kernels per row (65.24), plant height (cm) (38.90), ear height (cm) (32.39), grain yield (q/ha) (18.32). shelling percentage (%) (7.14), no. days to 75% dry husk (6.91), no. of days to 50% silking (6.87), no. days to 50% tasseling (6.68), cob length (cm) (3.34), cob girth (cm) (2.67), number of plants per plot (1.91), stem girth (cm) (1.89), kernels rows per cob (1.72), moisture percentage (%) (1.35), and the lowest was found in number of cobs per plant (0.39).

4.4.5 Genetic Advance as Percentage of Mean

It was found that the genetic advance as percentage of mean ranged from 5.50 per cent to 53.54 per cent. The highest genetic advance as percentage of mean was observed for ear height (cm) (53.54) followed by grain yield (q/ha) (43.71), number of cobs per plant (34.37), kernels per cob (28.70), kernels per row (28.69), stem girth (cm) (27.57), 1000 kernel weight (g) (27.23), cob length (cm) (24.08), cob girth (cm) (23.39), plant height (cm) (23.28), kernels rows per cob (15.29), no. days to 50% tasseling (12.44), no. of days to 50% silking (12.14), shelling percentage (%) (9.14) number of plants per plot (8.51), no. days to 75% dry husk (6.66) and the lowest was found in moisture percentage (%) (5.50).

Table 4.34: Estimates of genetic parameters among inbred lines under the present study

Characters	Genotypic Coefficient Variance (%)	Phenotypic Coefficient Variance (%)	Heritability (%)	Genetic Advance	Genetic advance as a percentage of mean (%)
No. of days to 50% tasseling	6.63	7.29	82.80	6.68	12.44
No. of days to 50% silking	6.41	6.98	84.43	6.87	12.14
No. of days to 75% dry husk	3.75	4.35	74.26	6.91	6.66
Plant height (cm)	13.44	15.98	70.75	38.90	23.28
Ear height (cm)	27.69	29.49	88.15	32.39	53.54
Kernels rows per cob	8.26	9.18	80.84	1.72	15.29
Kernels per row	15.73	17.77	78.32	65.24	28.69
Kernels per cob	15.74	17.78	78.33	65.25	28.70
Cob girth (cm)	12.70	14.20	79.98	2.67	23.39
Cob length (cm)	12.78	13.98	83.63	3.34	24.08
Stem girth (cm)	14.69	16.12	83.02	1.89	27.57
No. of cobs per plant	18.13	19.70	84.67	0.39	34.37
No. of plants per plot	5.68	7.82	52.87	1.91	8.51
1000 kernel weight (g)	15.03	17.10	77.33	71.25	27.23
Moisture percentage (%)	3.57	4.77	56.06	1.35	5.50
Shelling percentage (%)	5.37	6.00	68.30	7.14	9.14
Grain yield (q/ha)	23.33	25.65	82.72	18.32	43.71

4.5 Correlation Coefficient Analysis

Correlation coefficients were analyzed between all the possible combinations of the traits and were estimated and have been represented in Table 4.35.

4.5.1 Correlation between Grain Yield and Other Characters

Genotypic Correlation (rg)

The grain yield (q/ha) exhibited significant and positive correlation with plant height (cm) (0.222), ear height (cm) (0.285), kernels rows per cob (0.272), kernels per row (0.477), kernels per cob (0.477), cob girth (cm) (0.522), cob length (cm) (0.409), stem girth (cm) (0.420), number of cobs per plant (0.346), no. of plants per plot (0.138), 1000 kernel weight (g) (0.731), moisture percentage (%) (1.139), shelling percentage (%) (0.944), while positive but non- significant correlation with no. days to 50% tasseling (0.063), no. of days to 50% silking (0.125), no. days to 75% dry husk (0.095).

Phenotypic correlation (rp)

The grain yield (q/ha) exhibited significant and positive correlation with plant height (cm) (0.212), ear height (cm) (0.210), kernels rows per cob (0.300), kernels per row (0.489), kernels per cob (0.489), cob girth (cm) (0.487), cob length (cm) (0.389), stem girth (cm) (0.304), number of cobs per plant (0.345), number of plants per plot (0.127), 1000 kernel weight (g) (0.685), moisture percentage (%) (0.722), shelling percentage (%) (0.881), while positive but non- significant correlation with no. days to 50% tasseling (0.040), no. of days to 50% silking (0.097), no. days to 75% dry husk (0.027).

4.5.2 Correlation Between Morpho-agronomical Traits

4.5.2.1 No. of Days to 50% Tasseling

Genotypic Correlation (rg)

The no. of days to 50% tasseling exhibited a significant and positive correlation with no. of days to 50% silking (0.995), no. days to 75% dry husk (0.965), plant height (cm) (0.456), ear height (cm) (0.477), while positive but non- significant correlation with cob girth (cm) (0.098), cob length (cm) (0.183), number of cobs per plant (0.085), 1000 kernel weight (g) (0.051), moisture percentage (%) (0.034), shelling percentage (%) (0.061), grain yield (q/ha) (0.063). It exhibited a negative and non-significant correlation with kernels rows per cob (-

0.201), kernels per row (-0.056), kernels per cob (-0.056), stem girth (cm) (-0.054), number of plants per plot (-0.069).

Phenotypic Correlation (rp)

The no. of days to 50% tasseling exhibited a significant and positive correlation with no. of days to 50% silking (0.990), no. days to 75% dry husk (0.894), plant height (cm) (0.375), ear height (cm) (0.383), while positive but non- significant correlation with cob girth (cm) (0.092), cob length (cm) (0.144), number of cobs per plant (0.068), 1000 kernel weight (g) (0.019), shelling percentage (%) (0.014), grain yield (q/ha) (0.040). It exhibited a negative and non-significant correlation with kernels rows per cob (-0.164), kernels per row (-0.041), kernels per cob (-0.041), stem girth (cm) (-0.067), number of plants per plot (-0.045), moisture percentage (%) (-0.004).

4.5.2.2 No. of Days to 50% Silking

Genotypic Correlation (rg)

The no. of days to 50% silking exhibited a significant and positive correlation with no. days to 50% tasseling (0.995), no. days to 75% dry husk (0.971), plant height (cm) (0.486), ear height (cm) (0.503), cob length (cm) (0.247), while positive but non- significant correlation with cob girth (cm) (0.141), number of cobs per plant (0.073), 1000 kernel weight (g) (0.121), moisture percentage (%) (0.108), shelling percentage (%) (0.119), grain yield (q/ha) (0.125). It exhibited a negative and non-significant correlation with kernels rows per cob (-0.167), kernels per row (-0.009), kernels per cob (-0.009), stem girth (cm) (-0.008), number of plants per plot (-0.060).

Phenotypic Correlation (rp)

The no. of days to 50% silking exhibited a significant and positive correlation with no. days to 50% tasseling (0.990), no. days to 75% dry husk (0.893), plant height (cm) (0.403), ear height (cm) (0.414), while positive but non- significant correlation with kernels per row (0.003), kernels per cob (0.003), cob girth (cm) (0.133), cob length (cm) (0.206), number of cobs per plant (0.061), 1000 kernel weight (g) (0.073), moisture percentage (%) (0.051), shelling percentage (%) (0.057), grain yield (q/ha) (0.097). It exhibited a negative and non-significant correlation with kernels rows per cob (-0.132), stem girth (cm) (-0.025), number of plants per plot (-0.036).

4.5.2.3 No. of Days to 75% Dry husk

Genotypic Correlation (rg)

The no. of days to 75% dry husk exhibited a significant and positive correlation with no. days to 50% tasseling (0.965), no. of days to 50% silking (0.971), plant height (cm) (0.614), ear height (cm) (0.576), stem girth (cm) (0.054), number of cobs per plant (0.065), while positive but non- significant correlation with cob girth (cm) (0.064), cob length (cm) (0.206), 1000 kernel weight (g) (0.068), moisture percentage (%) (0.028), shelling percentage (%) (0.120), grain yield (q/ha) (0.095). It exhibited a negative and non-significant correlation with kernels rows per cob (-0.163), kernels per row (-0.012), kernels per cob (-0.012), number of plants per plot (-0.022).

Phenotypic Correlation (rp)

The no. of days to 75% dry husk exhibited a significant and positive correlation with no. days to 50% tasseling (0.894), no. of days to 50% silking (0.893), plant height (cm) (0.445), ear height (cm) (0.473), while positive but non- significant correlation with cob girth (cm) (0.100), cob length (cm) (0.149), stem girth (cm) (0.055), number of cobs per plant (0.030), number of plants per plot (0.004), 1000 kernel weight (g) (0.011), moisture percentage (%) (0.050), shelling percentage (%) (0.031), grain yield (q/ha) (0.027). It exhibited a negative and non-significant correlation with kernels rows per cob (-0.121), kernels per row (-0.036), kernels per cob (-0.036).

4.5.2.3 Plant Height (cm)

Genotypic Correlation (rg)

The plant height (cm) exhibited a significant and positive correlation with no. days to 50% tasseling (0.456), no. of days to 50% silking (0.486), no. days to 75% dry husk (0.614), ear height (cm) (0.956), cob length (cm) (0.386), 1000 kernel weight (g) (0.265), moisture percentage (%) (0.231), shelling percentage (%) (0.257), grain yield (q/ha) (0.222), while positive but non- significant correlation with kernels per row (0.053), kernels per cob (0.053), cob girth (cm) (0.088), stem girth (cm) (0.150), number of cobs per plant (0.036), number of plants per plot (0.114), It exhibited negative and non-significant correlation with kernels rows per cob (-0.146).

Phenotypic correlation (rp)

The plant height (cm) exhibited a significant and positive correlation with no. days to 50% tasseling (0.375), no. of days to 50% silking (0.403), no. days to 75% dry husk (0.445), ear height (cm) (0.788), cob length (cm) (0.252), 1000 kernel weight (g) (0.216), grain yield (q/ha) (0.212), while positive but non- significant correlation with kernels per row (0.051), kernels per cob (0.051), cob girth (cm) (0.011), stem girth (cm) (0.164), number of cobs per plant (0.044), number of plants per plot (0.068), moisture percentage (%) (0.156), shelling percentage (%) (0.183), It exhibited negative and non-significant correlation with kernels rows per cob (-0.132).

4.5.2.5 Ear Height (cm)

Genotypic Correlation (rg)

The ear height (cm) exhibited a significant and positive correlation with no. days to 50% tasseling (0.477), no. of days to 50% silking (0.503), no. days to 75% dry husk (0.576), plant height (cm) (0.956), cob length (cm) (0.306), number of plants per plot (0.214), shelling percentage (%) (0.274), grain yield (q/ha) (0.285), while positive but non- significant correlation with kernels per row (0.024), kernels per cob (0.024), stem girth (cm) (0.099), number of cobs per plant (0.177), 1000 kernel weight (g) (0.184), moisture percentage (%) (0.188n). It exhibited a negative and non-significant correlation with kernels rows per cob (-0.130), and cob girth (cm) (-0.027).

Phenotypic Correlation (rp)

The ear height (cm) exhibited a significant and positive correlation with no. days to 50% tasseling (0.383), no. of days to 50% silking (0.414), no. days to 75% dry husk (0.473), plant height (cm) (0.788), cob length (cm) (0.251), stem girth (cm) (0.211), grain yield (q/ha) (0.210), while positive but non- significant correlation with kernels per row (0.011), kernels per cob (0.011), number of cobs per plant (0.131), number of plants per plot (0.181), 1000 kernel weight (g) (0.115), moisture percentage (%) (0.159), shelling percentage (%) (0.196). It exhibited a negative and non-significant correlation with kernels rows per cob (-0.121), cob girth (cm) (-0.028),

4.5.2.6 Kernels Rows Per Cob

Genotypic Correlation (rg)

The Kernels rows per cob exhibited significant and positive correlation with kernels per row (0.695), kernels per cob (0.695), cob girth (cm) (0.485), cob length (cm) (0.251), stem girth (cm) (0.318), moisture percentage (%) (0.309), shelling percentage (%) (0.407), grain yield (q/ha) (0.272), while positive but non- significant correlation with1000 kernel weight (g) (0.183). It exhibited a significant and negative correlation coefficient with number of cobs per plant (-0.315), while a negative but non-significant correlation with no. days to 50% tasseling (-0.201), no. of days to 50% silking (-0.167), no. days to 75% dry husk (-0.163), plant height (cm) (-0.146), ear height (cm) (-0.130), number of plants per plot (-0.166).

