

ASSESSMENT OF GENETIC DIVERSITY IN MAIZE [*Zea mays* (L.)] INBRED LINES

काशी हिन्दू
विश्वविद्यालय



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THESIS SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

THESIS

Master Of Science (Agriculture)

In

Genetics And Plant Breeding

SUPERVISOR
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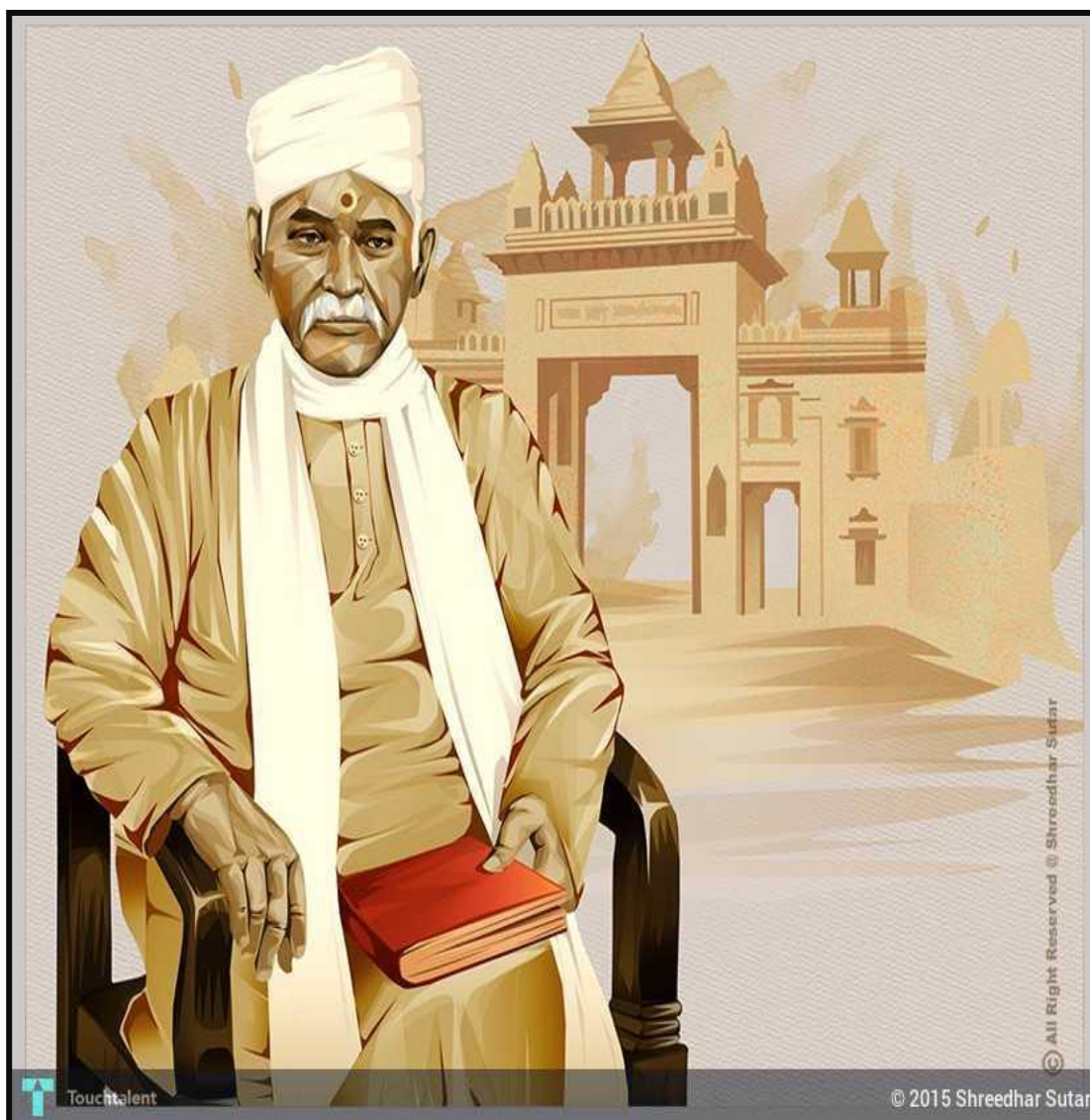
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Through: The Head, Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, B.H.U, and Varanasi.

Dear Sir,

I have great pleasure in forwarding the thesis entitled “**Assessment of Genetic Diversity in Maize [*Zea mays* L.]Inbred lines**” submitted by **Ms. Shivani Kharwar I.D. No. 19412GPB018**, in partial fulfillment of the requirements for the degree of **Master of Science (Agriculture) in Genetics and Plant Breeding**, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, and placing on record that she has completed the requisite residential requirements as contained in the statute of the University.

I certify that the entire scheme of investigation presented herein was planned and carried out solely by the candidate under my guidance and supervision. The data presented in the thesis, to the best of my knowledge and belief, are genuine and original.

Thanking you,

Yours Faithfully
Prof. J.P. Shahi
(Supervisor)

Forwarded by
Prof. B. Sinha
(Head of Department)

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Date:

Place: Varanasi

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CONTENT

CHAPTERS	PARTICULARS	PAGES
I	INTRODUCTION	1-7
II	REVIEW OF LITERATURE	8-26
III	MATERIALS AND METHODS	27-47
IV	EXPERIMENTAL RESULT	48-82
V	DISCUSSION	83-90
VI	SUMMARY AND CONCLUSION	91-94
VII	REFERENCES	i-ix
	APPENDIX	x-xii

LIST OF TABLES

Table no.	Particulars	Page no.
3.2.1	List of inbred lines taken under investigation	28
3.3.1	List of five different stages of crop growth for application of nitrogen	30
3.5.6.1	Analysis of variance of RCBD	35
3.5.7.2.1	Scale for GCV and PCV	37
3.5.7.3	Scale for Heritability	38
3.5.7.5	Scale for Genetic advance as percent mean	39
3.5.8	Scale for Correlation Coefficients	40
3.5.9.1	Scales for Path Coefficient	42
4.1.1	Analysis of variance for yield and yield contributing traits in maize	49
4.2.1	Mean performance and range for yield and yield contributing characters	52
4.3.1	Genetic variability parameters for yield and yield contributing traits	55
4.4.1.1	Phenotypic correlation between grain yield per plot (Kg) and its component traits in maize inbred lines	60
4.4.2.1	Genotypic correlation between grain yield per plot (Kg) and its component traits in maize inbred lines	65
4.5.1.1	Direct and indirect effect of component traits attributing to grain yield per plot (Kg) at the phenotypic level	69
4.5.2.1	Direct and indirect effect of component characters attributing to grain yield per plot (Kg) at the genotypic level	74
4.6.3.1	Cluster composition of thirty-five maize inbred lines	76
4.6.4.1	Average intra and inter-cluster distance among eleven characters for 35 maize inbred lines	78
4.6.5.1	Cluster mean for eleven characters in thirty-five inbred lines of maize	81
4.6.6.1	The relative contribution of eleven characters to genetic diversity in thirty-five inbred lines of maize	82

LIST OF FIGURES

Figure no.	Particulars	Page no.
3.3.1	Layout of Experimental Maize field plot	29
4.3.1	Genetic variability parameters (GCV, PCV, Heritability, and Genetic advance).	56
4.4.1.1 & 4.4.2.1	Correlation matrix of phenotypic and genotypic correlation for grain yield per plot (Kg/plot) in maize	61
4.5.1.1 & 4.5.2.1	Path diagram showing estimates of phenotypic and genotypic path correlation for grain yield per plot (Kg/plot) in maize inbred line	70
4.6.3.1	Clustering of inbred lines by Tocher's Method	77
4.6.4.1 & 4.6.6.2	Average intra and inter-cluster distance between inbred lines by Tocher's Method and Relative contribution of eleven characters in percent.	79

LIST OF ABBREVIATIONS

%	:	Percentage
ANOVA	:	Analysis of Variance
BHU	:	Banaras Hindu University
CD	:	Critical difference
CF	:	Correlation factor
°C	:	Degree centigrade
cm	:	Centimeter
cM	:	Centi Morgan
COV	:	Covariance
df	:	Degree of freedom
E	:	East
e.g.	:	For example
<i>et al.</i>	:	Co-authors [<i>et al</i> lii]
etc.	:	Etcetera
g	:	gram
GA	:	Genetic advance
GAM	:	Genetic advance as percent of mean
GCV	:	Genotypic coefficient of variation
$h_2(b)$	:	Heritability in broad sense
i.e.	:	that is
Kg/ha	:	Kilo gram /hectare
M	:	Meter

MMT	:	Million metric tons
m ²	:	square meter
Max.	:	Maximum
Min.	:	Minimum
MSL	:	Mean Sea level
Mha	:	Million hectare
mm	:	millimeter
MSe	:	Mean sum of square due to error
MSr	:	Mean sum of square due to replication
MS(Tr)	:	Mean sum of square of treatment
N	:	North
No.	:	Number
PCV	:	Phenotypic coefficient of variation
RCBD	:	Randomized Complete Block Design
S	:	Significant
SE	:	Standard error



INTRODUCTION

Maize (*Zea mays* L.) is a cereal crop belonging to the family of Poaceae (Gramineae) and tribe Maydeae having diploid chromosome number ($2n=2x=20$). It is a commercially important grain crop with wide adaptability and versatility under fluctuating agro-climatic conditions. Maize is also known as the queen of cereal crops because it has a high potential for productivity than other cereals of the Gramineae family. Maize, often known as Indian corn, is a robust annual plant grown for its grains during the rainy season. The roots are fibrous adventitious. After germination, the primary root dies and is replaced by fibrous adventitious roots from the stem's base. The stems are thick, sturdy, and have distinct nodes and internodes. The leaves are simple, with a full border, are larger and linear in shape, which are placed alternately. The set-up is distichous, or two-tiered. The bottom flag leaves are, 50–100 cm long and 5–10 cm wide, and the stems are erect, usually 1–3 m high, with several nodes consisting of flag leaves at each node and generally 20–30 cm long internodes are present. Sheathing leaf-base surrounds a portion of the internode above. At the base and blade intersection, there is a membranous ligule. The venation of leaves run parallel to each other and all of the organ have a rough surface due to the silica impregnation. The terminal staminate compound raceme or panicle and the axillary pistillate spadix are the two types of inflorescences. Spikelets make up the male inflorescence. The spikelet grows in pairs, with the lowest being sessile and the higher stalked. Two flowers appear on each spikelet. There are four glumes in a single glume. The first and second glumes at the base are sterile, whereas the blooming glume and the two-nerved palea enclose a flower. Flowers, by their very nature, are monosexual. Lodicules are fleshy scale-like entities that represent the perianth. Three free stamens with long, conspicuous linear anthers make up the androecium. A spadix grows from the axil of a lower leaf to produce female inflorescence.

Cob is formed when a significant number of spikelets are tightly packed along the fleshy axis. A few big hyaline bracts known as spathes remain surrounding it. Each spikelet has two flowers and protecting glumes, similar to a male spikelet. The higher blossom is normally viable, while the lower one fails. There aren't any lodicules. Monocarpellary gynoecium with a single anatropous ovule, the ovary is superior, one-chambered, and oval.

Long and silky styles are featured. From the tip of the cob, persistent styles dangle in tufts. The stigma is feathery and lengthy. Flowers are pollinated by the wind. The carpel's feathery stigma easily captures small dusty pollen grains. Fertilization occurs naturally. Fruit is a caryopsis with a single tightly fitting seed in which the fruit wall and seed coat are inextricably linked. On the spongy axis, a considerable number of fruits known as grains remain firmly packed. Albuminous seeds are those that contain a lot of protein. The absorbing organ is the solitary cotyledon, the scutellum. The germination process is hypogeal. The sporophyte, with diploid ($2n$) chromosomes in the nucleus of the cells, is the most prominent generation, whereas the gametophytes, with haploid (n) chromosomes, are represented by the embryo-sac and pollen tube. They're tiny, weak and dependent on the sporophyte for survival. Microspore-mother cell and megaspore-mother cell reduction division precedes the development of microspores and megaspores, respectively, in a gametophytic generation. The ' $2n$ ' number is restored after fertilization, and sporophyte development commences.

Cross-pollination occurs when pollen is blown by the wind and comes into contact with the emerging silks of the same or different plant. Fertilization of pollen grain results in the development of the kernel. The kernel is made up of two layers: an outside thin coating, an inner testa or real seed coat, and an outer pericarp. The endosperm, which accounts for approximately one-third of the overall volume. Except for sweet corn, this is virtually entirely made up of starch. The embryo is a small plant structure that, when planted, develops into a new plant. The pericarp of the fruit is fused with the caryopsis seed coat, which is characteristic of grasses, and the entire kernel is referred to as a seed. Normally, the ear holds about 600 kernels. White, yellow, blackish, bluish-gray, purple, green, red, and orange are some of the colors they come in. From sowing to complete ripening of the kernels, most corn varieties take 100 to 140 days, however other kinds can mature in as little as 80 days.