Phenotypic Correlation (rp)

The Kernels rows per cob exhibited significant and positive correlation with kernels per row (0.672), kernels per cob (0.672), cob girth (cm) (0.515), cob length (cm) (0.290), stem girth (cm) (0.247), moisture percentage (%) (0.214), shelling percentage (%) (0.419), grain yield (q/ha) (0.300), while positive but non- significant correlation with1000 kernel weight (g) (0.174n). It exhibited a significant and negative correlation coefficient with plant height (cm) (-0.132), ear height (cm) (-0.121), number of cobs per plant (-0.272), number of plants per plot (-0.139), while the negative but non-significant correlation with no. days to 50% tasseling (-0.164), no. of days to 50% silking (-0.132), no. days to 75% dry husk (-0.121).

4.5.2.7 Kernels Per Row

Genotypic Correlation (rg)

The Kernels per row exhibited significant and positive correlation with kernels rows per cob (0.695), kernels per cob (1.000), cob girth (cm) (0.735), cob length (cm) (0.685), stem girth (cm) (0.265), 1000 kernel weight (g) (0.430), moisture percentage (%) (0.594), shelling percentage (%) (0.673), grain yield (q/ha) (0.477), while positive but non- significant correlation with plant height (cm) (0.053n), ear height (cm) (0.024n). It exhibited a significant and negative correlation coefficient with number of cobs per plant (-0.401), number of plants per plot (-0.371), while a negative but non-significant correlation with no. days to 50% tasseling (-0.056n), no. of days to 50% silking (-0.009n), no. days to 75% dry husk (-0.012n).

Phenotypic Correlation (rp)

The Kernels per row exhibited significant and positive correlation with kernels rows per cob (0.672), kernels per row (), kernels per cob (1.000), cob girth (cm) (0.664), cob length (cm) (0.640), 1000 kernel weight (g) (0.332), moisture percentage (%) (0.359), shelling percentage (%) (0.657), grain yield (q/ha) (0.489), while positive but non- significant correlation with no. of days to 50% silking (0.003), plant height (cm) (0.051), ear height (cm) (0.011), stem girth (cm) (0.195), It exhibited significant and negative correlation coefficient with number of cobs per plant (-0.331), number of plants per plot (-0.315), while negative but non-significant correlation with no. days to 50% tasseling (-0.041), no. days to 75% dry husk (-0.036).

4.5.2.8 Kernels Per Cob

Genotypic Correlation (rg)

The Kernels per cob exhibited significant and positive correlation with kernels rows per cob (0.695), kernels per row (1.000), cob girth (cm) (0.735), cob length (cm) (0.685), stem girth (cm) (0.265), 1000 kernel weight (g) (0.430), moisture percentage (%) (0.594), shelling percentage (%) (0.673), grain yield (q/ha) (0.477), while positive but non- significant correlation with plant height (cm) (0.053), ear height (cm) (0.024). It exhibited a significant and negative correlation coefficient with number of cobs per plant (-0.401), number of plants per plot (-0.371), while a negative but non-significant correlation with no. days to 50% tasseling (-0.056), no. of days to 50% silking (-0.009), no. days to 75% dry husk (-0.012).

Phenotypic Correlation (rp)

The Kernels per cob exhibited significant and positive correlation with kernels rows per cob (0.672), kernels per row (1.000), cob girth (cm) (0.664), cob length (cm) (0.640), stem girth (cm) (0.195n), number of cobs per plant (-0.331), number of plants per plot (-0.315), 1000 kernel weight (g) (0.332), moisture percentage (%) (0.359), shelling percentage (%) (0.657), grain yield (q/ha) (0.489), while positive but non- significant correlation with no. of days to 50% silking (0.003), plant height (cm) (0.051), ear height (cm) (0.011), It exhibited negative and non-significant correlation with no. days to 50% tasseling (-0.041), no. days to 75% dry husk (-0.036).

4.5.2.9 Cob girth (cm)

Genotypic Correlation (rg)

The cob girth exhibited significant and positive correlation with kernels rows per cob (0.485), kernels per row (0.735), kernels per cob (0.735), cob length (cm) (0.759), stem girth (cm) (0.532), 1000 kernel weight (g) (0.493), moisture percentage (%) (0.647), shelling percentage (%) (0.672), grain yield (q/ha) (0.522), while positive but non- significant correlation with no. days to 50% tasseling (0.098), no. of days to 50% silking (0.141), no. days to 75% dry husk (0.064), plant height (cm) (0.088), It exhibited a significant and negative correlation coefficient with number of plants per plot (-0.365), while the negative but non-significant correlation with ear height (cm) (-0.027), number of cobs per plant (-0.158).

Phenotypic Correlation (rp)

The cob girth exhibited significant and positive correlation with kernels rows per cob (0.515), kernels per row (0.664), kernels per cob (0.664), cob length (cm) (0.734), stem girth (cm) (0.419), 1000 kernel weight (g) (0.368), moisture percentage (%) (0.425), shelling percentage (%) (0.560), grain yield (q/ha) (0.457), while positive but non- significant correlation with no. days to 50% tasseling (0.092), no. of days to 50% silking (0.133), no. days to 75% dry husk (0.100), plant height (cm) (0.011),It exhibited a significant and negative correlation coefficient with number of plants per plot (-0.241), while the negative but non-significant correlation with ear height (cm) (-0.028), number of cobs per plant (-0.156).

4.5.2.10 Cob Length (cm)

Genotypic Correlation (rg)

The cob length (cm) exhibited significant and positive correlation with no. of days to 50% silking (0.247), plant height (cm) (0.386), ear height (cm) (0.306), kernels rows per cob (0.251), kernels per row (0.685), kernels per cob (0.685), cob girth (cm) (0.759), stem girth (cm) (0.419), 1000 kernel weight (g) (0.448), moisture percentage (%) (0.505), shelling percentage (%) (0.480), grain yield (q/ha) (0.409), while positive but non- significant correlation with no. days to 50% tasseling (0.183), no. days to 75% dry husk (0.206), It exhibited a significant and negative correlation coefficient with number of cobs per plant (-0.258), number of plants per plot (-0.352).

Phenotypic Correlation (rp)

The cob length (cm) exhibited significant and positive correlation with plant height (cm) (0.252), ear height (cm) (0.251), kernels rows per cob (0.290), kernels per row (0.640), kernels per cob (0.640), cob girth (cm) (0.734), stem girth (cm) (0.340), 1000 kernel weight (g) (0.364), moisture percentage (%) (0.341), shelling percentage (%) (0.443), grain yield (q/ha) (0.389), while positive but non- significant correlation with no. days to 50% tasseling (0.144n), no. of days to 50% silking (0.206n), no. days to 75% dry husk (0.149n). It exhibited a significant and negative correlation coefficient with number of plants per plot (-0.255), while a negative but non-significant correlation with number of cobs per plant (-0.206).

4.5.2.11 Stem Girth (cm)

Genotypic Correlation (rg)

The stem girth (cm) exhibited significant and positive correlation with kernels rows per cob (0.318), kernels per row (0.265), kernels per cob (0.265), cob girth (cm) (0.532), cob length (cm) (0.419), 1000 kernel weight (g) (0.487), moisture percentage (%) (0.445), shelling percentage (%) (0.484), grain yield (q/ha) (0.420), while positive but non- significant correlation with no. days to 75% dry husk (0.054n), plant height (cm) (0.150n), ear height (cm) (0.099n), number of cobs per plant (0.029n), It exhibited negative and non-significant correlation with no. days to 50% tasseling (-0.054n), no. of days to 50% silking (-0.008n), number of plants per plot (-0.109n).

Phenotypic Correlation (rp)

The stem girth (cm) exhibited significant and positive correlation with ear height (cm) (0.211), kernels rows per cob (0.247), cob girth (cm) (0.419), cob length (cm) (0.340), 1000 kernel weight (g) (0.373), moisture percentage (%) (0.340), shelling percentage (%) (0.328), grain yield (q/ha) (0.304), while positive but non- significant correlation with no. days to 75% dry husk (0.055), plant height (cm) (0.164), kernels per row (0.195), kernels per cob (0.195), It exhibited negative and non-significant correlation with no. days to 50% tasseling (-0.067), no. of days to 50% silking (-0.025), number of cobs per plant (-0.011), number of plants per plot (-0.063).

4.5.2.12 Number of Cobs Per Plant

Genotypic Correlation (rg)

The number of cobs per plant exhibited a significant and positive correlation with stem girth (cm) (0.029n), number of plants per plot (0.272), moisture percentage (%) (0.303), shelling percentage (%) (0.232), grain yield (q/ha) (0.346), while positive but non- significant correlation with no. days to 50% tasseling (0.085), no. of days to 50% silking (0.073), no. days to 75% dry husk (0.065), plant height (cm) (0.036), ear height (cm) (0.177), It exhibited significant and negative correlation coefficient with kernels rows per cob (-0.315), kernels per row (-0.401), kernels per cob (-0.401), cob length (cm) (-0.258), while negative but non-significant correlation with cob girth (cm) (-0.158) and 1000 kernel weight (g) (-0.196).

Phenotypic Correlation (rp)

The number of cobs per plant exhibited a significant and positive correlation with shelling percentage (%) (0.223), and grain yield (q/ha) (0.345), while a positive but non-significant correlation with no. days to 50% tasseling (0.068), no. of days to 50% silking (0.061), no. days to 75% dry husk (0.030), plant height (cm) (0.044), ear height (cm) (0.131), number of plants per plot (0.161), It exhibited significant and negative correlation coefficient with kernels rows per cob (-0.272), kernels per row (-0.331), kernels per cob (-0.331), moisture percentage (%) (-0.214), while negative but non-significant correlation with cob girth (cm) (-0.156), cob length (cm) (-0.206), stem girth (cm) (-0.011), 1000 kernel weight (g) (-0.180),

4.5.2.13 Number of Plants Per Plot

Genotypic Correlation (rg)

The number of plants per plot exhibited significant and positive correlation with ear height (cm) (0.214), number of cobs per plant (0.272), while positive but non- significant correlation with plant height (cm) (0.114), moisture percentage (%) (0.056), grain yield (q/ha) (0.138). It exhibited a significant and negative correlation coefficient with kernels per row (-0.371), kernels per cob (-0.371), cob girth (cm) (-0.365), and cob length (cm) (-0.352), while the negative but non-significant correlation with no. days to 50% tasseling (-0.069), no. of days to 50% silking (-0.060), no. days to 75% dry husk (-0.022), kernels rows per cob (-0.166), 1000 kernel weight (g) (-0.115), shelling percentage (%) (-0.018), stem girth (cm) (-0.109).

Phenotypic Correlation (rp)

The number of plants per plot exhibited positive and non- significant correlation with no. of days to 75% dry husk (0.004), plant height (cm) (0.068), ear height (cm) (0.181), number of cobs per plant (0.161), grain yield (q/ha) (0.127), It exhibited significant and negative correlation coefficient with kernels per row (-0.315), kernels per cob (-0.315), cob girth (cm) (-0.241), cob length (cm) (-0.255), while the negative but non-significant correlation with no. days to 50% tasseling (-0.045), no. of days to 50% silking (-0.036), kernels rows per cob (-0.139), stem girth (cm) (-0.063), 1000 kernel weight (g) (-0.144), moisture percentage (%) (-

0.057), shelling percentage (%) (-0.013).

4.5.2.14 1000 Kernel Weight (g)

Genotypic Correlation (rg)

The 1000 kernel weight (g) exhibited significant and positive correlation with plant height (cm) (0.265), kernels per row (0.430), kernels per cob (0.430), cob girth (cm) (0.493), cob length (cm) (0.448), stem girth (cm) (0.487), moisture percentage (%) (0.898), shelling percentage (%) (0.688), grain yield (q/ha) (0.731), while positive but non- significant correlation with no. days to 50% tasseling (0.051), no. of days to 50% silking (0.121), no. days to 75% dry husk (0.068), ear height (cm) (0.184), kernels rows per cob (0.183), It exhibited a significant and negative correlation coefficient with number of plants per plot (-0.115), while negative but non-significant correlation number of cobs per plant (-0.196).

Phenotypic Correlation (rp)

The 1000 kernel weight (g) exhibited significant and positive correlation with plant height (cm) (0.216), kernels per row (0.332), kernels per cob (0.332), cob girth (cm) (0.368), cob length (cm) (0.364), stem girth (cm) (0.737), moisture percentage (%) (0.576), shelling percentage (%) (0.594), grain yield (q/ha) (0.685), while positive but non- significant correlation with no. days to 50% tasseling (0.019), no. of days to 50% silking (0.073), no. days to 75% dry husk (0.011), ear height (cm) (0.115), kernels rows per cob (0.174). It exhibited a negative and non-significant correlation with number of cobs per plant (-0.180), number of plants per plot (-0.144).

4.5.2.15 Moisture Percentage (%)

Genotypic Correlation (rg)

The moisture percentage (%) exhibited significant and positive correlation with plant height (cm) (0.231), kernels rows per cob (0.309), kernels per row (0.594), kernels per cob (0.594), cob girth (cm) (0.647), cob length (cm) (0.505), stem girth (cm) (0.445), number of cobs per plant (0.303), 1000 kernel weight (g) (0.898), shelling percentage (%) (1.079), grain yield (q/ha) (1.139), while positive but non- significant correlation with no. days to 50% tasseling (0.034), no. of days to 50% silking (0.108), no. days to 75% dry husk (0.028), ear height (cm) (0.188), number of plants per plot (0.056).

Phenotypic Correlation (rp)

The moisture percentage (%) exhibited significant and positive correlation with kernels rows per cob (0.214), kernels per row (0.359), kernels per cob (0.359), cob girth (cm) (0.425), cob length (cm) (0.341), stem girth (cm) (0.340), number of cobs per plant (0.214), 1000 kernel weight (g) (0.576), shelling percentage (%) (0.589), grain yield (q/ha) (0.722), while positive but non- significant correlation with no. of days to 50% silking (0.051), no. days to 75% dry husk (0.050), plant height (cm) (0.156), ear height (cm) (0.159), It exhibited negative and non-significant correlation with no. days to 50% tasseling (-0.004), number of plants per plot (-0.057).

4.5.2.16 Shelling Percentage (%)

Genotypic Correlation (rg)

The shelling percentage (%) exhibited significant and positive correlation with plant height (cm) (0.257), ear height (cm) (0.274), kernels rows per cob (0.407), kernels per row (0.673), kernels per cob (0.673), cob girth (cm) (0.672), cob length (cm) (0.480), stem girth (cm) (0.484), number of cobs per plant (0.232), 1000 kernel weight (g) (0.688), moisture percentage (%) (1.079), grain yield (q/ha) (0.944), while positive but non- significant correlation with no. days to 50% tasseling (0.061), no. of days to 50% silking (0.119), no. days to 75% dry husk (0.120). It exhibited a negative and non-significant correlation with number of plants per plot (-0.018n).

Phenotypic Correlation (rp)

The shelling percentage (%) exhibited significant and positive correlation with kernels rows per cob (0.419), kernels per row (0.657), kernels per cob (0.657), cob girth (cm) (0.560), cob length (cm) (0.443), stem girth (cm) (0.328), number of cobs per plant (0.223), 1000 kernel weight (g) (0.594), moisture percentage (%) (0.589), grain yield (q/ha) (0.881), while positive but non- significant correlation with no. days to 50% tasseling (0.014), no. of days to 50% silking (0.057), no. days to 75% dry husk (0.031), plant height (cm) (0.183), ear height (cm) (0.196). It exhibited a negative and non-significant correlation with number of plants per plot (-0.013).

Table 4.35: Estimates of genotypic (rg) and phenotypic (rp) correlation coefficients among 17 characters of maize inbred lines

		DT	DS	DDH	PH	EH	KRPC	KPR	KPC	CG	CL	SG	NCPP	NPPP	1000KW	MP	SP
DS	rg	0.995**															
	rp	0.990**															
DDH	rg	0.965**	0.971**														
	rp	0.894**	0.893**														
PH	rg	0.456**	0.486**	0.614**													
	rp	0.375**	0.403**	0.445**													
EH	rg	0.477**	0.503**	0.576**	0.956**												
	rp	0.383**	0.414**	0.473**	0.788**												
KRPC	rg	-0.201	-0.167	-0.163	-0.146	-0.130											
	rp	-0.164	-0.132	-0.121	-0.132	-0.121											
KPR	rg	-0.056	-0.009	-0.012	0.053	0.024	0.695**										
	rp	-0.041	0.003	-0.036	0.051	0.011	0.672**										
KPC	rg	-0.056	-0.009	-0.012	0.053	0.024	0.695**	1.000**									
	rp	-0.041	0.003	-0.036	0.051	0.011	0.672**	1.000**									
CG	rg	0.098	0.141	0.064	0.088	-0.027	0.485**	0.735**	0.735**								
	rp	0.092	0.133	0.100	0.011	-0.028	0.515**	0.664**	0.664**								
CL	rg	0.183	0.247*	0.206	0.386**	0.306**	0.251*	0.685**	0.685**	0.759**							
	rp	0.144	0.206	0.149	0.252*	0.251*	0.290**	0.640**	0.640**	0.734**							
SG	rg	-0.054	-0.008	0.054	0.150	0.099	0.318**	0.265*	0.265*	0.532**	0.419**						
	rp	-0.067	-0.025	0.055	0.164	0.211*	0.247*	0.195	0.195	0.419**	0.340**						
NCPP	rg	0.085	0.073	0.065	0.036	0.177	-0.315**	-0.401**	-0.401**	-0.158	-0.258*	0.029					
	rp	0.068	0.061	0.030	0.044	0.131	-0.272**	-0.331**	-0.331**	-0.156	-0.206	-0.011					
NPPP	rg	-0.069	-0.060	-0.022	0.114	0.214*	-0.166	-0.371**	-0.371**	-0.365**	-0.352**	-0.109	0.272**				
	rp	-0.045	-0.036	0.004	0.068	0.181	-0.139	-0.315**	-0.315**	-0.241*	-0.255*	-0.063	0.161				
1000KW	rg	0.051	0.121	0.068	0.265*	0.184	0.183	0.430**	0.430**	0.493**	0.448**	0.487**	-0.196	-0.115			
	rp	0.019	0.073	0.011	0.216*	0.115	0.174	0.332**	0.332**	0.368**	0.364**	0.373**	-0.180	-0.144			
MP	rg	0.034	0.108	0.028	0.231*	0.188	0.309**	0.594**	0.594**	0.647**	0.505**	0.445**	0.303**	0.056	0.898**		
	rp	-0.004	0.051	0.050	0.156	0.159	0.214*	0.359**	0.359**	0.425**	0.341**	0.340**	0.214*	-0.057	0.576**		
SP	rg	0.061	0.119	0.120	0.257*	0.274**	0.407**	0.673**	0.673**	0.672**	0.480**	0.484**	0.232*	-0.018	0.688**	1.079**	
	rp	0.014	0.057	0.031	0.183	0.196	0.419**	0.657**	0.657**	0.560**	0.443**	0.328**	0.223*	-0.013	0.594**	0.589**	
GY	rg	0.063	0.125	0.095	0.222*	0.285**	0.272**	0.477**	0.477**	0.522**	0.409**	0.420**	0.346**	0.138	0.731**	1.139**	0.944**
	rp	0.040	0.097	0.027	0.212*	0.210*	0.300**	0.489**	0.489**	0.457**	0.389**	0.304**	0.345**	0.127	0.685**	0.722**	0.881**

***, ** significant at 5% and 1% level, respectively**

***Abbreviations: DT= days to 50% tasseling, DS= days to 50% silking, DDH= days to 75% dry husk, PH= plant height (cm), EH= Ear height (cm), KRPC= kernels rows cob-^{1}, KPR= kernels row-^{1},KPC= kernels cob-^{1}, CG= cob girth (cm), CL= cob length (cm), SG= stem girth (cm), NCPP= No. of cobs plant-^{1}, NPPP=No. of plants plot-^{1} ,1000KW= 1000 kernel weight (g), MP= moisture percentage (%), SP= shelling percentage (%), GY= grain yield**

4.6 Path Coefficient Analysis

The results of path analysis depicting direct and indirect effects of independent variables (components characters) and dependent variable (grain yield) are given in Table 4.36 and Figure 4.1.

The positive direct effect on grain yield was exhibited by kernels per cob (1.3155), followed by cob length (1.1886), 1000 kernel weight (0.7600), no. of cobs per plant (0.3949), no. of days to 50% silking (0.3637), no. Of plants per plot (0.3601), plant height (0.3183) and stem girth (0.1997).

The negative direct effect on grain yield was exhibited by kernels per row (-0.9019), cob girth (-0.8975), ear height (-0.6596), no. of days to 75% dry hush (-0.2932), no. of days to 50% tasseling (-0.2089), moisture percentage (-0.0978), shelling percentage (-0.0811) and kernels rows per cob (-0.0768).

Kernels per cob having the highest direct effect (1.3155) were significantly and positively correlated with grain yield due to indirect positive effect via no. of days to 50% tasseling, no. of days to 75% dry husk, plant height, cob length, stem girth, and moisture percentage.

Kernels per row having a high direct negative effect (-0.9019) on grain yield also had a significant negative correlation due to indirect negative effects via no. of days to 50% silking, ear height, kernels row per cob, cob girth, no. of plants per plot, no. of plants per plot, 1000 kernel weight, moisture percentage, and shelling percentage. The residual effect was undefined.

No. of days to 50% tasseling had a positive but non-significant correlation with grain yield (q/ha) (r =0.0400) although it showed a high negative direct effect (-0.2089) towards grain yield (q/ha), along with its high indirect negative effect via days to 50% tasseling (-2.41). It also showed a positive indirect effect via days to 50% silking (2.91) which had adversely affected building up the positive association with grain yield (q/ha).

No. of days to 50% silking had a positive but non-significant correlation with grain yield (q/ha) (r=0.0971) which was due to its positive direct effect (0.3637) on grain yield (q/ha), along with its high indirect positive effect via cob length (0.1672), although the high negative indirect effect was also noticed via kernels per cob (-0.2993) which had adversely affected in building up the positive association with grain yield (q/ha).

No. of days to 75% dry husk had a positive but non-significant correlation with grain yield (q/ha) (r =0.0273) although it showed a high negative direct effect (-0.2932) towards grain yield (q/ha), along with its high indirect negative effect via kernels per cob (-0.3368). It also showed a positive indirect effect via no. of days to 50% silking (0.3316) which had adversely affected building up the positive association with grain yield (q/ha).

Plant height had a positive significant correlation with grain yield (q/ha) (r=0.2122) which was due to its positive direct effect (0.3183) towards grain yield (q/ha), along with its high indirect positive effect via cob length (0.4415) and 1000 kernel weight (0.3884) although the high negative indirect effect was also noticed via ear height (-0.6318) which had adversely affected in building up the positive association with grain yield (q/ha).

Ear height had a positive significant correlation with grain yield (q/ha) (r =0.2105) although it showed a high negative direct effect (-0.6596) towards grain yield (q/ha), along with its high indirect negative effect via kernels per row (-0.0731). It also showed a positive indirect effect via cob length (0.4166) and 1000 kernels weight (0.3201) which had adversely affected in building up the positive association with grain yield (q/ha).

Kernels row per cob had a positive significant correlation with grain yield (q/ha) (r =0.3004) although it showed a high negative direct effect (-0.0768) towards grain yield (q/ha), along with its high indirect negative effect via 1000 kernel weight (-0.4774). It also showed a positive indirect effect via kernels per cob (0.5941) which had adversely affected building up the positive association with grain yield (q/ha).

Kernels per row had a positive significant correlation with grain yield (q/ha) (r =0.4833) although it showed a high negative direct effect (-0.9019) towards grain yield (q/ha), along with its high indirect negative effect via cob girth (-0.6824). It also showed a positive indirect effect via kernels per cob (1.1965) which had adversely affected building up the positive association with grain yield (q/ha).

Kernels per cob had a positive significant correlation with grain yield (q/ha) (r=0.4892) which was due to its positive direct effect (1.3155) towards grain yield (q/ha), along with its high indirect positive effect via cob length (0.7957), although the high negative indirect effect was also noticed via kernels per row (-0.8203) which had adversely affected in building up the positive association with grain yield (q/ha).

Cob girth had a positive significant correlation with grain yield (q/ha) (r =0.4574) although it showed a high negative direct effect (-0.8975) towards grain yield (q/ha), along with its high indirect negative effect via kernels per row (-0.6857). It also showed a positive indirect effect via cob length (1.0934) which had adversely affected building up the positive association with grain yield (q/ha).

Cob length had a positive significant correlation with grain yield (q/ha) (r=0.3893) which was due to its positive direct effect (1.1886) towards grain yield (q/ha), along with its high indirect positive effect via kernels per cob (0.8806), although the high negative indirect effect was also noticed via kernels per cob (-0.7124) which had adversely affected in building up the positive association with grain yield (q/ha).