Maize has high nutritional content, which includes high starch levels as well as vital proteins and oils, is one of the reasons it is a staple diet around the world. Carbohydrates make up 70% of grain, whereas protein makes up 10%, fat makes up 5% to 7%, oil makes up 4%, fiber makes up 3% to 5%, and minerals make up 2%. Maize is high in vitamin B, folic acid, vitamin C, and provitamin A, which is a precursor to vitamin A. Manganese, phosphorus, magnesium, zinc, copper, iron, and selenium are all abundant in maize, which also contains a tiny amount of potassium and calcium. However, tryptophan and lysine, two of the 10 amino acids considered necessary to humans, are naturally lacking in maize. The

concentration and composition of numerous colored pigments known collectively as carotenoids vary greatly in maize. Beta-carotene is converted to vitamin A in the body through regular metabolic mechanisms. Vitamin A is essential for human health, notably in terms of vision and as an antioxidant. Maize is thus particularly vital for folks who do not have access to fresh veggies all year.

This crop requires 50-100 cm of rainfall to flourish, and it cannot be grown in locations with more than 100 cm of rainfall. During the rainy season, maize is harmed by lengthy dry spells. After the rain, maize benefits from the sun. Grain ripening is aided by cool, dry weather. Temperatures of 21°C to 27°C are ideal for this crop, yet it can withstand temperatures of up to 35°C. Maize is harmed by frost. The ideal soils for greater development and yield are fertile, well-drained alluvial and red loamy soils that are free of the coarse debris and rich in nitrogen. The best conditions for cultivation are well-drained plains, though they can also be found in hilly places. Maize is a facultative short-day plant that blooms when the temperature in the environment to which it is acclimated is more than 10°C. Maize is grown up to 3000 meters above mean sea level in most parts of the world. It is generally cultivated in tropics, subtropics and mild areas up to scope 58° north to 40° south from the equator to over 3000 m above mean sea level and region accepting yearly precipitation of 250 mm to 5000 mm over the world (Downswellet.*al.*, 1996). For photosynthetic carbon fixation, maize possesses a C4-type physiological mechanism. Maize ranks third after wheat and rice as commercially important crops (Poehlman, 2006). It has great potential for higher grain yield. It is believed to originate in southern Mexico or northern Guatemala (Weatherwax, 1995). Currently, nearly 1147.7 million MT of maize is being produced together by over 170 countries from an area of 193.7 million ha with average productivity of 5.75 t/ha (FAOSTAT, 2020). Production of maize is firmly concentrated in 4 countries U.S, China, Brazil, and Argentina which alone account for over 2/3rd of global production while Asian production is dominated by India and Indonesia. This crop is cultivated throughout the year in most of the country for different purposes including grain, feed, fodder, green cob, sweet corn, baby corn, flint corn, popcorn, and flour corn.

Maize consumption in India has grown up to 24 MMT comprising 13.5 MMT from poultry feed, 1.8 MMT from starch, 1.2 MMT from ethanol, and balance for food, seed, and other usages. In India, the production of maize crops by small farmers plays a vital role in alleviating poverty, income generation, and contributing to the local and national economy. Major maize growing states that contribute more than 80 percent of total maize production

are Andhra Pradesh (20.9%), Karnataka (16.55%), Rajasthan (9.9%), Maharashtra (9.1%), Bihar (8.9%), Uttar Pradesh (6.1%), Madhya Pradesh (5.7%), Himachal Pradesh (4.4%) followed by other states. Maize is predominantly a rain-fed *Kharif* crop, planted just before the monsoon begins and harvested after the monsoon has passed. In Uttar Pradesh, it is grown in both *Kharif* season crop in June and July and as a *Rabi* season crop in October-November, just before the winter season begins. The upper Gangetic plain of Uttar Pradesh is an important producer of maize in India. In U.P., Maize is grown in as many as 25 districts, with major production concentrated at Bulandshahar, Jaunpur, Etah, Ghaziabad, Bahraich, Farrukhabad, and Gonda. In Uttar Pradesh, the total area of maize was 6237 ha in 2018-2019, total production of maize was 10903 metric tons, and productivity was 17.78 q/ha in 2019-2020 (Directorate of economics and statistics, DAC and FW).

In India, maize production has increased linearly over the years, with breakthroughs at the dawn of the 21st century associated with the development and release of more hybrids over that period. Recent emphasis on developing inbred and high-yielding hybrids, preferring to remain dependent on composites, has yielded rich dividends as a potential field crop in India. The main breeding objective of maize improvement programs is to increase yield. Any plant breeder working with crop improvement programs must have a thorough understanding of genetic parameters such as variability, heritability, and genetic advancement, as well as the relationship between yield and its contributing characters in a given crop species for various economically important quantitative characteristics. The extent of genetic diversity in the base material for the desired character is a major factor in the generation of new varieties/hybrids. In estimating the amount of variability present in a particular trait, parameters like phenotypic and genotypic coefficients of variation can be relevant. An assessment of the variation contained in the material is required before initiating a varietal/hybrid development program. As a result, it's critical to investigate the nature and degree of heritable genetic variation in the sample. The presence of significant genetic variation in the base material ensures improved possibilities of generating superior cultivars, therefore understanding the type and degree of the genetic variability existing in the gene pool is quite valuable when we start any systematic breeding program. Yield is a complex character and an interactive effect of various traits, determining the components that contribute to high yield is a difficult task. To reach a high yield level, the plant breeder must simplify this complex situation by handling yield components that have correlations with one another. To implement this reasonable approach, data on the type and extent of the

relationship between the various yield components, as well as their mode of contribution to yield, is required. Heritability was discussed by Bhatt (1973), Paroda and Joshi (1970), and Lush (1949). Heritability is defined as the ratio of genotypic variance to the phenotypic or total variance. It's measured in percentages. As a result, heritability refers to the heritable component of phenotypic variance. It's a good indicator of character inheritance from parents to progeny.

Heritability estimation aids in the selection of elite genotypes, making it extremely useful for improving crop species through the selection of many features, including qualitative traits. The breeding value of an individual genotype is determined by the amount of heritability. To develop a successful breeding program for quantitative characters, reliable estimations of heritability are required. The improvement in the mean genotypic value of the selected population over the parental population is referred to as genetic advancement. It estimates the genetic gain as a result of selection. The genetic advance study, which analyses the genetic gain in a particular character based on selection, is just as significant as the genetic gain study. As a result, any crop improvement program based on selection must include the research of genetic variability and heritability, as well as genetic advancement. In determining the effect of selection for the best yielding genotypes and yield attributing traits, heritability combined with high genetic progress is extremely useful. The effectiveness with which genotypic variability can be exploited by selection is determined by the individual trait's heritability and genetic advancement. Yield is a complex quantitative character that is greatly influenced by the surrounding environment. As a result, genotype selection based on yield is ineffective. For the yield components, a decision must be made. The direction and degree of the relationship between yield and yield contributing component characteristics determine the efficiency of any breeding effort. Thus, by examining the relative influence of different characters on yield and each other, the correlation analysis assists in determining the character or combination of characters that could be useful as an indicator of high yield. As a result, knowledge of the correlation coefficients between grain yield and its component attributes is critical for yield enhancement. The phenotypic and genotypic correlation coefficients reflect the degree of the link between the various characters and, as a result, helps in the selection of characters that boost yield and yield attributing characters. F. Galton (1889) introduced the concept of correlation, which was later expanded upon by Fisher (1918).

The number of characters is examined in connection to one another, which indicates indirect selection. Indirect selection plays an equal role in influencing the final result, grain yield, in any crop species. The path coefficient analysis has developed as a valuable tool for this goal, as it identifies the direct and indirect causes of association, provides a notion of the specific forces at work to form a strong correlation, and measures the relative importance of each causal component. Path analysis is a standardized partial regression coefficient that divides the total correlation coefficient into direct and indirect effects, as well as measuring the direct and indirect contributions of each independent variable to the dependent variable. Path analysis is a technique for determining the direct and indirect effects of various features on grain production. Simple correlations cannot distinguish between each component's direct contribution to yield and indirect effects through linkage with other characters. The correlation between the independent character and the dependent character states grain yield is owing to their direct effect or indirect effects via other component characters, according to path analysis. Wright (1921) was created and described as a method for studying the direct and indirect effects of independent variables on dependent variables in genetics. Later, Dewey and Lu (1959) were used to boost crop yields.

All crop improvement programs, both self-pollinated and cross-pollinated, are built on genetic diversity. In the segregating generations, hybrids from more diversified crosses are likely to have substantially higher levels of heterosis and a wide spectrum of variability. As a result, understanding genetic variety is critical when choosing parents for a hybridization program to create appropriate heterotic crossings and obtain desired combinations in segregating generations. For the examination of genetic diversity in germplasm accessions, breeding lines, inbred lines, and populations, a variety of approaches are now used. Pedigree data, morphological data, agronomic performance data, biochemical data, and, more recently, molecular data were used to develop these approaches. D^2 statistics is one of the finest ways for measuring genetic diversity in crop species among all of these methodologies. P.C. Mahalanobis established the notion of D^2 statistics for the first time in 1928. C.R. Rao, on the other hand, was the first to propose using the Mahalanobis D^2 approach for estimating genetic diversity in plant breeding. This is a method based on numbers. A cluster diagram is used to depict genetic diversity in D^2 statistics. This information assists in the classification of germplasm into appropriate heterotic groups for future breeding operations, as genetically diverse genotypes are known to exhibit high hybrid vigor. Plant breeders need to know the group distance to determine the level of genetic variability in the material. The study of

genetic variation is thus becoming increasingly important for the generation of super and successful hybrids, in which diverse and desirable lines are selected and crossed to combine two or more traits in a single genotype.

In light of this, the current study, titled “**Assessment of Genetic Diversity in Maize [*Zea mays* L.] Inbred lines**” was conducted on 35 maize germplasm specimens including eleven traits with the following objectives:

1. To examine the amount of genetic variability, heritability, and genetic advancement among the maize inbred lines.
2. To determine the character relationship between yield and yield contributing characters.
3. To access the direct and indirect effects of yield contributing trait on the grain yield of the maize inbred lines under study.
4. To study the genetic diversity among the selected inbred lines.



Chapter-II**REVIEW OF LITERATURE**

A Literature review is a survey of scholarly sources that provides an overview of a particular topic. Writing a literature review involves finding relevant publications such as books and journal articles, research papers related to the investigation for critical analysis and explaining what we observe. Under the following headings, reviews of previous publications in maize genotypes that correspond to the present study are offered.

1. Genetic variability, heritability, and genetic advance
2. Correlation coefficient analysis
3. Path coefficient analysis
4. Genetic diversity analysis

2.1 Genetic variability, heritability, and genetic advance

Thapa Magar *et al.*, (2021) studied variation, broad-sense heritability, genetic progress, and association among characters for growth, yield, and its attributing traits in ten maize genotypes. The phenotypic coefficient of variation (PCV) was larger than the genotypic coefficient of variation (GCV) for all traits showing that there was an environmental influence. The grain yield had the highest PCV (26.91%) and GCV (25.9%), whereas the leaf width at maturity had the lowest PCV (4.07%) and GCV (25.9%). (6.05 percent) of Genetic Advancement. The genetic advance over a mean (GAM) for the characters ranged from 0.1 percent for days to 50% anthesis to 51.36 percent for grain yield. Test weight ($r = 0.706$), cob length ($r = 0.671$), cob diameter ($r = 0.573$), and number of rows per cob ($r = 0.539$) all had positive and substantial phenotypic correlations with grain yield. As a result, characters with a significant variance can be employed as selection indices in indirect selection

Diribu Tesfaye *et al.*, (2021) based on their study reported that thousand kernel weight, ear, and plant height had the biggest genotypic and phenotypic variations, implying that genotype selection based on the phenotypic performance of these parameters is beneficial. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all traits (GCV). On the other hand, the differences between the two

components were insignificant. Grain yield, ear height, and ear aspect all demonstrated substantial genetic progress as a percent of the mean, as well as high heritability, implying that additive gene action had a larger role in these characters. Selection for these traits will allow upland maize germplasm to be improved.