Stem girth had a positive significant correlation with grain yield (q/ha) (r=0.3041) which was due to its positive direct effect (0.1997) towards grain yield (q/ha), along with its high indirect positive effect via cob length (0.6007), although the high negative indirect effect was also noticed via kernels per row (-0.2352) which had adversely affected in building up the positive association with grain yield (q/ha).

No. of cobs per plant had a positive significant correlation with grain yield (q/ha) (r=0.3454) which was due to its positive direct effect (0.3949) towards grain yield (q/ha), along with its high indirect positive effect via 1000 kernel weight (0.1240), although the high negative indirect effect was also noticed via kernels per cob (-0.3289) which had adversely affected in building up the positive association with grain yield (q/ha).

No. of plants per plant had a positive but non-significant correlation with grain yield (q/ha) (r=0.1274) which was due to its positive direct effect (0.3601) towards grain yield (q/ha), along with its high indirect positive effect via 1000 kernel weight (0.2984), although the high negative indirect effect was also noticed via kernels per cob (-0.5069) which had adversely affected in building up the positive association with grain yield (q/ha).

1000 kernels weight had positive significant correlation with grain yield (q/ha) (r=0.6852) which was due to its positive direct effect (0.7600) towards grain yield (q/ha), along with its high indirect positive effect via kernels per row (0.2030), although high negative indirect effect was also noticed via kernels per cob (-0.5511) which had adversely affected in building up the positive association with grain yield (q/ha).

Moisture percentage had a positive highly significant correlation with grain yield (q/ha) (r =0.7221) although it showed a negative direct effect (-0.0978) towards grain yield (q/ha), along with its indirect negative effect via ear height (-0.3327). It also showed a positive indirect effect via cob length (0.6360) and 1000 kernels weight (0.4568) which had adversely affected building up the positive association with grain yield (q/ha).

Shelling percentage had a positive highly significant correlation with grain yield (q/ha) (r =0.8811) although it showed a negative direct effect (-0.0811) towards grain yield (q/ha), along with its indirect negative effect via cob girth (-0.2541). It also showed a positive indirect effect via cob length (0.4908) and 1000 kernels weight (0.4412) which had adversely affected building up the positive association with grain yield (q/ha).

Table 4.36: Path coefficients showing the direct and indirect effect of various traits on grain yield

	DT	**DS**	**DDH**	**PH**	**EH**	**KRPC**	**KPR**	**KPC**	**CG**	**CL**	**SG**	**NCPP**	**NPPP**	**1000KW**	**MP**	**SP**	**GY**
DT	**-0.2089**	0.35403	-0.28327	-0.1174	0.1793	0.01605	0.21672	-0.38984	-0.00849	-0.00087	0.01634	-0.00218	0.12375	0.03803	-0.0067	0.01164	0.0400
DS	-0.2034	**0.3637**	-0.2674	-0.0905	0.1200	0.0202	0.1360	-0.2993	-0.1308	0.1672	0.0441	0.0000	0.1246	0.1033	-0.0195	0.0023	0.0971
DDH	-0.2018	0.3316	**-0.2932**	-0.1658	0.2816	0.0082	0.1966	-0.3368	0.0037	-0.0644	0.0086	-0.0184	0.1295	-0.0914	0.0046	0.0173	0.0273
PH	0.0770	-0.1034	0.1527	**0.3183**	-0.6318	0.0125	-0.1019	0.1521	-0.0785	0.4415	-0.0065	0.1392	-0.0408	0.3884	-0.0572	-0.0264	0.2122*
EH	0.0568	-0.0661	0.1252	0.3049	**-0.6596**	-0.0002	-0.0731	0.2236	-0.0427	0.4166	-0.0205	0.0942	-0.0468	0.3201	-0.0493	-0.0239	0.2105*
KRPC	0.0437	-0.0956	0.0314	-0.0519	-0.0016	**-0.0768**	-0.0905	0.5941	0.1281	-0.1317	-0.1073	-0.1848	-0.0812	-0.4774	0.0600	0.0130	0.3004**
KPR	0.0502	-0.0548	0.0639	0.0360	-0.0535	-0.0077	**-0.9019**	1.1965	-0.6824	0.9389	0.0521	-0.0312	-0.1013	-0.1711	-0.0153	-0.0221	0.4833**
KPC	0.0619	-0.0828	0.0751	0.0368	-0.1121	-0.0347	-0.8203	**1.3155**	-0.5533	0.7957	0.0115	-0.0987	-0.1388	-0.3184	0.0031	-0.0171	0.4892**
CG	-0.0020	0.0530	0.0012	0.0278	-0.0314	0.0110	-0.6857	0.8109	**-0.8975**	1.0934	0.1426	-0.0479	-0.0265	0.0092	-0.0388	-0.0230	0.4574**
CL	0.0002	0.0512	0.0159	0.1182	-0.2312	0.0085	-0.7124	0.8806	-0.8256	**1.1886**	0.1009	-0.0226	-0.0254	0.1280	-0.0524	-0.0335	0.3893**
SG	-0.0171	0.0803	-0.0126	-0.0104	0.0678	0.0413	-0.2352	0.0757	-0.6408	0.6007	**0.1997**	-0.0059	0.0601	0.1878	-0.0396	-0.0185	0.3041**
NCPP	0.0012	0.0000	0.0137	0.1122	-0.1574	0.0359	0.0712	-0.3289	0.1089	-0.0679	-0.0030	**0.3949**	0.0506	0.1240	-0.0390	0.0021	0.3454**
NPPP	-0.0718	0.1258	-0.1054	-0.0361	0.0858	0.0173	0.2538	-0.5069	0.0661	-0.0837	0.0333	0.0555	**0.3601**	0.2984	-0.0069	-0.0357	0.1274
1000KW	-0.0105	0.0494	0.0353	0.1627	-0.2778	0.0482	0.2030	-0.5511	-0.0109	0.2001	0.0493	0.0644	0.1414	**0.7600**	-0.0588	-0.0471	0.6852**
MP	-0.0143	0.0723	0.0138	0.1861	-0.3327	0.0471	-0.1406	-0.0415	-0.3555	0.6360	0.0808	0.1573	0.0254	0.4568	**-0.0978**	-0.0237	0.7221**
SP	0.0300	-0.0104	0.0624	0.1037	-0.1941	0.0123	-0.2456	0.2768	-0.2541	0.4908	0.0456	-0.0103	0.1584	0.4412	-0.0286	**-0.0811**	0.8811**

***Abbreviations: DT= days to 50% tasseling, DS= days to 50% silking, DDH= days to 75% dry husk, PH= plant height (cm), EH= Ear height (cm), KRPC= kernels rows cob-^{1}, KPR= kernels row-^{1,}KPC= kernels cob-^{1}, CG= cob girth (cm), CL= cob length (cm), SG= stem girth (cm), NCPP= No. of cobs plant-^{1}, NPPP=No. of plants plot-^{1} ,1000KW= 1000 kernel weight (g), MP= moisture percentage (%), SP= shelling percentage (%), GY= grain yield(q/ha)**

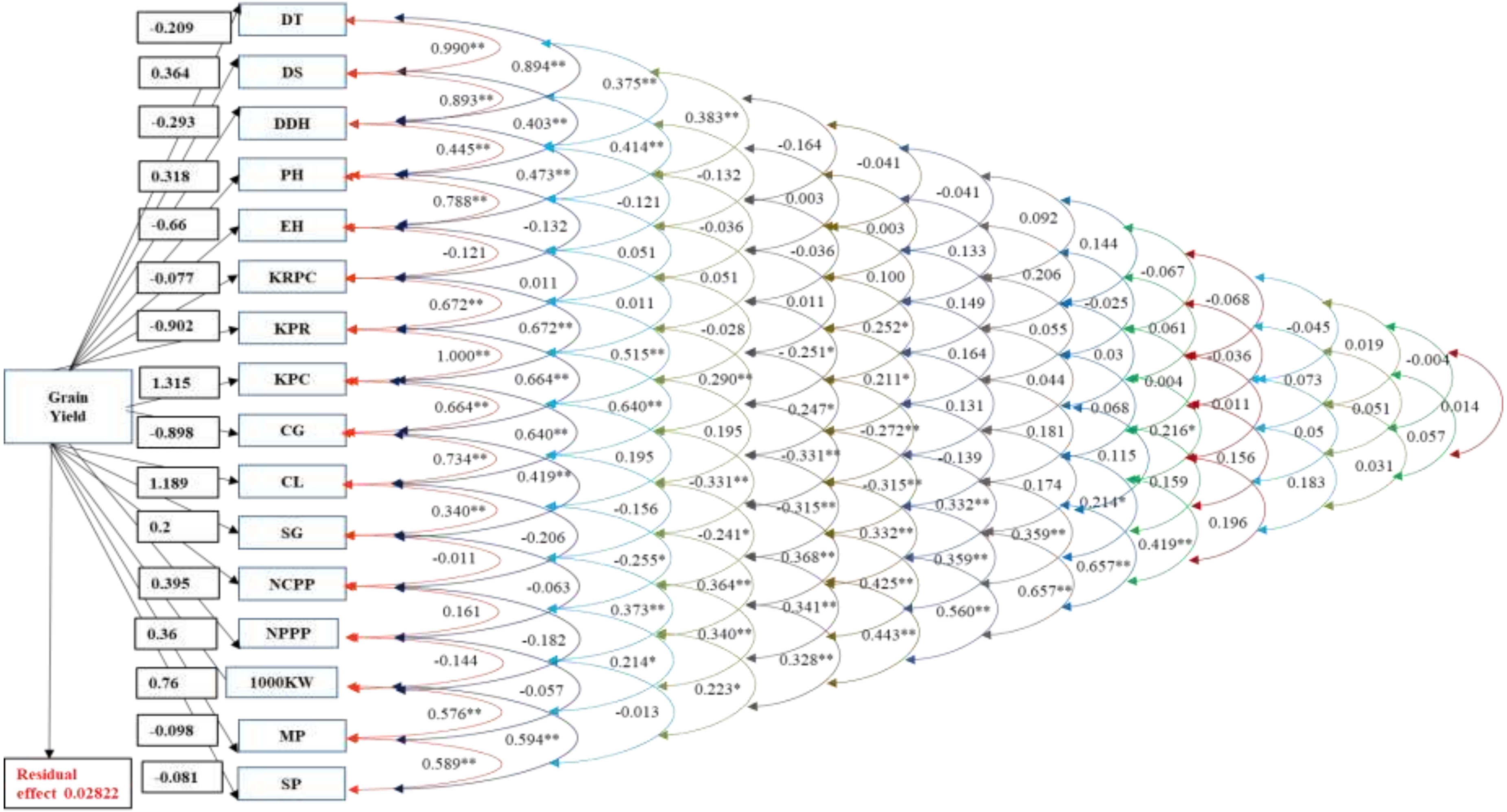

Figure 4.1 Phenotypic path diagram for Grain Yield

Table 4.37: Allocation of Maize inbred lines in various clusters based on D^2 statistics (Tocher's Method)

Cluster No.	No. of inbred lines	Description of Inbred lines
Cluster 1	3	EV 1465, HKI-1105-2-1, HKI-323-4-1
Cluster 2	3	WN 52362, WN 31984, UDMI-128-1-5
Cluster 3	5	WN 1207, HKI-536, EV 1463, WN 2489, HKI-193-1
Cluster 4	3	PFSR-10109, WN 2402-2, WN 2453
Cluster 5	1	WN 5279
Cluster 6	3	Z-490-26, WN 554, WN 2538
Cluster 7	3	WN 129, WN 24249-1, EV 1439
Cluster 8	2	WN 32296, WN 2199
Cluster 9	2	WN 1079, WN 9071-2
Cluster 10	1	WN 52188
Cluster 11	1	WN 4614-1
Cluster 12	2	WN 33153, SMSF 7752
Cluster 13	1	V-351

4.7 Estimation of Genetic Divergence Based on Morpho-agronomical and Yield Contributing Traits

4.7.1 Clustering of Maize Inbred Lines by Using the Tocher's method

On the basis of the relative magnitude of distances, thirty inbred lines were grouped into 13 clusters such that the intra-cluster distance of inbred lines within the cluster was smaller than the inter-cluster distance of inbred lines belonging to different clusters. The distribution pattern of inbred lines in each cluster is shown in Table 4.37 and Figure 4.2 in accordance with the Mahalanobis D^2 analysis utilizing Tocher's method (Rao, 1952).

Cluster 1 contain three inbred lines i.e, EV 1465, HKI-1105-2-1 and HKI-323-4-1; Cluster 2 contain three inbred lines i.e, WN 52362, WN 31984 and UDMI-128-1-5; cluster 3 contain five inbred lines i.e, WN 1207, HKI-536, EV 1463, WN 2489 and HKI-193-1. Cluster 4 contains three inbred lines i.e, PFSR-10109, WN 2402-2, and WN 2453. Cluster 5 contains only one inbred line i.e, WN 5279. Cluster 6 contains three inbred lines i.e, Z-490-26, WN 554, and WN 2538. Cluster 7 contains three inbred lines i.e, WN 129, WN 24249-1, and EV 1439. Cluster 8 contains two lines i.e, WN 32296 and WN 2199. Cluster 9 contains two inbred lines i.e, WN 1079 and WN 9071-2. Clusters 10, 11, and 13 contain only one inbred line each i.e, WN 52188, WN 4614-1, and V-351 respectively. Cluster 12 contains two inbred lines i.e, WN 33153 and SMSF 7752.

4.7.2 Mean Values of Different Clusters

The cluster means of different clusters for seventeen morpho-agronomical traits have been presented in Table 4.38. The genetic differences between the clusters are reflected as cluster mean which differed from each other for one or more characters.

The inbred lines of cluster 8 (61.00) took a maximum no. of days to 50 per cent tasseling followed by cluster 10 (57.33). The inbred lines with lesser no. of days to 50 per cent tasseling were concentrated in cluster 12 (49.50).

The inbred lines of cluster 8 (63.67) took maximum days to 50 per cent silking followed by cluster 10 (61.00). The inbred lines with lesser no. of days to 50 per cent silking were concentrated in cluster 12 (52.17).

The inbred lines with lesser no. of days to 75% dry husk were grouped in cluster 12 (98.50) followed by cluster 13 (98.67). The inbred lines of cluster 8 (112.67) showed the highest mean for

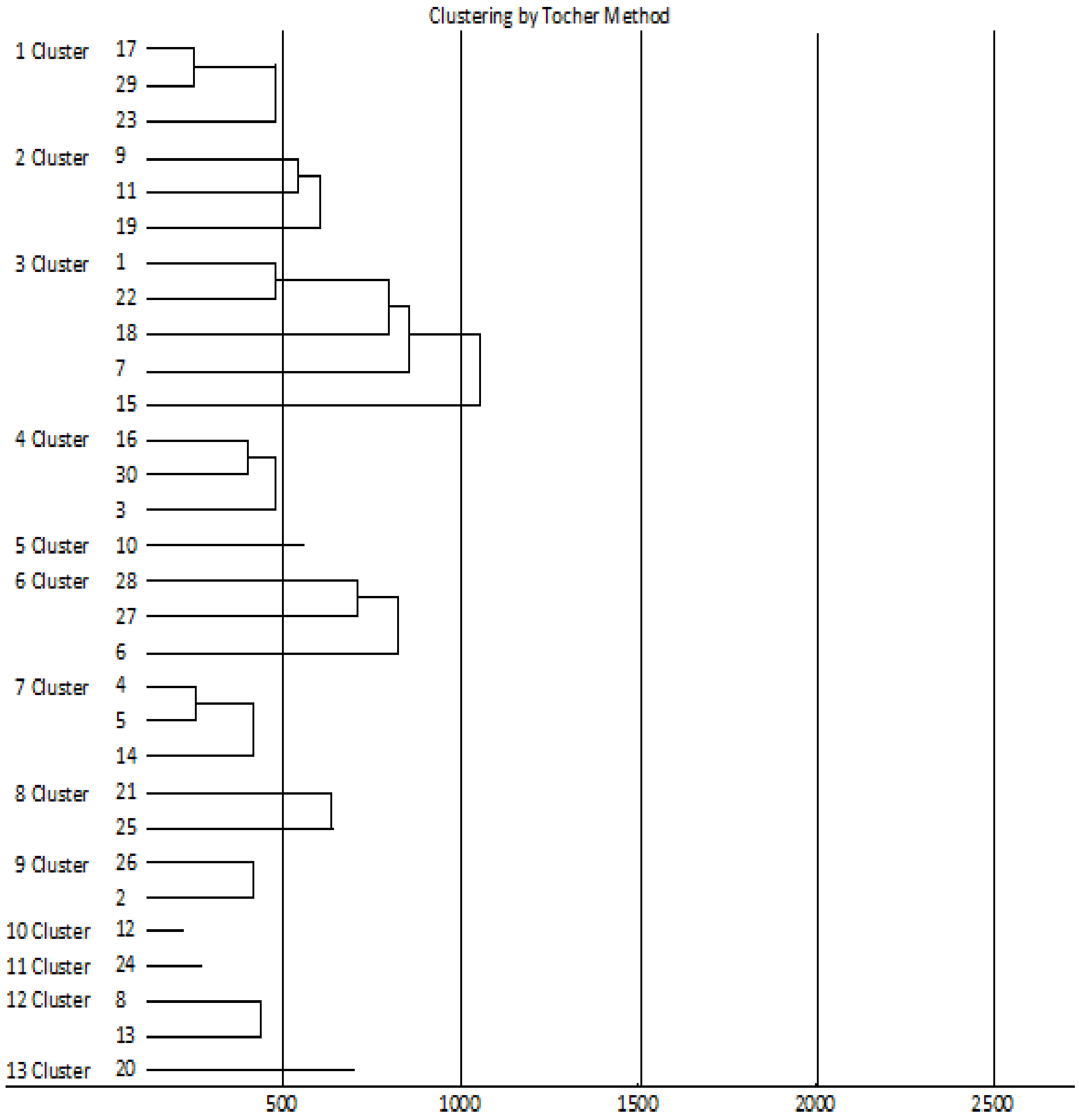

Figure 4.2: Dendrogram showing clustering pattern of maize inbred lines by Tocher's Method

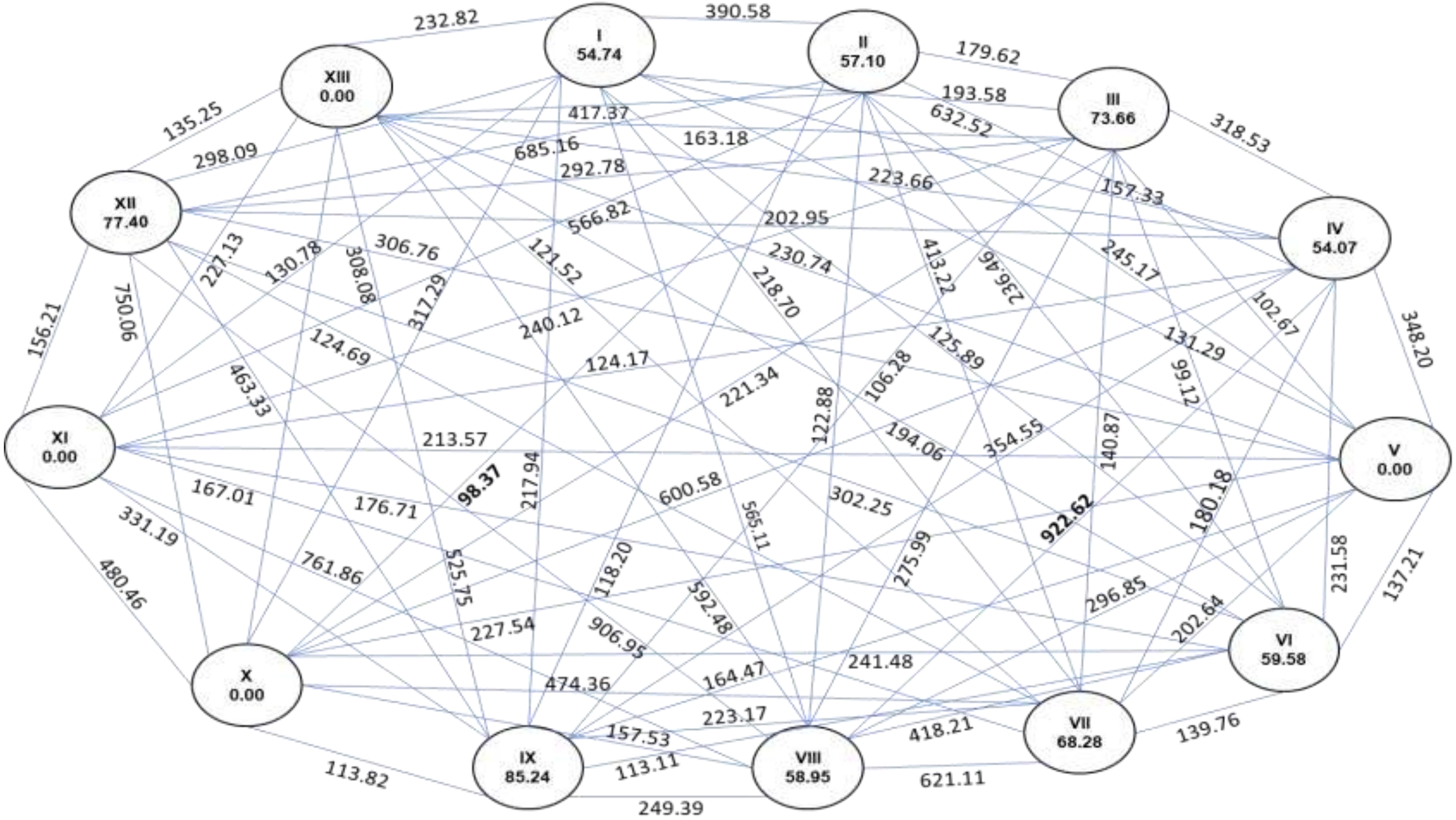

Fig 4.1 : Inter and Intra cluster distance

Figure 4.3: Tocher’s method- Mahalanobis Euclidean Distance

no. of days to 75% dry husk.

The inbred lines with the highest plant height were grouped in cluster 10 (214.40) followed by cluster 9 (203.73) and cluster 8 (198.70). The inbred lines of cluster 13 (125.80) showed the lowest mean for plant height.

The inbred lines with the highest ear height were grouped in cluster 10 (90.80) followed by cluster 8 (83.02) and cluster 9 (78.62). The inbred lines of cluster 13 (26.00) showed lowest mean for ear height.

Cluster 7 (12.47) showed the highest cluster means for kernel row per cob followed by cluster 11 (12.27) and cluster 9 (11.80). However, cluster 13 (9.20) had the lowest cluster value for this character.

For the character, kernels per row the cluster mean was highest in cluster 4 (22.71) followed by cluster 2 (22.50), while, the lowest cluster mean was recorded in cluster 13 (10.18).

The inbred lines with the highest number of kernels per cob were grouped in cluster 9 (263.12) followed by cluster 7 (263.03) and cluster IV (12.86). The inbred lines of cluster 13 (139.36) showed the lowest mean for kernels per cob.

The cluster means for cob girth ranged from 13.79 in cluster 4 followed by cluster 9 (12.67) and cluster 1 (12.58). The inbred lines with minimum mean for cob girth were grouped in cluster 13 (8.60).

The cluster means for the character, cob length was maximum for cluster 10 (16.53) followed by cluster 9 (15.83). The inbred line with minimum cob length was concentrated in cluster 13 (9.87).

The highest cluster means for stem girth was exhibited by cluster 11 (8.37) followed by cluster 4 (8.04), while, the lowest cluster mean was noted in cluster 13 (5.22).

The highest cluster means for number of cobs per plant was observed in cluster 5 (1.73), followed by cluster 1 (1.42). While, Clusters 2, 4, 7, 9, and cluster 13 contained the lowest cluster mean of 1.00.

The highest cluster means for number of plants per plot was observed in cluster 6 (23.78) and Cluster 10 contained the lowest cluster mean of 18.67.

The inbred line with the highest mean for 1000 kernel weight was grouped in cluster 10 (321.70) followed by cluster 6 (316.86) and cluster 11 (300.36). The inbred lines of cluster 12 (190.73) showed the lowest cluster mean for 1000 kernel weight.

The highest cluster means for moisture percentage was exhibited by cluster 6 (25.94) followed by cluster 1 (25.70), while, the lowest cluster mean was noted in cluster 13 (23.00).

The highest cluster mean for shelling percentage was observed in cluster 6 (82.17), followed by clusters 10 (82.14) and 1 (82.02). The inbred lines which had a very low shelling percentage were grouped in cluster 13 (67.70).