Yaregal Damtie *et al.*, (2021) determined the magnitude of genetic variability, heritability, and genetic advance of traits, to confirm genotypic and phenotypic associations between important traits, and to use path coefficient analysis to determine the relationship of traits with grain yield and direct and indirect effects. The experiment was carried out at Pawe Agricultural Research Centre with 23 inbred lines in replications utilizing RCB design. The results showed that there was a considerable difference in genetic variability among widely produced maize inbred lines. Keeping all the characters under consideration, lines A7033, CML197, and CML202 were found promising. Better soil nutrient and carbon assimilation for photosynthesis, which may have built up in each ear size and number, thus providing higher grain production, can be attributed to positive significant direct effects of plant and ear height and a number of ears collected in each plot on grain output.

Bartula *et al.*, (2019) evaluated ten maize genotypes in a completely randomized block design (RCBD) in a Lamahi Municipality field in Nepal's Dang district with three replicates. All of the characters had significant differences, according to the analysis of variance. For all traits, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV). Among all other characters, grain yield and field weight had the highest PCV and GCV, but test weight and plant height had the lowest PCV and GCV. With low genetic advancement, the test weight had the highest heritability. Grain yield, number of kernels per cob, and kernel rows per cob with high GCV and PCV that can be exploited in crop improvement programs.

Beulah *et al.*, (2018) evaluated eleven genotypes based on analysis of variance, heritability, and genetic advancement. For all of the traits evaluated, there was high significant variation. For all characters, the PCV values were higher than the GCV values. The heritability of traits including anthesis-silking interval, grain yield, plant height, cob height, days to maturity, and grain rows per cob were quite high. Other traits examined in the study have a moderate degree of heritability. For the field weight and grain yield per plot, a high value of genetic advance was seen. All of the characters investigated had a relatively low genetic advancement.

Dar et al., (2018) conducted the field experiment at the Budgam Dryland Agriculture Research Station (DARS) during 2017 *Kharif* season under natural rainfed conditions. Thirteen maize varieties were evaluated in a Randomized Block Design with three replications. He discovered that the days to 50% anthesis, days to 50% silking, and the anthesis-silking gap had the largest genotypic and phenotypic coefficients of variation, whereas the number of cobs per plant had the lowest.

Sravanthi et al., (2017) examined variability, heritability, and genetic advancement of 42 maize genotypes for yield and its contributing variable. The analysis of variance revealed that the maize genotypes under consideration had a large degree of variability. They found that ear height had the highest PCV (27.52) and GCV (26.42) of all the features studied, whereas days to maturity had the lowest PCV (3.45) and GCV (3.45). Ear height and grain yield per plot had high heritability and high genetic advance, indicating that additive gene action was dominant in controlling the traits.

In South-West Nigeria, **Sesay et al., (2016)** evaluated twelve maize hybrids at various places and claimed that the ten hybrids in the study had various levels of diversity, heritability, and genetic advance based on the traits examined. The number of kernel rows was observed to have a moderate to medium genotypic variation coefficient (GCV) and phenotypic coefficient variation (PCV). For all of the measured characters, such as germination %, 100 seed weight, and shelling percentage of top-cross hybrids, low to high heritability and genetic advance values were also provided. In top-cross hybrids, field weight and grain yield showed low GCV, high heritability, and genetic advance values.

During *Kharif* 2013, **Sandeep et al., (2015)** performed experiment on a college farm, College of Agriculture, PJTSAU Rajendranagar, Hyderabad, to quantify genetic diversity in sixty inbred lines of maize. The genotypic coefficient of variation (GCV) was lower than the phenotypic coefficients of variation (PCV) for all of the traits investigated, indicating an environmental effect. For traits like grain yield per plant and ear height, strong PCV and GCV as well as high genetic progress were detected. For the shelling percentage, the difference between the PCV and GCV estimations were quite small, showing that the environment has a minor impact on the manifestation of these traits.

Nzuve et al., (2014) studied 42 maize genotypes planted in full diallel mating design. Heritability of grain yield and related agronomic parameters were determined at three

locations in various agro-ecological zones in Kenya. He noted that substantial differences were found for all of the examined features, indicating the diversity of maize genotypes. The prevalence of additive gene action in ear height and plant height was revealed by the high heritability and wide genotypic variation.

Dar et al., (2014) included 80 maize genotypes in the study and reported that the Mss due to genotypes exhibited substantial differences for all the characters studied, confirming the presence of variation, based on the analysis of variance. High heritability and genetic advancement have been reported for traits such as yield per plant, plant height, ear height, number of kernels per row, and the 100-kernel weight, demonstrating that the heritability is most likely due to the consequences of high additive gene effects, and selection for these traits is effective in early generations. Days to 50% tasselling, days to 50% silking, shelling percent, ear length, days to maturity, ear diameter, and the number of kernel rows per ear have all showed high to moderate heritability and low genetic progress.

Panwar et al., (2013) studied eighty-three maize genotypes for genetic variability and interrelationships among grain yield and its components (*Zea mays* L.). For all of the characters tested, there were extremely few variations in genotypic and phenotypic coefficients of variation, indicating that environmental effects on the development of these traits were minimal and that these characters were largely regulated by genetic factors. High heritability associated with high genetic advance was detected for grain production per plant, leaves in the plant, 100-seed weight, and harvest index and ear length, showing the additive genetic control in the inheritance of these variables.

Bharathiveeramani et al., (2012) analysed a total of 144 maize inbred lines using 15 distinct quantitative features. All of the traits investigated had a lot of variation, according to the analysis of variance and phenotypic range. Except for anthesis-silking interval, cob production per plant, and grain yield per plant, the difference between PCV and GCV was very small, indicating that these traits had minimal environmental influence. GCV, PCV, heritability, and genetic progress as a proportion of the mean were all high during the anthesis-silking phase. PCV and GCV values were low for traits including grain yield per plant, cob yield per plant, and ear height, moderate to high heritability with moderate genetic gain.

Shanthi *et al.*, (2011) conducted an experiment at two locations, Hyderabad and Allahabad, and in two seasons, *Kharif* 2003 and 2004 to assess genetic variability parameters in QPM genotypes for several economic traits such as grain yield, different growth, maturity, and quality parameter in QPM genotypes. A randomized block design was used to raise the experimental sample, which included 10 parents, 45 single cross hybrids, and two standard checks, Shaktiman-2 and DHM-105. Grain yield and its component characters such as total anthers dehiscence period, the total period of silk appearance, active pollination period, cob weight, number of seeds per cob, protein yield, and oil yield all showed high GCV and PCV estimates, as well as high heritability of more than 85% and high genetic advance in this experiment. The presence of genetic variants for these traits was most likely due to their strong additive gene effects, implying that there was a better chance of improving these features through direct selection.

Chauhan *et al.*, (2010) assessed variability and genetic progress of 20 quantitative parameters in 20 baby corn cultivars. Days to first and last cob harvesting intervals, cob production per plant, ear yield per plant, harvest index, and tassel weight per plant all had high genotypic and phenotypic coefficients of variation (GCV and PCV) values. Traits with high heritability, such as stalk weight, biological yield, cob yield plant, ear yield per plant, fodder yield per plant, and plant height, were accompanied by substantial genetic progress, showing that additive gene action drives the expression of these traits. Days until the first and last cob picking intervals, as well as cob weight, showed lower values for heritability and genetic advance.

During the 2005 and 2006 cropping seasons **Bello *et al.*, (2012)** assessed eight open-pollinated maize cultivars at the Teaching and Research Farm of Ilorin University in Nigeria for genetic characteristics. According to the findings, high and significant PCV, GCV, and heritability, as well as high genetic advance, were recorded for grain yield, 100 seed weight, grains per ear, ear weight, plant height, and ear heights, indicating that these parameters were controlled by additive gene effects and that effective selection for these characters could be possible for yield improvement.

Beyene *et al.*, (2005) tested 180 genotypes in a Randomized Complete Block Design. For all of the traits studied, the genotypes exhibited significant variation. Grain yield, field weight, kernels per row, rows per ear, and ear height were directly selected by peasants and had high PCV values, but indirectly selected traits such as ear diameter, ear height, days to 50%

tasselling, and silking had low PCV values. The number of kernel rows and kernels per row had the highest heritability and genetic progress and may be employed as a selection criterion to boost grain yield. Overall, the data indicated that maize genotypes had a wide range of features that can be exploited through hybridization and selection.

Mahmood *et al.*, (2004) found grain yield per plant (0.993) had the highest heritability with genetic advance estimates, followed by plant height (0.99) and test weight (0.887), respectively. The study's genetic progress values for several characters ranged from 43.80 for grain yield plant to 1.33 for the number of kernel rows per ear.

Yanhua *et al.*, (1999) conducted a field experiment to estimate genetic parameters among 20 maize inbred lines for quantitative features. The heritability of days to 50% silking, plant height, kernel number per row, leaves, number per plant, grain production per plant, and kernel weight was higher; thus, these traits might be regarded early generation selection. The grain production per plant and kernel weight had a better genetic advance, and the direct selection impacts were the best. The grain yield per plant kernel weight was more closely linked to ear diameter, kernel number per row, 100 seed weight, and their selection index.

2.2 Correlation analysis

Bal Krishna *et al.*, (2021) tested 13 inbred lines, 3 testers, 39 hybrids, and 2 checks in a Randomized Block Design with three replications at the Irrigation Research Station Farm, Araria, Bihar. The purpose was to determine the direct and indirect effects of traits on maize grain yield, as well as the phenotypic and genotypic relationships between traits. Character association studies will aid in evaluating the relationship between the yield and its components to increase the effectiveness of the selection. In light of this, the current study analysed the correlation coefficient and path analysis among 39 F₁S, 13 inbred, three testers, and two checks of maize using twelve quantitative traits. Plant height (cm), ear height (cm), ear length (cm), ear diameter (cm), 1000 kernels weight, kernel rows per ear, and the number of kernels per row all showed a significant positive association with grain yield (Kg/ha) as well as among themselves at the phenotypic and genotypic level, according to correlation studies. As a result, selecting for any one of these characters will improve the other characters while also increasing grain production (Kg/ha). Ear length, ear diameter, kernel rows per ear, kernels per row, 1000 kernels weight, ear height, and days to 50% silking had the largest positive direct influence on grain yield, according to path coefficient analysis. As a result, the

current research could help with the reliable selection of parental lines based on the above-mentioned characters, as well as the development of high-yielding varieties for future breeding programs.

Vishal Verma *et al.*, (2020) undertook a field experiment with 30 maize inbred lines was at Horticulture Research Farm, Institute of Agricultural Sciences, Bundelkhand University, Jhansi (U.P.) to investigate the correlation and path coefficient analysis for seed yield and its component traits in maize. The seed yield per plant correlation coefficient was extremely significant and positive with seed yield per cob, number of seed per cob, shelling percent, and biological yield per plant, indicating that these components may be used to improve maize output effectively. The most important characters contributing to seed yield per plant were biological yield per plant, harvest index, seed yield per cob, seed per cob, seeds per row, 100 seed weight, days to 50% germination, cob ear weight, cob length, and days to 50% tasselling, days to 50% silking, days to 50% maturity, cobs per plant, and selection based on these characters would be more effective for improvement in seed yield per plant.

Reddy & Jabeen (2016) conducted a study to assess the correlation and path coefficient analysis of maize hybrids. For the characters under study, the genotypic correlation was found to be greater than the phenotypic correlation, indicating a positive and significant relationship between grain yield and other traits such as test weight, number of kernel rows, ear diameter, ear length, plant height, and ear height. The number of kernels per row, the weight of 100 kernels, and the girth of the ears had the greatest direct effect on the yield of grain per plant, followed by days to 50% silk. Characters including days to 50% tasselling, days to 50% silking, ear height, number of kernels per row, 100-seed weight, ear girth, and days to maturity, length of ear, and yield of grain per plant have high heritability combined with genetic progress.

Ghimire *et al.*, (2015) examined 14 maize genotypes and determined correlation for several yield attributing factors. Grain yield had a positive relationship with ear height, plant height, ear length, ear girth, ear weight, number of kernel rows per ear, number of kernels per row, and 500 kernel weights, according to the findings. Days to 50% tasselling and days to 50% silking were likewise shown to have a highly significant and negative association with grain yield, while days to maturity were found to have a negative and nonsignificant link with grain yield. According to correlation analysis, the highest yield determinant factors were plant height, ear height, ear length, ear girth, number of kernels per row, and ear weight.

Rafiq *et al.*, (2014) found negative association between fertility and plant size. If the optimum grain yield is to be achieved, a compromise between these two characters must be reached.

Amini *et al.*, (2013) examined six generations of maize seed yield and their components in a randomized full block design with three replications. In most situations, the genotypic correlation between traits was stronger than the phenotypic values, according to correlation studies; for example, plant height had a strong positive genotypic association with seed yield. Path analysis also showed a high positive direct effect of the yield components on the yield of seed per plant. However, ear seed weight had a substantial negative correlation with seed yield due to large negative indirect effects on other yield components, despite having a very high positive direct effect on seed production per plant.