The highest cluster mean for grain yield (q/ha) was observed in cluster 6 (55.10), followed by cluster 1 (54.62) and cluster 11 (53.59). Cluster 13 contained the lowest cluster mean of 21.22.

4.7.3 Contribution of Each Character Towards Total Diversity

The analysis of each character's contribution to the expression of genetic divergence is presented in Table 4.38. A review of the data reveals that the stem girth, followed by the number of cobs per plant, contributed a maximum of 46.62 and 11.26 percent, respectively, to the total genetic divergence among the thirty maize inbred lines studied. These characteristics were followed by grain yield (q/ha) (9.30), 1000 kernel weight (7.59), cob girth (4.14), kernel row per cob (3.68), kernels per cob (3.45), days to 50% tasseling (2.53) and cob length (2.53), kernels per row (2.30), ear height (2.07), shelling percentage (1.55), number of plants per plot (1.15), moisture percentage (1.14), Days to 50% silking (0.46), the sum of which account for 99.77 per cent of total divergence. Plant height (0.23) and days to 75% dry husk (0.00), accounted for the least contribution to total divergence

4.7.4 Average Intra and Inter-Cluster Distances

The estimates of intra and inter-cluster distance for thirteen clusters are presented in Table 4.39 and Figure 4.3. The highest intra-cluster distance was found in cluster 9 (85.24), followed by cluster 12 (74.40), cluster 3 (73.66), and cluster 7 (68.28). The inter-cluster distance ranged from 98.37 (between cluster 2 and cluster 10) to 922.62 (between cluster 4 and cluster 8). The maximum inter-cluster distance was recorded between cluster 8 and cluster 4 (922.62) followed by cluster 8 and cluster 12 (906.95), cluster 8 and cluster 11 (761.86), cluster 10 and cluster 12 (750.06), and cluster 2 and cluster 12 (685.16). Low inter-cluster distances were observed between cluster 2 and cluster 10 (98.37), cluster 3 and cluster 6 (99.12), and cluster 3 and cluster 5 (102.67).

4.7.5 Suitable Parent in a Cluster for Different Characters

Parents based on genetic distance and superior *per se* performance for different morpho-agronomical traits are presented in Table 4.40. The inbred line WN 33153 in cluster 12 exhibited desirable no. of days 50% tasseling (47.67) and no. of days to 50% silking (50.33) and no. of days to 75% dry husk (98.40) based on *per se* performance of these traits. WN 52188 belonging to cluster 10 was found to have the highest plant height (214.40 cm), ear height (90.80 cm), cob length (16.53 cm), and 1000 kernel weight (253.08 g) based on *per se* performance. WN 129 belonging to cluster 7 was found to have the highest kernels rows per cob (12.65) based on *per se* performance. In cluster 4 inbred line PFSR-10109 exhibited the highest kernels per row (24.72) and inbred line WN2453 exhibited the highest cob girth (14.35 cm) based on *per se* performance of these traits. WN 9071-2 was found to be having highest kernels per cob (304.28) based on *per se* performance. WN 4614-1 was found be having highest stem girth (8.37 cm) based on *per se* performance. WN 5279 was found be having a desirable number of cobs per plant (1.73) based on *per se* performance. Inbred line Z-490-26 belonging to cluster 6 exhibited desirable moisture percentage (26.37 %), shelling percentage (82.52 %), grain yield per q/ha (56.55 q/ha), and number of plants per plot (24), also inbred line WN 554 belonging to same cluster exhibit a highest number of plants per plot (24) based on *per se* performance of these traits.

Table 4.38: Cluster means among seventeen morpho-agronomical traits in maize inbred lines by Tocher's Method

CLUSTER N0.	DT	DS	DDH	PH	EH	KRPC	KPR	KPC	CG	CL	SG	NCPP	NPPP	1000KW	MP	SP	GY
CLUSTER 1	53.56	56.56	103.00	162.42	65.04	10.67	19.88	212.36	12.58	14.55	7.78	1.42	22.44	296.59	25.70	82.02	54.62
CLUSTER 2	54.89	57.78	104.22	177.89	74.42	10.18	22.50	227.42	10.48	15.47	6.01	1.00	23.11	255.02	23.80	75.96	37.92
CLUSTER 3	54.00	56.80	103.27	161.98	59.79	11.57	19.05	219.63	10.99	12.83	6.26	1.11	22.93	250.70	23.95	77.21	38.98
CLUSTER 4	55.89	58.78	105.89	159.33	46.14	11.27	22.71	255.34	13.79	15.70	8.04	1.00	21.44	282.89	24.69	80.62	43.31
CLUSTER 5	53.33	56.00	104.33	170.67	71.40	10.67	19.61	205.29	9.70	12.28	6.92	1.73	23.33	210.28	24.67	81.04	47.90
CLUSTER 6	50.44	53.78	100.89	174.79	58.66	11.73	21.34	251.77	11.72	13.84	6.69	1.04	23.78	316.86	25.94	82.17	55.10
CLUSTER 7	49.56	52.22	100.33	144.42	48.47	12.47	21.06	263.03	12.12	13.75	6.81	1.00	21.44	234.36	23.97	78.51	36.59
CLUSTER 8	61.00	63.67	112.67	198.70	83.02	10.23	17.60	177.59	9.85	12.08	5.57	1.23	23.33	203.00	23.48	72.33	31.27
CLUSTER 9	54.50	57.67	105.33	203.73	78.62	11.80	22.15	263.12	12.67	15.83	7.49	1.00	21.83	278.89	24.87	80.45	43.90
CLUSTER 10	57.33	61.00	108.67	214.40	90.80	11.27	22.26	251.64	11.43	16.53	7.77	1.20	18.67	321.70	25.67	82.14	50.87
CLUSTER 11	56.33	59.33	108.00	159.33	55.20	12.27	19.44	235.98	10.97	13.43	8.37	1.20	22.67	300.36	25.50	81.84	53.59
CLUSTER 12	49.50	52.17	98.50	135.50	35.50	11.33	16.31	190.56	9.88	12.31	7.01	1.20	22.67	190.73	23.33	70.97	28.16
CLUSTER 13	51.33	53.33	98.67	125.80	26.00	9.20	10.18	139.36	8.60	9.87	5.22	1.00	20.67	261.98	23.00	67.70	21.22
Contribution of various traits to divergence (percentage)	2.53	0.46	0.00	0.23	2.07	3.68	2.30	3.45	4.14	2.53	46.62	11.26	1.15	7.59	1.14	1.55	9.30

***Abbreviations: DT= days to 50% tasseling, DS= days to 50% silking, DDH= days to 75% dry husk, PH= plant height (cm), EH= Ear height (cm), KRPC= kernel rows cob-^{1}, KPR= kernels row-^{1,}KPC= kernels cob-^{1}, CG= cob girth (cm), CL= cob length (cm), SG= stem girth (cm), NCPP= No. of cobs plant-^{1}, NPPP=No. of plants plot-^{1},1000KW= 1000 kernel weight (g), MP= moisture percentage (%), SP= shelling percentage (%), GY= grain yield (q/ha)**

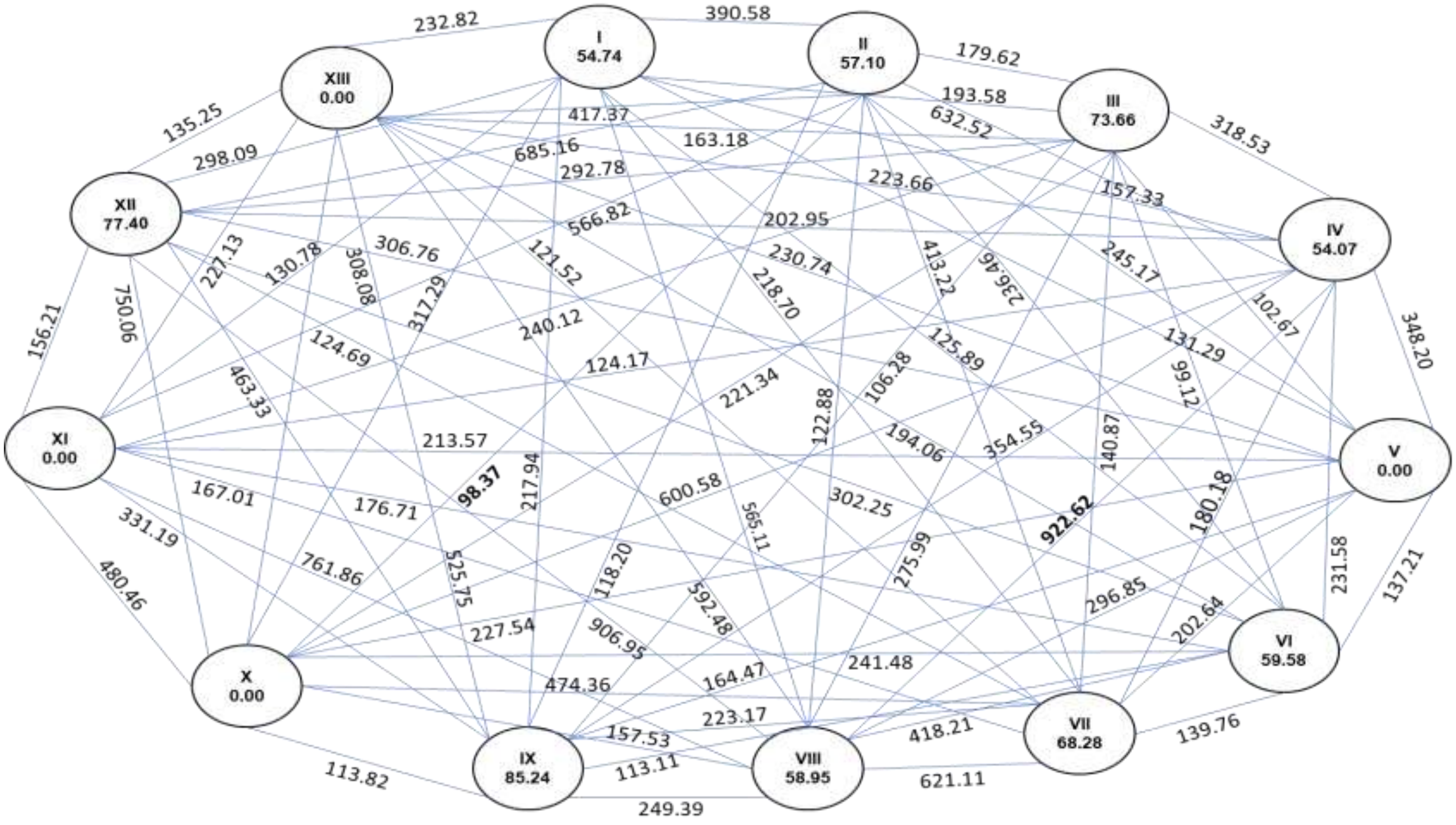

Fig 4.1 : Inter and Intra cluster distance

Figure 4.3: Tocher’s method- Mahalanobis Euclidean Distance

Table 4.39: Mean inter and Intra cluster distance among thirteen clusters in maize inbred lines by Tocher's method

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11	Cluster 12	Cluster 13
Cluster 1	**54.74**	390.58	193.58	157.33	131.29	125.89	218.70	565.11	217.94	317.29	130.78	298.09	232.82
Cluster 2		**57.10**	179.62	632.52	245.17	236.46	413.22	122.88	118.20	98.37	566.82	685.16	417.37
Cluster 3			**73.66**	318.53	102.67	99.12	140.87	275.99	106.28	221.34	240.12	292.78	163.18
Cluster 4				**54.07**	348.20	231.58	180.18	922.62	354.55	600.58	124.17	202.95	223.66
Cluster 5					**0.00**	137.21	202.64	296.85	164.47	227.54	213.57	306.76	230.74
Cluster 6						**59.58**	139.76	418.21	113.11	241.48	176.71	302.25	194.06
Cluster 7							**68.28**	621.11	223.17	474.36	167.01	124.69	121.52
Cluster 8								**58.95**	249.39	157.53	761.86	906.95	592.48
Cluster 9									**85.24**	113.82	331.19	463.33	308.08
Cluster 10										**0.00**	480.46	750.06	525.75
Cluster 11											**0.00**	156.21	227.13
Cluster 12												**77.40**	135.25
Cluster 13													**0.00**

Black Bold figures represent the intra-cluster distance

Table 4.40: Diverse maize inbred lines based on genetic distance and superior *per se* performance for different morpho-agronomical traits

S.no.	Characters	Cluster	Suitable parents in cluster	*per se* performance
1.	**No. of days to 50 % tasseling**	12	WN 33153	47.67
2.	**No. of days to 50 % silking**	12	WN 33153	50.33
3.	**No. of days 75 % dry husk**	12	WN 33153	98.00
4.	**Plant height (cm)**	10	WN 52188	214.40
5.	**Ear height (cm)**	10	WN 52188	90.80
6.	**Kernel row per cob**	7	WN 129	12.65
7.	**Kernels per row**	4	PFSR-10109	24.72
8.	**Kernels per cob**	9	WN 9071-2	304.28
9.	**Cob girth (cm)**	4	WN 2453	14.35
10.	**Cob length (cm)**	10	WN 52188	16.53
11.	**Stem girth (cm)**	11	WN 4614-1	8.37
12.	**No. of cobs per plant**	5	WN 5279	1.73
13.	**No. of plants per plot**	6	Z-490-26 WN 554	24.00
14.	**1000 kernel weight (g)**	10	WN 52188	321.70
15.	**Moisture percentage (%)**	6	WN 2538	26.37
16.	**Shelling percentage (%)**	6	Z-490-26	82.52
17.	**Grain yield per plot (g)**	6	Z-490-26	56.55

CHAPTER-5

DISCUSSION

Maize is a cereal crop that is widely cultivated throughout the world and has the highest yield among all cereals (FAOSTAT, 2020). It is one of the crop species with the greatest variation in morphological and physiological characteristics. Genetically, maize is a well-characterized crop species that has gained more genetic enhancement than any other crop over the last few decades. Wide environmental adaptability, greater genetic diversity, and simple development of successive generations from parental lines are the primary reasons for maize's wide acceptability in genetic and biometric research.

Maize is one of the domesticated crop species with the highest level of genetic diversity. Genetic diversity is an important component of crop improvement programs (Mohammadi *et al*., 2003; Kitti *et al*., 2012). Morphological characters have been recognized to constitute universally undisputed descriptors for varietal characterization of crop species and establishing the distinctness, uniformity, and stability (DUS) of crop species in Plant Variety Protection (PVP) systems (Begum and Kumar, 2011). As the demand for maize will increase exponentially in the coming years, the primary objective of maize breeders is to improve yield-related characteristics (Fisher *et al.*, 2015). Maize inbred lines represent a fundamental resource for studies in genetics and breeding and are used extensively in hybrid corn production (Anderson *et al*., 1952). The assessment of genetic diversity within and among populations has been the concern of several researchers in the past and it is especially important for plant genetic resource management given by (Hamrick *et al*., 1989; Bretting *et al*., 1995).

Creating new inbred lines and introductions are the foundational steps for reversing population growth. Developing hybrids requires the selection of prospective parental lines. Heterosis is probably contingent on the nature of genetic divergence between parental lines (Saxena *et al.,* 2010). Consistently, maize breeders emphasize the significance of diversity among maize parental genotypes, which has a substantial impact on the production of heterotic hybrids (Azad *et al.,* 2012). Multiple studies on maize have demonstrated that inbred lines derived from diverse stock tend to be more productive than crosses between inbred lines of the same variety (Vasal, 1998). Typically, the manifestation of heterosis is determined by the genetic divergence of the two parental lines (Saxena *et al.*, 1998). The development of high-yielding maize varieties is the most fundamental goal of any maize breeder to increase yield. Grain yield is the collective product of inherited and environmental factors. Genetic variability in maize genotypes plays a vital role in grain yield variation (Tahir *et. al*., 2008).

Characterization of maize inbred lines for morpho-agronomical traits has been utilized extensively to increase knowledge of genetic diversity in maize germplasm. In addition, it facilitates the expansion of the genetic base of essential maize genetic resources for sustaining genetic improvement and guides the selection of parents for the creation of new hybrids with high seed yield production potential (Ihsan *et al*., 2005). Morphological traits are the functional manifestation of an organism's underlying genetic constitution; consequently, they are an essential set of genetic diversity markers.

The materials for the present study consisted of 30 maize inbred lines grown in Randomized Block Design (RBD). The present study entitled "**Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region"** was carried out at Maize Research Station, SKUAST-J, Udhampur, J&K during *Kharif* 2021. The research work's findings are explored in the context of pertinent literature under the following headings:

5.1 Characterization of Inbred lines as DUS and Agro-morphological Traits

5.2 Analysis of Variance

5.3 Estimation of Genetic Parameters of Variability

5.4 Correlation and Path Coefficient Analysis

5.5 Genetic Divergence Studies

5.1 Characterization of Inbred Lines as DUS and Agro-morphological Traits

For each of the 30 maize inbred lines, 31 DUS characters were assessed. The observations that were noted are leaf: angle between blade and stem, leaf: attitude of blade, stem: anthocyanin colouration of brace roots, tassel: time of anthesis, tassel: anthocyanin colouration at base of glume, tassel: anthocyanin colouration of glumes excluding base, tassel: anthocyanin colouration of anthers, tassel: density of spikelets, tassel: angle between main axis and lateral branches, tassel: attitude of lateral branches , ear: time of silk emergence, ear: anthocyanin colouration of silks, leaf: anthocyanin colouration of sheath, tassel: length of main axis above lowest side branch, plant: length, plant: ear placement, leaf: width of blade, ear: length without husk, ear: diameter without husk, ear: shape, ear: number of rows of grains, ear: type of grain, ear: colour of top of grain, ear: anthocyanin colouration of glumes of cob, kernel: row arrangement, kernel: poppiness, kernel: sweetness, kernel: waxiness, kernel: opaqueness, kernel: shape and kernel: 1000 kernel weight (g). From all these observations in 30 maize inbred lines, it was concluded that there is a wide range of variations present among the maize inbred lines.

Yadav and Singh (2010) evaluated eleven morphological characteristics according to the DUS test on 30 maize inbred lines which were divided into three major groups based on dissimilarity matrix analysis, indicating all 30 lines were found to differ from each other. Pinnisch *et al*. (2012) characterized 27 maize inbred lines and suggested that grain yield, thousand-kernel weight, ear length, and kernel morphology were the traits suitable for the inbred line to use as a seed parent. Selvi *et al*. (2013) initiated a DUS characterization study on 17 maize inbred lines divided into 6 clusters based on a dissimilarity matrix. Madhukeshwara and Sajjan (2015) analyzed 13 morphometric characterizations for 7 genotypes including 2 hybrids revealed more variation in plant height, tassel attitude, tassel angle, ear shape, and thousand seed weight.

Thus, the study indicated that morphological variations exist with inbred lines due to variations in genetic makeup and could be better utilized by breeders in the selection of inbred lines according to their specific requirements in maize breeding programs.

5.2 Analysis of Variance

Analysis of variance for the experiment involving 30 maize inbred lines for 17 morpho-agronomical traits i.e, no. days to 50% tasseling, no. of days to 50% silking, no. days to 75% dry husk, plant height (cm), ear height (cm), kernels rows per cob, kernels per row, kernels per cob, cob girth (cm), cob length (cm), stem girth (cm), number of cobs per plant, number of plants per plot, 1000 kernel weight (g), moisture percentage (%), shelling percentage (%), grain yield (q/ha).

The analysis of variance revealed that the mean sum of squares for treatments was significant for all traits indicating considerable variation among the inbred lines. Analysis of variance indicated the existence of sufficient variation in the material studied. Similar results of significant mean sum of squares due to inbred lines for all the traits studied were observed by (Yusuf *et al.,* 2010; Rafiq *et al.,* 2010; Nagabhushan *et al.,* 2011; Suresh *et al*., 2012; Nayak *et al.,* 2013; Natraj *et al.,* 2014; Shazia *et al.,* 2017; Aci *et al.,* 2018; Khan *et al.,* 2018.) Among the inbred lines, a high amount of variability was present for no. days to 50% tasseling (43.67-62.33), no. of days to 50% silking (46.67-64.67), no. days to 75% dry husk (96.67-113.33), plant height (cm) (125.47-214.40), ear height (cm) (27.60-90.80), kernels rows per cob (9.20-12.67), kernels per row (10.18-25.06), kernels per cob (139.36-314.64), cob girth (cm) (8.60-14.35), cob length (9.87-17.67) stem girth (cm) (5.11-8.61), number of cobs per plant (1-1.73), number of plants per plot (18.67-24), 1000 kernel weight (g) (184.91-338.72), moisture percentage (%) (23-26.37), shelling percentage (%) (67.70-82.30), grain yield (q/ha) (21.22-56.55). Similar results were obtained by (Haydar *et al.,* 2015; Kapoor and Batra, 2015; Rahman *et al.,* 2017; Hassan *et al.,* 2018; Najar *et al.,* 2018).

5.3 Estimation of Genetic Parameters of Variability

The estimates of phenotypic variance were observed to be higher than the genotypic variance, indicating thereby, the influence of the environment in the expression of these characters. The phenotypic and genotypic variance coefficient of variation was low (<10%) for no. days to 50% tasseling, no. days to 50% silking, no. of days to 75% dry husk, kernels rows per cob, number of plants per plot, moisture percentage, shelling percentage. Moderate value (10- 40%) was for plant height (cm), ear height (cm), kernels per row, kernels per cob, cob girth, cob length (cm), stem girth (cm), no. of cobs per plant, 1000 kernel weight (g) and grain yield (q/ha). Hence, these characters can be relied upon and simple selection can be practiced for further improvement. These results align with (Singh *et al.,* 2009; Reddy *et al*., 2012; Sandeep *et al.,* 2015; Chaudhary *et al.,* 2015; Bhusal *et al*., 2017; Najar *et al.,* 2018; Sharma *et al*., 2018).

Heritability estimates (broad sense) and expected genetic gain were calculated for all the characters. Heritability estimates were observed to be low to high for all the traits and ranged from 52.87-88.15 per cent. Almost similar results were reported by (Sandeep *et al.,* 2015; Rahman *et al.,* 2017; Hasan *et al.,* 2018; Rocandio-Rodríguez *et al.,* 2020). Whereas High values of heritability (>60%) were exhibited by no. of days to 50 % tasseling, no. of days to 50% silking, no. of days to 75% dry husk, plant height, ear height, kernels rows per cob, kernels per row, kernels per cob, cob girth, cob length, stem girth, no. of cobs per plant,1000 kernel weight, shelling percentage, and grain yield.

Moderate values of heritability (30-60%) were observed for no. of plants per plot and moisture percentage. Heritability estimates revealed the heritable portion of variability present in different characters. The knowledge of heritability enables the plant breeder to decide the course of selection procedure to be followed under a given situation (Li *et al.,* 1985). The genetic advance was estimated at 5 per cent of selection intensity and converted into an expected genetic gain (per cent of mean). The expected genetic gain was low for no. of days to 75% dry husk, number of plants per plot, moisture percentage, and shelling percentage. It was found to be moderate (10-20%) no. of days to 50% tasseling, no. of days to 50% silking, and kernels rows per cob. High genetic gain (>20%) was for plant height, ear height, kernels per row, kernels per cob, cob girth, cob length, stem girth, no. of plants per plot, 1000 kernel weight, and grain yield. The results were in agreement with the reports of (Lal and Singh, 2014; Haydar *et al.,* 2015; Shazia *et al.,* 2017; Hasan *et al.,* 2018). The estimates of genetic parameters as variances, coefficients of variation, heritability, genotypic, phenotypic, and environmental correlations, allow knowing the magnitude of the genetic variability of a population, and the selection gains. A critical analysis of genetic variability present in the germplasm of a crop and its estimation is a prerequisite for initiating any crop improvement program as well as adopting appropriate selection techniques (Sravanti *et al*., 2017).

However, heritability values coupled with genetic advances would be more reliable and useful in formulating a selection procedure. In this present experiment, high heritability with high genetic advance was observed for the traits plant height, ear height, kernels per row, kernels per cob, cob girth, cob length, stem girth, no. of cobs per plant, 1000 kernel weight, and grain yield. High genetic advance coupled with high heritability was observed by (Larik *et al*. 2000; Bharathiveeramani *et al.,* 2012; Sandeep *et al.,* 2015; Kinfe and Tsehaye, 2015) for grain yield.

Other traits that showed high to low heritability along with moderate to low genetic advance can be improved by inter-mating superior inbred lines from source populations.

5.4 Correlation and Path Coefficient Analysis

Yield, as it is well known, is a complex trait and its performance is the result of the interaction of several characters. Estimates of genotypic and phenotypic correlations among the characters have, therefore, been found useful in planning and evaluating breeding programs (Johnson *et al.,* 1955; Al-Jibouri *et al.,* 1958). The association between two characters can directly be observed as genotypic and phenotypic correlation. Therefore, their primary utility is in strengthening interpretations based on genotypic and phenotypic correlation and in better predicting correlated responses to selection.