Raghu *et al.*, (2011) investigated 45 maize genotypes using correlation analysis. Plant height, ear height, ear girth, number of kernel rows per ear, number of kernels per row, and test weight all had strong positive associations with grain yield. Days to 50% tasselling and days to 50% silking, on the other hand, were found to have a substantial negative correlation with grain yield.

Bello *et al.*, (2010) found PCV and GCV to be positive and significant for days to 50% tasselling, days to 50% silking, plant height, and ear height. Grain yield had substantial negative relationships with plant height, number of kernels per ear, and ear weight; however, grain yield had a positive and significant environmental correlation with plant and ear height, and ear weight.

Malik *et al.*, (2005) analysed the genetic link between 36 maize hybrids and their parent lines for quantitative traits in Randomized Complete Block Design with two replicates. Ear heights, leaves per plant, leaf length, leaf breadth, leaf area, ear weight, and kernels row per ear all exhibited a significant positive link with grain yield per plant. Grain yield was found to be negatively correlated with days to 50% silking, days to 50% tasselling, and grain wetness at harvest. The most significant contributor to grain yield was discovered as kernel rows per ear ($r = 0.76$), followed by leaf area ($r = 0.69$), plant height ($r = 0.67$), and leaves per plant ($r = 0.43$). Plant height, leaf area, leaves per plant, ear weight, kernels per row, and grain yield all have a strong positive genetic association, indicating that selecting these traits can help increase maize grain yield.

Xis *et al.*, (2003) performed correlation and path analysis on 11 features of glutinous maize. It has been reported that the yield is closely related to the average weight of the ear and the biological yield. The average weight of the ear makes the highest contribution to total production, followed by biological yield. The biological yield was related to the mean ear weight. There was a significant positive relationship between ear width and length, as well as the axile breadth and net ear weight.

Zhang *et al.*, (2003) examined the relationship between ear length and the other seven factors that contribute to yield. The results showed that, except rows per ear, the correlation coefficients of ear length and other seven agronomic parameters in grain yield were all positive; the correlation coefficients of kernels per row and ear length with grain yield were all significant.

Xiao *et al.*, (2001) evaluated 17 maize hybrids for yield and the relationship between yield and yield contributing traits in a Randomized Complete Block Design. He claimed that 1000 kernel weight ($r=0.541$) had the greatest impact on yield, followed by ear diameter ($r=0.4767$), shelling % ($r=0.4067$), and ear length ($r=0.14$). The correlation value between plant height and ear height ($r=0.822$), plant height and stem diameter ($r=0.760$), and ear length and row number ($r=0.706$) demonstrated extremely significant differences at 1% significance.

2.3 Path coefficient analysis

Pallabi Rani Roy *et al.*, (2021) tested twenty-five maize genotypes to evaluate genetic variability, correlations, and path co-efficient analyses affected yield and yield contributing characters. The genotypes showed very significant differences in sixteen yield contributing factors when analysed using analysis of variance. Estimates of genetic components for yield contributing traits revealed a larger phenotypic coefficient of variation than genotypic coefficient of variation, indicating that the studied traits are more influenced by the environment. The heritability of the traits under investigation ranged from modest to high. 1000 kernel weight (79.79) had the highest heritability, seed numbers ear 1 had the highest genetic advance (55.45), and shoot lodging (223.07) had the largest genetic advance in the percentage of the mean. The largest significant positive connection (0.746) with yield per plant was seen in thousands of kernel weight, followed by husk girth (0.620) and ear length (0.432). Days to anthesis, days to maturity, and seed counts per row all had a negative

connection with yield per plant. The thousands kernel weight had the most beneficial direct effect on grain yield, followed by ear girth and ear length, according to path co-efficient study. The results of this experiment showed that selecting maize based on thousands of kernel weight, ear girth, and ear length increased grain yield. As a result, the findings of the study will be valuable in identifying and selecting traits for future maize breeding efforts.

Yaregal Damtie *et al.*, (2021) determined the magnitude of genetic variability, heritability, and genetic advance of traits, to confirm genotypic and phenotypic associations between important traits, and to use path coefficient analysis to determine the relationship of traits with grain yield and direct and indirect effects. The experiment was carried out at Pawe Agricultural Research Centre with 23 inbred lines in replications utilizing RCB. The results showed that there was a considerable difference in genetic variability among widely produced maize inbred lines. At Pawe Agricultural Research Centre, there is a requirement for further varietal improvement. The findings suggested that there is enough potential for improved exploitation of the intended maize inbred for carefully preferred features in maize development initiatives, as variability persisted in the twenty-three maize inbred lines assessed. Keeping in mind that all of the character A7033, CML197, and CML202 lines investigated in breeds are promising. Better soil nutrient and carbon assimilation for photosynthesis, which may have built up in each ear size and number, thus providing higher grain production, can be attributed to positive significant direct effects of plant and ear height and several ears collected in each plot on grain output.

O. P. Taiwo *et al.*, (2020) used correlation and path coefficient analyses to examine character association and show the impact of various yield contributing characters in some maize varieties to identify relevant plant traits for selection to improve maize grain yield. In a humid climate in Port Harcourt, Nigeria, seventeen maize cultivars were sown in a Randomized Complete Block Design with three replications in 2018. Days to 50% anthesis, days to 50% silking, anthesis-silking interval, plant height (cm) and ear height (cm), number of plants per plot, number of plants harvested, number of ears harvested, moisture content (percent), field weight (Kg), and grain yield were all kept a record of (t ha⁻¹). The number of plants per plot, harvested plants, harvested ears, and field weight all associated positively and significantly with grain yield, both phenotypically and genotypically. Field weight and days to 50% anthesis were the features with the greatest positive direct effect on grain yield, according to

path coefficient analysis at the genotypic level. As a result, indirect selection for these traits could enhance maize grain production.

Ubi *et al.*, (2019) reported that characters such as grain yield per plant, ear length, ear height, test weight, and ear diameter all had high estimations of GCV and PCV with strong heritability and genetic progress. The path coefficient analysis found that test weight had the greatest significant direct effect on grain yield per plant, followed by the number of grains per row, kernel rows per ear, ear length, and ear diameter. The majority of the traits used test weight, the number of kernel rows per ear, and the number of kernels per row to exert their considerable beneficial indirect impacts.

Rani *et al.*, (2017) observed that ear length, number of kernel rows, 100 test weight, and Harvest index revealed substantial positive associations with grain yield at both genotypic and phenotypic levels, based on path analysis studies using 21 maize hybrids. According to the path analysis, the biological yield and harvest index had the greatest significant positive direct effect on grain yield per plant and grain yield per hectare, followed by ear length, plant height, and grain protein content.

Nataraj *et al.*, (2014) based on Path analysis revealed that the following factors had the greatest significant positive direct effect on grain yield per plant: ear weight, number of kernel rows per ear, number of kernels per row, and 100 kernels weight. Plant height, ear height, and ear diameter had a significant direct effect on grain yield per plant, whereas the remaining characters had a negative direct effect.

Hepziba *et al.*, (2013) based on the study of 70 distinct inbred lines discovered that ear weight, test weight, number of kernel rows, ear weight, and number of kernels per row all had a strong positive relationship with grain yield per plot. The number of kernel rows had the greatest beneficial direct influence, followed by ear length and ear height, according to path analysis. The positive indirect effects of the number of kernels per row, days to 50% tasselling, ear height, and ear length on grain yield are responsible for the substantial relationship between test weight and the number of kernel rows.

Zarei *et al.*, (2012) investigated the relationship between yield and yield attributing traits, in randomized full block design with four replications to examine eleven hybrids. Kernel yield is positively correlated with plant height, ear height, days to physiological maturity, kernel length, number of kernel rows, the total number of kernels per ear, and test weight. The

strongest associations were found between the plant's height and the length of the ear ($r=0.65$) and the weight of the kernel and the number of kernels per row ($r=0.61$). Grain yield per plant is directly affected by ear length, kernel volume, 100 kernel weight, and the total number of kernels per ear, according to path analysis. The number of kernels per ear had the largest direct effect, followed by the test weight (0.25). The test weight and ear length had the greatest indirect influence. The negative indirect effects of test weight on grain yield through the number of rows per ear and the number of kernels per row largely offset the much higher positive direct effect of test weight on grain yield.

Pavan *et al.*, (2011) analysed the direct and indirect effects of grain yield among twelve quantitative traits, researchers used a Randomized Complete Block Design with two replicates to test 87 inbred. Plant height, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, 100-grain weight, shelling percent, grain yield per plant, and fodder production per hectare all exhibited a positive relationship with grain yield per plant. Days to 50% silking, plant height, number of kernel rows, number of kernels per row, test weight, shelling percent, grain yield per plant, and fodder yield have the greatest direct effect on grain production, according to the path coefficient analysis.

Beiragi *et al.*, (2011) conducted an experiment using a randomized full block design with three replications to investigate the direct and indirect impacts of different characters on total corn production under normal irrigation and drought stress conditions in 28 novel maize hybrids, as well as 6 controls. According to path coefficient analysis, the number of kernels per row showed the highest association with grain yield under stress conditions, whereas the lowest correlation with grain yield was identified under standard irrigation ear diameter. According to this study, the total yield is more closely and strongly connected with kernel number per ear.

Wannows *et al.*, (2010) found grain yield to have a positive and significant relationship with kernel number per row (0.589), ear length (0.465), and leaf area index (0.497). The path coefficient analysis was performed to determine the relative value of features that directly or indirectly contribute to grain yield. Plant height, leaf area index, ear diameter, and physiological maturity all had high and positive direct significant effects on grain output per plant, according to the study.

Nemati *et al.*, (2009) undertook an experiment at the Mohaghegh Ardabili University's agricultural research farm. The kernel/ear is the highest connected with grain yield ($r = 0.53$), according to the path analysis results. Grain yield and kernel yield were both negatively correlated with grain thickness per ear ($r = -0.33$ and $r = -0.52$, respectively). Grain protein and thickness also had a negative and significant relationship ($r = -0.52$). The path coefficient study revealed that selecting maize cultivars with high kernels per ear aids in the improvement of grain yield. Grain yield was controlled by kernel length and the number of kernels per row.

Saidaiyah *et al.*, (2008) performed path coefficient analysis on 40 maize hybrids, 14 parents, and two checks for 11 characteristics. Path analysis found that 100 kernel weights had the most beneficial direct effect on grain yield, followed by plant height and the number of leaves above the ear. Plant height, ear height, number of leaves above the ear, chlorophyll content at 50% silk, flag leaf area, ear length, ear girth, and grain yield were all found to have a positive indirect effect on grain yield.

Saleem *et al.*, (2007) conducted an experiment at the Maize and Millets Institute of Science in Sahiwal. Days to 50% tasselling, days to 50% silking, 1000 kernel weight, and biomass per plant are all substantially associated with grain yield. Plant output was also strongly linked to days of 50 percent tasselling, days to 50 percent silking, plant height, cob height, flag leaf size, and biomass per plant. Plant height had the greatest direct impact on grain yields, followed by the number of rows per ear and the height of the ear. Day to 50% silking had the greatest direct impact on grain yield, followed by ear height and flag leaves.

Cheng *et al.*, (2002) examined 90 maize genotypes in a completely randomized block design in three replications. The path analysis revealed that eight quantitative characters, including ear length, ear diameter, kernel weight, number of kernel rows, kernel number per row, kernel length, kernel width, and 100 kernel weights, are associated with grain yield.

2.4 Genetic diversity analysis

Mamud Aman (2021) showed that plant breeding and agricultural production rely heavily on genetic heterogeneity. The degree of diversity in a crop's germplasm collections is the most essential factor in breeding for better varieties, especially genetic variability for a given attribute, which is a necessity for systematic breeding improvement. Any crop improvement program's effectiveness is determined not just by the amount of genetic variation present in the population, but also by how heritable it is, which determines the amount of progress that

can be made by selection. The amount of genetic improvement that might result from selective breeding is not determined solely by heritability. Furthermore, the efficiency of selection in any breeding program is largely dependent on knowledge of trait associations. Information on the nature and magnitude of population variation, character correlation with yield and among themselves, and the extent of environmental influence on the expression of these characters are all required for efficient selection. The most essential techniques for describing the relationship of features in maize breeding programs are the correlation coefficient and path coefficient analyses.

Muhammad Syafii1 *et al.*, (2021) performed selection of sweet corn lines based on genetic factors that are directly linked to yield. The research was carried out at PT. East-West Seed Indonesia's Experimental Station in Cempaka Village, Purwakarta Regency, from July to December 2018. 14 MS-Unsika sweet corn lines and three commercial sweet corn lines were used as genetic material. The results revealed that the sweet corn lines tested had a wide range of characteristics. Plant height, ear height, ear diameter, ear length, ear weight per plant, the weight of 100 seeds, and several rows per ear all demonstrated high heredity and a strong association with tonnes per hectare production. The MS 08 line is the ideal option for hybrid parents.