Hence, in the present study, genotypic and phenotypic correlations among the 17 characters of maize genotypes were computed. Grain yield per plot exhibited significant and positive genotypic and phenotypic correlation with plant height, ear height, kernels rows per cob, kernels per row, kernels per cob, cob girth, cob length, stem girth, no. of cobs per plant, 1000 kernels weight, moisture percentage, and shelling percentage. These results align with (Pavan *et al.,* 2011; Mahesh *et al.,* 2013; Bhusal *et al.,* 2017). So, direct selection for the positively correlated characters will be helpful in improvement of grain yield per plot

High positive contribution shown by various characters might have a direct impact on grain yield improvement. However, sometimes correlation coefficients give misleading results because the correlation between two variables may be due to a third factor. It is therefore necessary to analyze the cause-and-effect relationship between the dependent and independent variables to entangle the nature of the relationship between the variables. Path coefficient analysis (Dewey and Lu, 1959) furnished a method partitioning the correlation coefficient into direct and indirect effects and provides information on the actual contribution of a trait to the yield. If the correlation between yield and a character is due to the direct effect of a character, it reveals a true relationship between them, and direct selection for this character will be rewarding for yield improvement. However, if the correlation coefficient is mainly due to indirect effects of the character through another component trait, indirect selection through such trait will be effective for yield improvement. The direct positive effect on grain yield per plot was exhibited by no. of days to 50% tasseling, plant height, kernels per cob, cob length, stem girth, no. of cobs per plant, no. of plants per plot, and 1000 kernel weight. Hence, direct selection for these traits could be practiced for developing high grain yield maize genotypes. Almost similar results were reported by (Bhusal *et al*., 2017).

5.5 Genetic Divergence Studies

Precise information about genetic divergence is critical for a productive breeding program, as genetically diverse parents are known to produce high heterotic effects increasing consequently yield of desirable segregants. High-yielding parents with greater genetic diversity are required to develop productive hybrids. For identifying genetically diverse parents for hybridization, multivariate analysis (Mahalanobis D^2 statistics, 1936) has been used in almost all crop species. The D^2 statistic has been extensively used by numerous workers in classificatory problems (Rao, 1952) in understanding the nature of genetic divergence. The cluster formation was done by following Tocher's method, as described by (Rao, 1952). Classification of genotypes led to the formation of 13 clusters in accordance with the results of various workers (Kage *et al.,* 2013; Shazia *et al.,* 2017; Sood *et al.,* 2017; Singh *et al.,* 2019). Cluster 3 contained the maximum number of inbred lines (5) followed by clusters 1, 2, 4, 6, 7 having 3 inbred lines, clusters 8, 9, and 12 having 2 inbred lines, clusters 5, 10, 12 having 1 inbred line each. The inbred lines exhibited a random pattern of distribution into various clusters showing that genetic diversity and geographical diversity are not related. This means that geographic diversity, though important, was not the only factor in determining genetic divergence (Yadav *et al.,* 2001). The clustering pattern of inbred lines revealed that the inbred lines had significant genetic divergence among themselves. Similar results were reported by (Bhusal *et al*., 2016; Ranawat *et al*., 2013). The clustering of inbred lines from different eco-geographic locations into one cluster could be attributed to the exchange of breeding materials from one place to another; this may also be due to the fact that the unidirectional selection practiced for a particular trait at several places produced similar phenotypes which were aggregated in one cluster irrespective of their distant geographic origin (Singh and Bains, 1968).

Mean Intra and inter-cluster distances revealed that intra-cluster distance was maximum in cluster 9, followed by cluster 12. The inter-cluster distance was maximum between cluster 4 and cluster 8 followed by cluster 8 and cluster 12. So, crossing between lines belonging to these clusters may result in high heterosis, which could be exploited in maize improvement programs, as the crossing among the inbred lines leads to the formation of different transgressive segregants which are utilized to study heterotic effects. The distance between clusters 2 and 10 was minimum indicating that the inbred lines belonging to these clusters were comparatively less diverse.

The genetic differences between clusters were reflected in their cluster means. Cluster means for different morpho-agronomical traits revealed that substantial variability existed for all the characters. The highest mean values for plant height, ear height, cob length, and 1000 kernel weight were observed in cluster 10. Kernels rows per cob were found maximum in cluster 7. The highest mean values for kernels per row and cob girth were observed in cluster 4. Kernels per cob were found maximum in cluster 9 whereas no. of cobs per plant was found maximum in cluster 5. Stem girth was found highest in cluster 11. No. of plants per plot, moisture percentage, shelling percentage, and grain yield were observed highest in cluster 6. Required minimum no. of days to tasseling, no. of days to silking, and no. of days to 75% dry husk were observed in cluster 8 indicating the early inbred lines in this group.

The highest cluster mean for grain yield was exhibited by cluster 6 (Z-490-26). Considering all the characters the inbred lines in cluster 6 had a good performance. Hence, for the improvement of different characters viz. grain yield, no. of plants per plot, moisture percentage, shelling percentage, shelling percentage, no. of days to tasseling, no. of days to silking, no. of days to 75% dry husk, plant height, ear height cob length, and 1000 kernels weight under the present study, inbred lines should be selected from clusters 6, 12 and 10.

The per cent contribution of traits towards total divergence revealed that stem girth was the main factor contributing to divergence followed by number of cobs per plant, grain yield (q/ha), 1000 kernel weight, cob girth, kernel row per cob, kernels per cob, days to 50% tasseling and cob length, kernels per row, ear height, shelling percentage, number of plants per plot, moisture percentage, Days to 50% silking, the sum of which account for 99.77 per cent of total divergence. Plant height (0.23) and days to 75% dry husk (0.00), accounted for the least contribution to total divergence. These results agreed with various workers (Azam *et al*., 2012; Kage *et al.,* 2013; Haydar *et al.,* 2015; Rahman *et al.*,2017; Matin *et al.,* 2017). The traits contributing maximum towards D^2 value need to be given greater emphasis for deciding on the clusters to be chosen for further selection and choice of parents for hybridization (De *et al.,* 1998).

Table 5.1: Identification of diverse inbred lines and recommendation of cross combination for superior recombinants for yield character

Diverse cluster	**Diverse inbred**	**Flowering**	**Mean Per se performance for Yield (q/ha)**	**Colour**	**Recommended cross combination**
Cluster 4	PFSR-10109	Late	39.78	Yellow	**WN 2453 ×WN 32296** **PFSR 10109 ×WN 32296**
	WN 2402-2	Medium	41.23	Orange	
	WN 2453	Late	48.93	Yellow	
Cluster 8	WN 32296	Late	33.27	Yellow	
	WN 2199	Late	29.26	Yellow	

It was found that Cluster 4 and Cluster 8 had highest inter-cluster distance. Cluster 4 contain three inbred lines i.e, PFSR-10109 with late flowering time, mean *per se* performance for yield q/ha (39.78) and yellow kernel colour, WN 2402-2 with medium flowering, mean *per se* performance (41.23), and orange kernel colour, WN 2453 with late lowering mean *per se* performance with late flowering, mean *per se* performance for yield q/ha (48.93) and yellow kernel colour. Cluster 8 contains two inbred lines i.e, WN 32296 with late flowering, mean *per se* performance for yield q/ha (33.27), and yellow kernel colour, WN2199 with late flowering, mean *per se* performance for yield q/ha (29.26) and yellow kernel colour. Based on genetic diversity, mean *per se* performance, and their DUS traits, (Table 5.1) WN 2453 ×WN 32296 and PFSR 10109 ×WN 32296 were found to be the most diverse parent, and their combination for grain yield and recommended for superior recombinants.

CHAPTER –6

SUMMARY AND CONCLUSION

The present study entitled "Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region" was undertaken by keeping in view the following two objectives *viz.*

1. To characterize the maize inbred lines for morpho-agronomical traits as per DUS guidelines
2. To study genetic divergence among maize inbred lines

The basic plant materials in the present study comprised 30 inbred lines. The seed material was sown out in Randomized Block Design at Maize Research Station, SKUAST-J, Udhampur, J&K during *Kharif* 2021. Row to row and plant to plant spacing were maintained at 60 cm and 20 cm, respectively. Recommended agronomic practices were followed to ensure healthy plant stands and to provide the optimum level of management of crop growth. The research was undertaken to DUS characterize the maize inbred lines for morpho-agronomical traits as per DUS guidelines and to generate information on the 17 morpho-agronomical traits viz. no. days to 50% tasseling, no. of days to 50% silking, no. days to 75% dry husk, plant height (cm), ear height (cm), kernels rows per cob, kernels per row, kernels per cob, cob girth (cm), cob length (cm), stem girth (cm), number of cobs per plant, number of plants per plot, 1000 kernel weight (g), moisture percentage (%), shelling percentage (%), grain yield (q/ha).

A wide spectrum of variation was found in the frequency distribution of inbred lines for various characters. The phenotypic variance estimates were found to be greater than the genotypic variance estimates. The phenotypic and genotypic variance coefficients were low (10%) for no. of days to 50% tasseling, no. of days to 50% silking, no. of days to 75% dry husk, kernels rows per cob, number of plants per plot, moisture percentage, shelling percentage. Moderate values (10-40%) were found for plant height (cm), ear height (cm), kernels per row, kernels per cob, cob girth, cob length (cm), stem girth (cm), no. of cobs per plant, 1000 kernel weight (g) and grain yield (q/ha). Estimates of heritability for all traits ranged from 52.87 to 88.15 percent, falling between low and high values. The plant displayed high levels of heritability (>60%) to no. of days to 50 % tasseling, no. of days to 50% silking, no. of days to 75% dry husk, plant height, ear height, kernels rows per cob, kernels per row, kernels per cob, cob girth, cob length, stem girth, no. of cobs per plant, 1000 kernel weight, shelling percentage, and grain yield.

For no. of plants per plot and moisture, percentage demonstrated moderate levels of heritability (30-60%) were found. The expected genetic gain for no. of days to 75% dry husk, number of plants per plot, moisture percentage, and shelling percentage was low (10%). It was discovered that no. of days to 50% tasseling, no. of days to 50% silking, and kernels rows per cob were all moderate (10-20%). For plant height, ear height, kernels per row, kernels per cob, cob girth, cob length, stem girth, no. of plants per plot, 1000 kernel weight, and grain yield, high genetic gain (>20%) was observed. Following the Mahalanobis D^2 analysis utilizing Tocher's method, 30 inbred lines were categorized into 13 clusters based on their performance (Rao, 1952). Cluster 3 had the most genotypes (5), followed by clusters 1,2,4,6, and 7 with 3 inbred lines each, clusters 8,9,12 with 2 inbred lines each, and clusters 5,10,11, and 13 with only one inbred line each. Inter-cluster distances are greater than intra-cluster distances. As a result, the genotypes within a cluster exhibited less diversity. The percentage contribution of various characteristics to divergence revealed that the greatest contribution was made by the percentage of stem girth (46.62).

Conclusion

- Analysis of variance revealed significant differences among the inbred lines for all the traits recorded, while DUS traits were also found to be distinct indicating sufficient variation in the inbred lines.
- The characters like grain yield, kernels per row, kernels per cob, 1000 kernel weight, ear height, and plant height showed high heritability and genetic advance while, kernels rows per cob, kernel per cob, cob girth, cob length, stem girth, plant height, ear height, 1000 kernel weight, moisture percentage, and shelling percentage had a highly significant positive and direct association with grain yield. Hence, estimation of direct and indirect effects before selection based on such component characters may increase the grain yield in maize inbred lines.
- D^2 analysis grouped thirty maize inbred lines into thirteen clusters. The high number of clusters and their value for genetic divergence study showed the presence of a significant amount of genetic diversity.
- Based on genetic diversity, mean *per se* performance, and their DUS traits, WN 2453 ×WN 32296 and PFSR 10109 ×WN 32296 were found to be the most diverse parent, and their combination for grain yield and recommended for superior recombinants.
- Thus, these inbred lines can further be utilized for crossing programs to achieve high-yielding hybrids in maize.

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CERTIFICATE-IV

Certified that all necessary corrections as suggested by the external examiner and advisory committee have been duly incorporated in the thesis entitled **"Genetic Characterization of Maize (*Zea mays* L.) Inbred Lines under Sub-Tropical Conditions of Jammu Region"**, submitted by **Mr. Surjeet Singh**, Registration No. **J-20-M-748**.

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