D. Bhadru *et al.*, (2020) performed an experiment to gain a better understanding of the genetic characteristics and genetic diversity among the eighteen maize inbred lines, which is crucial for evaluating breeding strategies and predicting hybrid performance. The inbred lines under investigation showed a wide range of diversity. Plant height, ear height, grain yield per ear, ear length, and several kernels per row showed a medium to high range of PCV and GCV estimates, heritability, and genetic advance as a percent of mean for traits like plant height, ear height, grain yield per ear, ear length, and several kernels per row. As a result, these qualities are critical for genotype selection to increase maize production. Cluster II had the greatest intra-cluster distance (60.49), while cluster I had the smallest (43.81). Solitary clusters are clusters III, IV, V, and IV. Clusters IV and V had the maximum inter-cluster distance of 386.89, followed by clusters I and IV (326.90), clusters I and VI (309.98), clusters II and V (297.76), cluster III and V (239.32), and Cluster I and III (239.32). (252.68). It will be rewarding to generate high heterotic hybrids in maize using inbred such as lines from cluster I and testers from clusters III, IV, and VI, as well as lines from cluster II and clusters III and V.

S B Singh *et al.*, (2020) assessed the genetic diversity of 97 newly produced winter maize inbred lines and 13 released inbred using morphological characteristics. For 13 of the characters investigated, analysis of variance revealed significant differences. All of the inbred lines were classified into fifteen clusters, ten of which were solitary. Cluster I has the most inbred lines (37) according to the D^2 statistics, followed by Cluster II (24), Cluster III (16), Cluster IV (14), and Cluster V (13). (9). Cluster V and cluster XV had the greatest inter-cluster distance (26.96), followed by cluster IV and XV (26.12), and cluster V and XII (24.55), indicating a higher possibility of heterotic recombination. Cluster IV has the greatest distance between clusters (11.59). 100 kernel weight (39.45%) generated the most genetic diversity in percentage terms, followed by days to anthesis (22.64), grain filling duration (10.31), and grain yield (10.31). (10.50). Inbred lines IMLSB-2005, IMLSB-1000-2, IMLSB-182-1, IMLSB-719-1, IMLSB-164-1, IMLSB-457-2, IMLSB-2083, IMLSB-1298-2, IMLSB-1298-5, and IMLSB-246-2 were identified based on per se performance, intra and inter-cluster distance, and could be used in maize improvement programmes to develop superior hybrid combinations.

Lone (2017) assessed 47 inbred maize inbred lines based on genetic diversity of physical traits. The experiment was conducted in *Kharif* 2015 at the Dryland Agriculture Station in Budgam, Jammu, and Kashmir, utilizing Randomized Complete Block Design. Tocher's Method was used to perform D^2 analysis and clustering. Seven clusters have been formed from all inbred lineages. Cluster number IV had the most inbred lines (29) whereas clusters III and VI had the least inbred lines (2). When parents were chosen from these group pairs, a higher probability of heterotic hybrids was seen in Cluster II and V, V and VI, VI, and VII. Days to 50% tasselling and days to maturity were the most important contributing characters to genetic divergence.

Sharma *et al.*, (2015) analysed 20 distinct maize genotypes using D^2 statistics for eleven characters to estimate genetic diversity; it allowed all genotypes to be grouped into five clusters. 100 seed weight, leaf area index, harvest index, days to 50% flowering, and plant height were the significant contributors to genetic variability in the genotypes. Cluster II has the most genotypes (6), followed by Cluster III, which has five genotypes. Genotypes 4, 3, and 2 were found in groups I, V, and IV, respectively. Cluster III had the greatest intra-cluster distance, while clusters I and III had the greatest inter-cluster distance.

Maruthi *et al.*, (2015) investigated genetic divergence for 43 maize genotypes for eleven traits at the College Farm, College of Agriculture, and Hyderabad. They discovered that all characters had a wide range of variability, as well as strong heritability and genetic gain. All 43 genotypes were classified into six groups based on the D^2 analysis. The distance between clusters I and V (39.38) was the greatest. Grain yield (38.43 percent), plant height (14.29 percent), 100-grain weight (12.85 percent), and the number of kernels per row all contributed significantly to overall diversity (12.07 percent).

Rahman *et al.*, (2015) assessed the genetic diversity of nine maize genotypes. The statistical analysis revealed substantial differences between maize genotypes. Grain yield per plant had the highest GCV and PCV of all the traits. Test weight was found to have a very high genetic advance, followed by total kernel numbers per ear. In this investigation, nine genotypes were clustered into three separate groups. All of the clusters demonstrated the existence of a wide genetic variety across maize genotypes, which can be better exploited in future breeding operations to improve maize germplasm.

Amin *et al.*, (2013) looked at the genetic diversity of 24 inbred QPM lines using the Mahalanobis D^2 statistics for 11 characters. Four groups of genotypes have been identified. Inter-cluster distances were much bigger than intra-cluster distances, indicating that there was more genetic diversity among the genotypes of different groupings. Clusters I and III have the greatest number of genotypes. Kernel yield per plant, test weight, number of kernels per ear, and kernel yield per plant had the highest mean values in Cluster III. Cluster II had the longest average ear length. Days to 50% anthesis and days to 50% silking had the lowest mean values in Cluster IV. The greatest inter-cluster distance was found between Clusters I and III and Clusters II and IV. Cluster I had the greatest intra-cluster distance, whereas Cluster IV had the smallest. The overall divergence was influenced by the number of kernels per row, ear length, kernel yield per plant, days to pollen anthesis, and kernel yield per plant, all of which contributed considerably and in a higher percentage than other parameters.

Ranawa *et al.*, (2013) grouped all maize genotypes using D^2 Mahalanobis statistics into three clusters based on their morphological diversity. Cluster II (15.44) had the greatest intra-cluster distance, and cluster II-III (25.46) had the greatest inter-cluster distance. For all physical features, diversity analysis revealed considerable differences between parental lines. According to the findings, the characters under investigation are essential to yield

contributing characters and are highly connected. To choose a high-yielding maize genotype, those traits should be considered either simultaneously or separately.

Khan et al., (2013) used Mahalanobis D^2 statistics based on morphological character relevant to grain yield to quantify genetic divergence in 17 CIMMYT maize inbred lines, including one check. During the winter of 2010-2011, at the Regional Agricultural Research Station, Ishurdi, Pabna, the experiment was conducted in an alpha lattice design with two replications. The genotypes were divided into four distinct groups. Cluster II has the most germplasm lines, with six, while Cluster I only had one genotype. Cluster I and Cluster IV had the greatest inter-cluster distance, while Cluster I and Cluster II had the smallest distance. Cluster IV had the greatest intra-cluster distance, whereas Cluster I had the smallest. Cluster III genotypes had a shorter growth life, a lower stature, a shorter ear height, a higher shelling %, and a fair grain yield. The ear played a significant role in genetic divergence. Days for pollen anthesis, days to 50% silking, maturity, and 1000 grain weight were identified to be the key causes of genetic divergence.

Zaman & Islam (2013) performed an experiment during the *Rabi* season 2010-11, on the research farm of the Regional Agricultural Research Station BARI, Ishuardi, Pabna, experimented to examine of the genetic divergence of exotic maize hybrids. The genotypes were split into seven clusters based on the results of the research. Cluster VI had a maximum of 13 genotypes, showing general genetic similarity amongst genotypes within the cluster. Clusters III and V, which each had one genotype, included the minimum genotype. Cluster V and Cluster III had the greatest inter-cluster distance, followed by Clusters I and III and Clusters III and VII; Cluster VII had the greatest intra-cluster distance, while Cluster III and V had only one genotype, therefore their intra-cluster distance was zero. Cluster IV has a medium plant height, days to maturity, days to 50% tasselling, days to 50% silking, and shelling percent, as well as a mean yield. Cluster V's mean values revealed a middling overall yield with all traits contributing to yield.

Kage et al., (2013) carried out an examination to investigate genetic diversity among maize inbred lines in *Kharif* 2011. Seventy-nine inbred lines were analysed with three checks, and observations for 13 yield attributing traits were recorded in this experiment. The difference between all inbred lines is quite substantial, according to the analysis of variance. The genetic diversity of inbred lines was determined by grouping them into 14 clusters. Cluster I had the most genotypes (67); the highest inter-cluster distance was recorded between clusters II and

XII (22.41); the highest intra-cluster distance was detected in cluster XII (5.46); and mean cluster performance for the characters analysed showed considerable variation. These genetically diverse inbred lines can then be exploited to create higher hybrids, as well as synthetic and composite materials.

Hepziba *et al.*, (2013) investigated 70 distinct inbred lines during the month of *Kharif* 2010. He explained that 70 inbred lines were divided into ten groups based on biometrical characteristic scores. Cluster I included 19 inbred lines, cluster II contained 12 inbred lines, cluster III contained eight inbred lines, and clusters IV through X contained 1, 2, 7, 3, 6, 9, and 7 inbred lines, respectively.

Azad *et al.*, (2012) analysed 30 inbred lines of normal maize at Danesh Science and Technology University at experimental field in 2010-11, to determine genetic diversity using the D^2 statistic. According to the findings, 30 inbred lines were classified into six distinct groups. Within each of the six clusters, the intra-cluster distance was extremely low, indicating that all genotypes in the group are similar or that genotypes in the same cluster are closely related. Cluster I and Cluster IV had the greatest inter-cluster distance, while Cluster II and Cluster III had the smallest. Clusters V and IV, which have nine and three genotypes respectively, have the greatest and lowest genotypes. Except for days to 50% tasselling and days to 50% silking, Cluster VI had the highest mean values for kernel yield and all yield contributing factors. Cluster II had the shortest and shortest average ear height and length. Between 30 inbred lines, days to maturity and ear diameter contributed the most to overall variability.

Singh *et al.*, (2007) used Multivariate analysis employing the Mahalanobis D^2 statistics to examine 101 maize inbred lines as well as four checks on genetic divergence information. All variables differ considerably between the genotypes, according to the analysis of variance. The study discovered 105 genotypes divided into 23 clusters, with cluster III containing the most entries (51). Clusters II and XXIII had the greatest distance, followed by Clusters II and XIII, Clusters II and XIII, Clusters II and XVI, and Clusters II and XVII. Based on inter-cluster distance and per se performance, grain production per plant was found to contribute the most to genetic differences, followed by plant height and ears per plant. Grain yield per plant was shown to contribute the most to genetic variations, followed by plant height and ears per plant. Based on the inter-cluster distance and per se performance of the selected genotype, 15 inbred lines that might be used to make high heterotic crosses were chosen.

Hemavathy *et al.*, (2006) split maize genotypes into seven clusters based on the D^2 values, indicating that maize genotypes exhibited a lot of variation. Cluster III had the most inbred (20), followed by Clusters III and IV, which had seven and five breeds, respectively. A genetic difference was discovered when inbred lines were grouped. The highest inter-cluster distance ($D^2 = 162.12$) was reported between Cluster IV and Cluster VI. To create high yield inbred lines with acceptable features, inter-crossing between Cluster V, VI, and VII genotypes were recommended.

Showemimo *et al.*, (2004) used the D^2 statistic to examine the genetic diversity of 53 maize quality protein genotypes for 12 attributes during three years (1999, 2000, and 2001). The genotypes were divided into 11 groups based on the results of the research. The inter-cluster D^2 value ranged from 60.4 (between Cluster 1 and VI) to 501.9. (Between Cluster V and IX). Plant height, days to physiological maturity, and days to 50% silking, as well as protein content and grain yield, account for more than 70% of the genetic variability.



MATERIAL AND METHODS

The present investigation is entitled “**Assessment of Genetic Diversity in Maize [*Zea mays* L.] Inbred lines**” was carried out during crop season *Rabi* of the year 2020-21 at the Agriculture Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. This chapter comprises information concerning the following heads:

- 3.1 Location and agro-climatic and weather condition of the experimental site
- 3.2 Experimental material
- 3.3 Experimental design and layout
- 3.4 Observation recorded on quantitative traits
- 3.5 Statistical analysis
- 3.6 Assessment of genetic parameters

3.1 Location and agro-climatic and weather condition of the experimental site

Varanasi is a spiritual city of North India situated on the banks of the Ganga River in the state of Uttar Pradesh. The Experiment was conducted at the Agriculture Research Farm, Institute of Agricultural Sciences (I.Ag.Sc.), Banaras Hindu University (BHU) which is situated in the South-eastern part of Varanasi city at 25° 18' North latitude and 83° 03' East longitude at an elevation of 128.93 m above the mean sea level in the north Gangetic plain.

Soil and climate: The climate of Varanasi city is moist subtropical with a high range of differences between the summer and winter seasons. The normal temperature of the city is between 32°C to 46°C in the summer season and 5°C to 15°C in the winter season. The average annual rainfall in this area is around 1110 mm; a major part of which is received during September and the mean relative humidity is 67%. The soil type is fertile alluvial loam, and soil texture is sandy loam to sandy clay loam which contains organic carbon ranging from 0.60 to 0.50 percent. The pH of soil ranged from 7.2 to 9.7 (**Rai et al., 2011**) which is the characteristic plains and is suitable for growing the experimental material.

3.2 Experimental material

The experimental material comprises 35 different inbred lines (Year 2020-2021) of maize which was obtained from laboratory of Department of Genetics and Plants breeding Banaras Hindu University for the assessment of diversity parameters. The details of the experimental material listed in the Table 3.2.1.

Table 3.2.1 List of inbred lines taken under investigation

S.no	Entry	Genotype	R₁	R₂
1	359	LM-13	1	53
2	332	HUZM68-1	2	50
3	470	HUZM470	3	56
4	491	HUZM491	4	59
5	348	HUZM637-1	5	63
6	416	HUZM416	6	44
7	320	HUZM256	7	62
8	484	HUZM484	8	51
9	355	HUZM1108-2	9	41
10	419	DMR113-1	10	49
11	420	HUZM-1-13	11	45
12	328	HUZM328	12	69
13	363	CML-41	13	52
14	444	HUZM-2A-1	14	64
15	442	HUZM-22-4	15	58
16	423	HUZM-53-10	16	57
17	477	HUZM-405-1	17	70
18	425	CML-163	18	65
19	461	HUZM-111-8	19	37
20	349	HUZM642-1	20	67
21	303	HUZM6	21	61
22	430	HUZM72087	22	36
23	385	HUZM9043A	23	39
24	481	HUZM-3-2-1	24	38
25	327	HUZM294	25	66
26	447	MM721-2	26	43
27	454	HUZM-4-32	27	54
28	489	HUZM489	28	60
29	455	HUZM455	29	68
30	451	HUZM451	30	42
31	393	HUZM393	31	48
32	475	SCFEMALE	32	47
33	408	HUZM-100-10	33	46
34	441	HUZM-44-111	34	40
35	448	HUZM-88-3	35	55

3.3 Experimental design and layout

The experimental design used in the study was a Randomized Complete Block Design (RCBD). It is based on two-way classification and one-way control of the error. It deals with one more source of systematic variation other than the treatment or genotypes



DOUBLE BORDER ROW		SINGLE BORDER ROW	
07	1	07	1
69	2	69	2
89	3	89	3
79	4	79	4
99	5	99	5
59	6	59	6
69	7	69	7
63	8	63	8
29	9	29	9
19	10	19	10
09	11	09	11
65	12	65	12
58	13	58	13
75	14	75	14
95	15	95	15
55	16	55	16
55	17	55	17
53	18	53	18
52	19	52	19
15	20	15	20
05	21	05	21
67	22	67	22
87	23	87	23
77	24	77	24
97	25	97	25
57	26	57	26
47	27	47	27
43	28	43	28
42	29	42	29
14	30	14	30
04	31	04	31
39	32	39	32
38	33	38	33
37	34	37	34
36	35	36	35
SINGLE BORDER ROW		DOUBLE BORDER ROW	

Material and Methods

Sowing: The experimental study had begun with the line sowing of the 35 inbred lines on the 7th of December 2020 (*Rabi* season). It was sown in a Complete randomized block design with two replications. Each genotype was planted in a single row of 20×20 cm in length and width of 60×38 cm. A spacing of 60 cm between rows and 20 cm between plants was maintained. All the recommended agronomic package and practices were followed to raise a good crop.

Manure and Fertilizers: The rate of nutrient application depends mainly on the soil nutrient availability/balance and cropping system for obtaining a desirable yield, the doses of applied nutrients should be matched with the soil supplying capacity and plant demand. Therefore, for a higher economic yield of maize, application of 1 Kg FYM per m², 10-15 days before sowing is given in addition to 16 grams Nitrogen, 6 grams Phosphorus, 6 grams Potassium, and 2.5 grams Zinc Sulfate in meter square of the field. A full dosage of P₂O₅ and K₂O was given at the time of sowing as basal application. Nitrogen is applied in 5 split dosages for higher productivity and use efficiency. The application of nitrogen during the grain filling stage results in better grain yield.

Table 3.3.1 Nitrogen was given at five different stages of crop growth as mentioned below.

S. No.	Crop stage	Nitrogen rate in %
1	Basal (at sowing)	20
2	V4 (four-leaf stage)	25
3	V8 (eight leaf stage)	30
4	VT (tasseling stage)	20
5	GF (grain filling stage)	5

Irrigation: The rainfall during the *Rabi* season is insufficient for high-yielding maize inbred line to be successfully grown hence six irrigations are administered, one (important) at the time of flowering, two after blooming, and one at the early grain-filling stage were applied at a 20-25 days interval. One irrigation at the vegetative stage can be avoided if only five irrigations are given, and irrigation after the dough stage can be avoided if only four irrigations are given. However, if appropriate rains are received, the irrigation system can be adjusted accordingly.

Weed management: To keep weeds under control, light hoeing was done as needed. Broad-leaved weeds and most grasses were effectively managed with a pre-emergence spray of Atrazine or Simazine @ 0.5-1.0Kg a.i./ha in 1000 lit of water. To manage weeds in zero-till maize production, pre-plant applications of non-selective herbicides such as Glyphosate @ 1.0 Kg a.i./ha-1 in 400–600-liter water or Paraquat @ 0.5 Kg a.i./ha-1 in 600-liter water are given (10-15 days before seeding). Paraquat was also applied as a shielded spray utilizing hoods in areas where there are a lot of weeds.

3.4 Recording of observations

Observations on various pre-and post-harvest parameters were recorded on five plants selected at random from each entry in each replication. The following observation were recorded during the course of investigation.

Pre-harvest characters

3.4.1 Days to 50% anthesis (days)

Days to 50 % anthesis were recorded as the number of days taken from the sowing date to the day on which 50 % of the plants shed pollen from their tassel.

3.4.2 Days to 50% silking (days)

Days to 50 % silking was recorded as the number of days from the sowing to the day on which 50 percent of plants showed silk emergence.

3.3.3 Anthesis-silking interval (ASI)

Anthesis-silking interval is defined as the difference between the Days to 50% tasselling and Days to 50% silk emergence.

3.4.4 Plant height (cm)

It is the height of the mature plant from the ground level to the base of the fully opened flag leaf. It is measured using a centimetres-scale and its average was recorded at least for five plants from each plot avoiding border plants.

3.4.5 Ear height (cm)

It was recorded from ground level to the base of the uppermost ear in centimetres (cm). The observations were taken on five representative plants within each plot by avoiding border plants.

Post-harvest Characters

3.4.6 Ear length (cm)

It is the length of the ear that was measured from the base to the tip of the ear in cm using a centimetres-scale.

3.4.7 Ear girth (cm)

It is the average diameter at the middle portion with maximum circumference after de-husking of the best five ears which was measured using the vernier calliper's scale and recorded in centimetres.

3.4.8 Number of kernel rows per ear

The number of kernel rows per ear was counted and the average was recorded based on the best five ears.

3.4.9 Number of kernels per row

The number of kernels in each row for five ears for each inbred lines counted and the average was recorded.

3.4.10 Shelling percentage

The shelling percentage was taken 80% for all the inbred lines.

$$\text{Shelling\%} = \frac{\text{Grain weight}}{\text{Ear weight}} \times 100$$

3.4.11 Field weight:

Ears harvested from individual plots weighted separately. Used for calculating the shelling percentage.

3.4.12 Test weight (g)

It is defined as the weight of 100 seeds which were drawn at random from each plot and weighed using an electronic pan balance. The mean value for each inbred from both replications was recorded individually.

3.4.13 Moisture content (per cent)

Moisture content was taken 15% for all inbred lines.

3.4.14 Grain yield per plot (Kg)

Grain yield per plot is estimated using field weight, moisture percentage, and shelling percentage using a following formula.

$$\text{GYPP} = \frac{\text{Field weight} \times \text{Shelling percentage}}{100} \times \left[1 - \frac{\text{grain moisture}}{100}\right] \times 1.176$$

3.5 Statistical analysis

The mean data of the various characters was carried out using a random selection of five plants from the individual plots which are used for statistical analysis over two replications. The analysis of variance was carried out separately for all the eleven characters by RCBD. The estimation of variance is a method suggested by **Gomez and Gomez (1984)** and **Singh and Chaudhary (1977)**. The following statistical methods were adopted under the sub-heads.

3.5.1 Mean

The mean of each character was determined by dividing the summing up all the observations by corresponding no. of the observation.

$$\bar{x} = \frac{\sum_{i=1}^N x_i}{N}$$

Where,

$\bar{x}$ = Mean

$\sum_{i=1}^N x_i$ = Sum of all observations

N= Number of observations

3.5.2 Range

The difference of the lowest and the highest value based on individual plant observation for each character was recorded (minimum and maximum value of any character) is known as the range for that character.

$$\text{Range} = \text{Upper limit} - \text{Lower limit}$$

3.5.3 Standard error of the difference between two means [S.E.d (M)]

[S.E.d (M)] was calculated with the help of the error mean square from the ANOVA table.

$$\text{S.E.d. (M)} = \sqrt{2\text{M} \cdot \text{S} \cdot \text{E} / \text{r}}$$

Where,

r = Number of replications

MSE = Mean sum of square due to error

3.5.4 Coefficient of variance / Relative standard deviation

It is defined as the percent ratio of the Standard deviation to the mean value.

$$\text{C} \cdot \text{V} \cdot (\%): \frac{\text{SD}}{\bar{x}} \times 100$$

Where,

SD = Standard deviation

x = Mean of the character

3.5.6 Analysis of variance

The analysis of variance for study the characters was carried out using mean data to assess the genetic variability between inbred lines as given by **Cochran and Cox (1957)**. The level of significance was tested at 5% and 1% levels using the F test. The model of ANOVA used is presented in Table 3.5.6.1 The total variation for each character was partitioned into variations due to genotype, replication, and unassignable causes (error). A random-effect model was followed for each character. The analysis of variance, a test of significance of variance component was done as suggested by **Panse and Sukhatme (1967)**.

Analysis of variance for Randomized complete block design with the expectation of mean sum square was set up as mentioned. The form of the ANOVA table is given below:

Table 3.5.6.1 Analysis of variance of RCBD

Source of variation	d.f	Sum of squares	Mean sum of squares	F value
Treatment	n-1	SS (Tr)	$MS(Tr) = \frac{SS(Tr)}{n-1}$	$F(Tr) = \frac{MS(Tr)}{MSE}$
Replication	m-1	SS (R)	$MS(R) = \frac{SS(R)}{m-1}$	$F(R) = \frac{MS(R)}{MSE}$
Error	(n-1) (m-1)	SSE	$MSE = \frac{SSE}{(n-1)(m-1)}$	
Total	nm-1	SST		

Where,

m = Number of replications.

n = Number of treatments (genotypes)

SS (R) = Sum of square of replication.

SS (Tr) = Sum of square of treatment (genotype)

SSE = Sum of square due to error

MS (R) = Mean sum of square of replication.

MS (Tr) = Mean sum of square of treatment (genotype)

MSE = Mean sum of square due to error

The mean squares of treatments, and replications were investigated against the corresponding mean square of error. The calculated 'F' value was compared with the table value of 'F' at 5% and 1% level of significance. The general statistics were calculated as follows:

$$SE_{\pm} = \sqrt{2EMS \div r}$$

$$\text{Critical differences (C.D.)} = \text{S.E.} \times t$$

Where,

S.E. = Standard error of differences

T = Table value of ‘t’ at 5% and 1% level of significance corresponding to error degrees of freedom

3.5.7 Assessment of genetic variability parameters

Genetic variability parameters among the 35 inbred lines for traits related to yield in maize were assessed according to the method given by **Lush (1940)**.

3.5.7.1 Phenotypic and Genotypic variance

Phenotypic and genotypic components of variance were estimated by using the formula given by **Cochran and Cox (1957)**.

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e = \frac{(\text{MSg}) - (\text{MSe})}{r} + \text{Me}$$

$$\text{Genotypic variance } (\sigma^2_g) = \frac{(\text{MSg}) - (\text{MSe})}{r}$$

Where,

σ^2_g = Genotypic Variance

σ^2_p = Phenotypic Variance

σ^2_e = Error Variance

MSt= Treatment means sum of square

MSe = Error mean sum of square

r = Number of replications

3.5.7.2 Coefficient of Variation

It is a unit less statistical measurement, used for comparing the magnitude of variation among several traits and expressed in percent. It was calculated by using the following formula. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to **Burton and Devane (1953)**.

$$CV = \frac{ErMSS}{\bar{X}} \times 100$$

Where,

ErMSS = Error mean sum of square

$\bar{X}$ = Grand mean

3.5.7.2.1 Phenotypic Coefficient of Variation (PCV)

The PCV was computed by dividing the phenotypic variance by the general mean for the respective trait and multiplying it by 100 and expressed in percent.

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_p = Phenotypic standard deviation

$\bar{X}$ = General mean for the character

3.5.7.2.2 Genotypic Coefficient of Variation (GCV)

The GCV was computed by dividing the genetic variance by the general mean for the respective trait and multiplying it by 100 and expressed in percent.

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

$\bar{X}$ = General mean for the characters

Table 3.5.7.2.1 Scale for GCV and PCV were classified by (Robinson *et al.*, 1949)

S. No.	Value of GCV and PCV (percent)	Rate or Scale
1.	0 to 10	Low
2.	10 to 20	Moderate
3.	More than 20	High

3.5.7.3 Heritability in broad sense [$h^2(b)$]

Heritability in a broad sense was computed as the ratio of genetic variance to the total phenotypic variance. In general, heritability is of two type's narrow-sense and broad-sense heritability. Narrow-sense heritability is the ratio of additive genetic variance to the total phenotypic variance as suggested by **Hanson *et al.*, (1956)** and expressed in percentage.

Heritability (in a broad sense) for different traits was assessed by using the components of variance as per **Hanson *et al.* (1956)** in the following manner.

$$h^2 \text{ (Broad sense)} = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

h^2 = Heritability (broad sense)

Heritability in a broad sense was categorized as per the classification given by **Robinson *et al.*, (1949)**.

Table 3.5.7.3 Scale for Heritability was classified by (Robinson *et al.*, 1949)

S. No.	Value of heritability broad sense (%)	Rate or Scale
1.	0 to 30	Low
2.	30 to 60	Medium
3.	More than 60	High

3.5.7.4 Expected Genetic advance

It is the measurement of genetic gain under selection and it was estimated by using the formula suggested by **Lush (1949)**, followed by **Johnson *et al.* (1955)** and **Allard (1960)**.

$$\text{Genetic Advance (GA)} = K \times \sigma_p \times h^2(b)$$

Where,

K = Selection differential at 5% selection intensity which accounts to a constant value of (2.06).

h²(b) = Heritability in broad sense.

σ_p = Phenotypic standard deviation.

3.5.7.5 Genetic advance as percent of the mean (GAM)

$$\text{GAM} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

X = Grand mean of the character

Table 3.5.7.5 Scale for Genetic advance as percent mean was classified by (Johanson *et al.*, 1955)

S. No.	Values of Genetic Advance (%)	Rate or scale
1.	Less than 10	Low
2.	10 to 20	Medium
3.	More than 20	High

3.5.8 Correlation coefficient analysis

It was computed to find out the association of the independent variables with yield and also among the yield components. Both genotypic and phenotypic coefficients of correlation between two characters were determined by using the variance and covariance components as suggested by **Al-Jibouri *et al.*, (1958)**. But the modified version for phenotypic and genotypic correlations was worked out by using the formulae suggested by **Falconer (1964)**.

3.5.8.1 Phenotypic correlation between character X and Y

$$r_{xy} (p) = \frac{\text{CovXY}(p)}{\sqrt{\text{varX}(p) \times \text{varY}(p)}}$$

Where,

Cov x,y (p) = Phenotypic co-variance between two characters X and Y

Var X (p) = Phenotypic variance for character X.

Var Y (p) = Phenotypic variance for characters Y.

The observed value of correlation coefficient (r) was compared with the tabulated value for (n-2) degree of freedom to know the significance of the correlation coefficient. (**Snedecar and Cochran 1967**). If the observed value of 't' is greater than the table value of 't' the correlation coefficient is said to be significant. The test of statistics is as follow:

$$t = \frac{r(\sqrt{n-2})}{\sqrt{1-r^2}}$$

Where,

t = Test of significance

r = Correlation coefficient.

n = Number of genotypes.

Table 3.5.8 Scale for Correlation Coefficients (Searle, 1965)

S. No.	values of the correlation coefficient	scale
1	>0.65	Very strong
2	0.50 to 0.64	Moderately strong
3	0.30 to 0.49	Moderately weak
4	<0.30	Very weak

3.5.8.2 Genotypic coefficient of correlation (R_G)

$$r(x_i, x_j)_g = \frac{\text{Cov}(x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

r (x_i.x_j)_g = Genotypic correlation between ith and jth character

Cov(x_i.x_j)_g = Genotypic covariance between ith and jth character

V (x_i)_g = Genotypic variance of ith character

V enclose = Genotypic variance of jth character

3.5.8.3 Environment coefficient of correlation (R_E)

$$r_{x_1x_2}(e) = \frac{Cov \cdot x_i, x_j}{\sqrt{\sigma^2 x_i(e) * x_j(e)}}$$

Where,

Cov. $x_i x_j$ = Environmental covariance between character x_i and x_j

σx_i = Genotypic variance for i^{th} character

σx_j = Genotypic variance for j^{th} character

3.5.8.4 Test of significance

The calculated value of correlation coefficients was tested for its significance by comparing the observed value of correlation coefficients with the table value of 'are given by **Fisher and Yates (1963)** available in standard books at $(n - 2)$ degrees of freedom as follows:

$$t = \frac{r}{\sqrt{1-r^2}} \cdot \sqrt{n-1}$$

Where,

r = Correlation coefficient

n = Number of genotypes used for the pair of characters

3.5.9 Path coefficient analysis

It is defined as portioning the total correlation into direct and indirect effects due to the dependent characters. It was proposed by **S. Wright (1934)** this analysis and it was further expounded by **Dewey and Lu (1959)**. In simple words, it is a partial regression coefficient, which individually provides a measure of the direct effect of the causal factor or independent variables on the dependent variable. These allow partitioning of the correlation between the causal factor and the effect of a variable into components of direct and indirect effects and this makes the association of causal factor with the effect of a variable clearer. Standard path coefficients which are the standardized partial regressing coefficients were obtained as follow:

It is mathematically represented by following simultaneous equations:

$$r_{1y} = P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + r_{1k} P_{ky}$$

$$r_{2y} = r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \dots + r_{2k} P_{ky}$$

$$r_{iy} = r_{i1} P_{1y} + r_{i2} P_{2y} + r_{i3} P_{3y} + \dots + r_{ik} P_{ky}$$

$$r_{ky} = r_{k1} P_{1y} + r_{k2} P_{2y} + r_{k3} P_{3y} + \dots + r_{kk} P_{ky}$$

Where,

r_{1y} to r_{ky} = Coefficient of correlations between factors 1 to k and dependent character y.

r_{12} to $r_{k-1, k}$ = Coefficient of correlations among independent variables.

P_{1y} to P_{ky} = Direct effects of characters 1 to k on character y

The indirect effect of the i^{th} variable via j^{th} variable is attained as $(r_{ij} \times P_{ij})$.

3.5.10 Residual effect

The contribution of the remaining unknown factors is measured as the residual factors. The residual effect was estimated with the help of direct effects and simple correlation coefficients using the following formula.

$$I = P^2 R_y + \sum P_{iy} \cdot r_{iy}$$

Where,

$P^2 R_y$ = Square of the residual effect.

Table 3.5.9.1 Scales for Path Coefficient (Lenka and Mishra, 1973)

S. No	Values of direct and indirect effects	Scale
1.	0.00 to 0.09	Negligible
2.	0.10 to 0.19	Low
3.	0.20 to 0.29	Moderate
4.	0.30 to 0.99	High
5.	>1.00	Very High

3.5.11 Genetic Divergence analysis/ Mahalanobis' D² analysis**Genetic divergence studies by Mahalanobis' D² Statistics:**

Genetic divergence is the process in which two or more population of an ancestral species accumulates independent genetic changes through the time when they become reproductively isolated. Mahalanobis D² statistics was initially developed by Mahalanobis' D² in 1928 and are one of the most effective tools to measure the genetic distance between genotypes. The genetic difference between cultivars, as measured by allele frequencies at a sample of loci (Nei,1987). Mahalanobis' D² statistics can be used for the selection of genetically diverse parents for the hybridization program.

The various steps involved in the analysis of D² values are given below.

$$D^2_{ij} = \sum_{t=1}^p Y_{it} - Y_{jt}$$

Where,

Y_i^t is the uncorrelated mean value of i^{th} genotype for 't' characters

Y_j^t is the uncorrelated mean value of j^{th} genotype for 't' characters

D^2_{ij} is D² between the i^{th} and j^{th} genotypes.

3.5.11.1 Test of significance

Variances were estimated for all the characters studied and a test of significance was done. Analysis of covariance for the pairs of characters was estimated based on mean values (Panse and Sukhatme, 1967). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of several correlated variables concerning the pooled effect of characters was carried out using the 'V' statistic, which in turn utilizes Wilk's criterion. The sum of squares and sum of products of error and error + genotype, variance, and covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship:

$$\Delta = \frac{E}{E+V}$$

$$= \frac{\text{Determination of error variance and covariance matrix (E)}}{\text{Determination of error variance + genotype and covariance matrix}}$$

Where,

Λ = Wilk's criterion

E = Determinant of error matrix and

$E+V$ = Determinant of error + genotypes sum of squares and sum of the product matrix.

$$V \text{ statistic} = -m \log_e \Lambda = -\left(n - \frac{p+q+1}{2}\right) \log_e \Lambda$$

Where,

$$m = \left(n - \frac{p+q+1}{2}\right)$$

n = Degrees of freedom for error + genotypes

$$\log_e \Lambda = 2.3026 \log_{10} \Lambda$$

P = Number of variables or characters

q = Degrees of freedom for population (i.e., number of genotypes – 1)

V (Statistic) is distributed as chi-square (χ^2) with pq degrees of freedom as the degrees of freedom for χ^2 exceeded 100.

$Z = \sqrt{2\chi^2} - \sqrt{2n - 1}$ was treated as a normal deviate. If the difference between the means with respect to the pooled effect of 'p' traits between different genotypes is significant then the data matrix was subjected to multivariate analysis (D^2) for further differentiation.

3.5.11.2 Transformation of correlated variables

In the present model, the computation of D^2 values was reduced to the simple summation of the differences in the mean values of various characters of the two genotypes i.e., $\Sigma-d_i^2$. Therefore, the transformation of the correlated variables into uncorrelated ones was done before working out the D^2 values. The transformation was done using the pivotal condensation method.

3.5.11.3 Computation of Mahalanobis' D² values

In the present investigation, genetic divergence was assessed based on Mahalanobis' generalized distance as described by **Rao (1952)**. Original variable means were transformed into uncorrelated variables by the essential condensation method of the inversion matrix. For the given combination of i and j genotype, the mean deviation i.e., $Y_{it}-Y_{jt}$ for $t = 1, 2 \dots p$ variables are computed and the D² values were calculated as

$$D^2_{ij} = \sum_{t=1} (Y_i^t - Y_j^t)^2$$

Where,

Y_i^t is the uncorrelated mean value of ith genotype for 't' characters

Y_j^t is the uncorrelated mean value of jth genotype for 't' characters

D²_{ij} is D² between the ith and jth genotypes.

3.5.11.4 Testing the significance of D² values

The D² value obtained for a population pair is taken as a calculated value of χ^2 and is tested against the tabulated value of Chi-Square (χ^2) for P degrees of freedom where P is the number of characters estimated. In the present study P is 18.

3.5.12 Contribution of individual characters towards divergence

In all combinations, each character was ranked based on its contribution towards divergence between two entries ($d_i = Y_i^j - Y_j^k$). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters. The percentage contribution towards genetic divergence was calculated using the following formula.

$$(d_i = Y_i^j - Y_j^k)$$

Where,

d_i = mean deviation

Y_i^j = mean value of the jth genotype for the ith character

Y_i^k = mean value of the kth genotype for the ith character

Material and Methods

The number of cases where a particular trait ranked first was counted, the proportion of this to the total number of trait combinations expressed in percentage will quantify the contribution of that character to the overall genetic divergence between the genotypes.

$$\text{Percent contribution of the character} = x = \frac{N}{M} \times 100$$

Where,

X = percent contribution of character

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of the number of genotypes considered.

3.5.13 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using Tocher's method as described by **Rao (1952)**. The criterion was that the two varieties belonging to the same cluster at least on average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by **Singh and Chaudhary (1977)**. To start with, two populations having the minimum distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At a certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster. The genotypes of the first cluster were then eliminated and the rest were treated similarly. This procedure was continued till all the genotypes were included in one or another.

3.5.13.1 Average intra-cluster distance

For the measurement of intra-cluster distances, the formula used was given by **Singh and Chaudhary (1977)**.

$$\text{Square of intra-cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

ΣD_i^2 = the sum of distances between all possible combinations (n) of the populations included in a cluster.

n = Number of all possible combinations

3.5.13.2 Average inter-cluster distance

Clusters were taken one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the members of the other clusters divided by the product of the number of genotypes in both the clusters under consideration. The inter-cluster distances were calculated by the formula given by **Singh and Chaudhary (1977)**.

$$\text{Average inter-cluster distance} = \frac{\Sigma D_i^2}{n_i \cdot n_j}$$

Where,

ΣD_i^2 = Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the clusters (i and j).

n_i = Number of entries in cluster i

n_j = Number of entries in the cluster

Statistical analysis of data was carried out by using the RSTUDIO cluster and INDOSTAT software.



Chapter-IV**EXPERIMENTAL RESULT**

In the present investigation entitled “**Assessment of Genetic Diversity in Maize [*Zea mays* L.] Inbred lines**” a collection of 35 maize inbred lines were assessed for the estimation of heritability, variability, genetic advance as percent mean, correlation coefficient, path-coefficients, and genetic divergence the inbred lines were evaluated for eleven characters *via*, days to 50% anthesis, days to 50% silking, silking anthesis interval, plant height (cm), ear height(cm), ear length (cm), ear girth (cm), number of kernel rows, number of kernel per row, test weight (100-grain weight) and grain yield per plot (Kg). The result obtained from the experiment presented in this chapter under the following headings:

4.1 Analysis of Variance**4.2 Analysis of Mean Performance and Range****4.3 Genetic Parameters (variability, heritability, and genetic advance)****4.4 Correlation coefficient Analysis****4.5 Path Coefficient Analysis****4.6 Genetic Divergence Analysis****4.1 Analysis of variance**

Analysis of variance for eleven characters is presented in table 4.1.1. The analysis of variance revealed a significant difference among the inbred lines for all eleven traits.

Table 4.1.1 Analysis of variance for the yield and yield contributing characters of maize inbred lines laid in RCBD.

Source of variation	Replication	Treatment	Error
Degree of freedom	1	34	34
	Mean sum squares		
Days for 50% Anthesis (days)	0.0893	7.9506*	5.8834
Days for 50% Silking (days)	0.1286	7.3042*	5.8638
Anthesis silking interval	0.7000	0.9932*	0.3176
Plant height (cm)	87.9873	390.0544*	118.7553
Ear height (cm)	0.8360	116.015*	38.2435
Ear length (cm)	0.5580	5.7224*	0.9190
Ear diameter (cm)	0.0408	0.1855*	0.0505
Number of kernel rows (No.)	6.4813	5.8296*	1.6995
Number of kernels per row (No.)	4.7633	26.5139*	3.3019
Test weight (g)	2.2357	29.8297*	2.5436
Grain yield per plot (Kg)	0.0024	2.5777*	0.8223

Where * = is significant at 0.05 level.

4.2 Analysis of mean performance and Range

The average performance of 35 inbred lines included in the study is calculated by taking the mean of five randomly selected plants in each replication. The mean and range value of all the traits studied for 35 inbred lines are presented in table 4.2.1.

4.2.1 Days to 50% anthesis (days)

Days to 50% anthesis ranged from 112 to 119 days with a mean of 115 days. Among all the inbred lines HUZM68-1, HUZM470, HUZM416, HUZM-2A-1 and LM-13 showed early anthesis (112 days), whereas HUZM-88-3, HUZM-3-2-1 and SCFEMALE showed very late anthesis (119 days). The 7 inbred lines were earlier in anthesis when compared to the general mean (115 days) of the days to 50% anthesis.

4.2.2 Days to 50% silking (days)

Days to 50% silking ranged from 115 days to 122 days with an average of 119 days. Among all the 35 inbred lines HUZM68-1, HUZM470 and HUZM-2A-1 showed early silking (115 days), whereas HUZM-88-3 and SCFEMALE showed very late silking (122 days). The 18 inbred lines were earlier in silking when compared to the general mean of (119 days) of the days to 50% silking.

4.2.3 Anthesis-silking interval (days)

Anthesis-silking interval ranged from 2 days to 4 days with a mean maturity of 2 days. The inbred lines HUZM68-1, HUZM491, HUZM-1-13, HUZM-328, CML-163, HUZM642-1, HUZM72087, HUZM9043A, HUZM-3-2-1, HUZM-94, MM-721-2, HUZM-4-32, HUZM455 and HUZM-44-111 has the lowest anthesis-silking interval (2 days) while inbred lines HUZM416, HUZM484, DMR-113-1, CML-41, HUZM-405-1, HUZM393 had the largest anthesis-silking interval (4 days). Only 20 inbred lines had the larger anthesis-silking interval when compared to the average (2 days) anthesis-silking interval.

4.2.4 Plant height (cm)

The mean values of plant height among 35 inbred lines ranged from 38.935 cm to 112.5 cm with a general mean height of 78.72 cm. Among all the inbred lines, HUZM-44-111 was the shortest (38.935 cm), whereas HUZM489 was the tallest (112.5 cm). The 16 inbred lines were shorter in plant height compared to the general mean (78.72 cm).

4.2.5 Ear height (cm)

The average ear height for 35 inbred lines was from 18.335 cm to 48.4 cm with a general mean of 31.99 cm. The shortest ear height was recorded by HUZM-111-8 (18.335 cm), whereas the longest ear height was recorded by HUZM-4-32 (48.4 cm). The 19 inbred lines showed lower ear height when compared to the general mean (31.99 cm) of this character.

4.2.6 Ear length (cm)

A range of 7.3 cm to 14.84 cm ear length was observed with a general mean of 10.85 cm. The maximum ear length was recorded by HUZM-22-4 (14.845 cm), whereas the minimum was by HUZM9043A (7.3 cm). The 17 inbred lines showed greater ear length when compared to the general mean of (10.8556 cm) of this character.

4.2.7 Ear girth (cm)

A range of 2.2 cm to 3.25 cm ear girth was observed with a general mean of 2.79 cm. The maximum ear girth was recorded by HUZM-22-4 and HUZM-3-2-1 (3.25 cm), whereas the minimum was by DMR-113 (2.2 cm). The 19 inbred lines showed greater ear girth when compared with a general mean of (2.79 cm) for this character.

4.2.8 Number of kernel rows (No.)

The number of kernel rows in the ear varied from 8 to 14 with a general mean of 10.21 cm. The highest number of kernel rows was recorded by CML-163 and HUZM642-1 (14 cm), whereas the lowest number of kernel rows was recorded by HUZM328, CML-41, HUZM-2A-1, HUZM-22-4, HUZM6, HUZM-3-2-1, HUZM451 and HUZM393 (8 cm). The 18 inbred lines had the lower number of kernel rows when compared to the general mean (10.21).

4.2.9 Number of kernels per row (No.)

This character ranged from 16.91 to 29.45 with a mean value of 22.88. CML-163 recorded the highest number of kernels per row (29.45), whereas HUZM-22-4 registered the lowest number of kernels per row (16.91). Out of 35 inbred lines, 19 inbred lines showed below the general mean (22.88) for this trait.

4.2.10 100-grain weight (g)

The 100-grain weight of 35 inbred lines in the study varied from 16.84 grams to 34.39 grams with a mean of 24.09 grams. LM-13 recorded a maximum 100-grain weight (34.39 gram), whereas HUZM455 recorded a minimum 100-grain weight (16.84 gram). 17 inbred lines exceeded the general mean for the 100-grain weight (24.09 gram).

4.2.11 Grain yield per plot (Kg)

This trait ranged from 0.48 to 1.12 kilogram with a mean of 0.83 kilograms. Inbred line HUZM451 registered maximum grain yield per plot (1.12 Kg), while CML-41 recorded minimum grain yield per plot (0.48 Kg). The 20 inbred lines exceeded the general mean.

Experimental Result

Table 4.2.1 Mean performance and range for yield and yield contributing characters

Inbred lines	Days to 50% anthesis (days)	Days to 50% silking (days)	Anthesis-silking interval	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows (No.)	Number of kernels per row (No.)	Test weight (g)	Grain yield per plot (Kg per plot)
LM-13	116	119	3	93.35	33.35	12.9	2.735	11	28.4	34.39	0.92
HUZM68-1	112	115	3	53.65	29.25	12.64	2.645	11	20.1	22.96	0.92
HUZM470	112	115	3	53.65	19.52	8	2.3	9.3	19.5	28.55	0.94
HUZM491	118	120	2	80.05	25.8	10.38	2.75	11.5	26	25.68	0.8
HUZM637-1	118	121	3	65.885	19.52	13.645	2.945	12	27.7	22.35	0.92
HUZM416	112	117	5	73.205	24.4	13.38	3.025	11	17.95	18.15	0.5
HUZM256	116	119	3	91.5	41	12.2	3	12	25	22.7	0.92
HUZM484	117	121	4	82.5	35	12.395	2.925	10	22	21.09	0.64
HUZM1108-2	116	119	3	67.2	26.7	12	3.16	11	20.5	28.61	1.08
DMR113-1	118	122	4	91.7	37.55	9.735	2.2	9	23.85	24.45	0.92
HUZM-1-13	115	118	3	75.45	28.3	10.35	2.3	10	22	21.36	0.76
HUZM328	116	118	2	70.5	31.5	11.1	2.65	8	19	18.05	0.64
CML-41	113	117	4	87.85	43.935	7.805	2.44	8	19.7	23.05	0.48
HUZM-2A-1	112	115	3	63.4	34.15	10.7	2.8	8	19	28.4	0.67
HUZM-22-4	114	117	3	80.5	29.25	14.845	3.25	9	16.91	26.39	0.64
HUZM-53-10	116	120	4	88.4	40.9	10.7	2.45	10	24.5	25.87	0.56
HUZM-405-1	114	118	4	82.55	25.55	11.3	3	10.5	26.15	25.67	1
CML-163	116	119	3	95	40.85	10.68	2.48	14	29.45	28.5	0.93
HUZM-111-8	115	118	3	64.2	18.335	9.2	2.835	11	25	20.49	0.92
HUZM642-1	118	121	3	80.85	38.35	14.3	3.15	14	20.6	19.73	0.94
HUZM6	117	120	3	88.4	35.85	9.7	2.85	8	19	22.51	0.77
HUZM72087	117	119	2	93.3	37.55	11.135	3	9	19.645	29.43	0.83
HUZM9043A	116	118	2	70.9	28.3	7.3	2.78	9	22.2	23.38	0.73
HUZM-3-2-1	119	121	2	86.65	33.35	10.37	3.25	8	25	24.73	0.89
HUZM294	117	119	2	79.15	30.85	10.44	2.7	10	19	21.59	0.86
MM721-2	117	120	3	99.15	40.8	10.45	3	13	20.6	27.09	1.01
HUZM-4-32	116	118	2	88.4	48.4	10.73	2.9	10	19.7	22.18	0.65
HUZM489	118	121	3	112.5	27.5	12.405	3.22	9	26.5	24.56	1.04
HUZM455	117	119	2	73.35	30.85	9.15	2.25	9.65	25.9	16.84	0.94
HUZM451	115	118	3	57.55	20	8.335	3	8	26.5	29.99	1.12
HUZM393	115	119	4	97.5	40	9.21	2.58	8	21.235	21.69	0.72
SCFEMALE	119	122	3	64.2	27.55	12.395	2.73	11.7	20.225	20.33	0.89
HUZM-100-10	115	118	3	66.7	24.2	11.45	2.3	10	29.35	20.22	0.94
HUZM-44-111	116	119	3	38.935	30.05	10.54	2.925	11.7	23.615	25.6	0.76
HUZM-88-3	119	122	3	69.57	41.415	11.08	3.15	12.2	29.27	26.54	0.92
Mean	115	118	3	78.72	31.99	10.85	2.79	10.21	22.88	24.09	0.83
C.V.	2.08	2.03	5.07	9.84	8.32	8.83	8.05	9.76	7.93	6.62	10.68
S.E.	1.71	1.71	0.39	7.7	4.37	0.67	0.15	0.92	1.12	1.12	0.14
Range lowest	112	115	2	38.935	18.335	7.3	2.2	8	16.91	16.84	0.48
Range highest	119	122	4	112.5	48.4	14.84	3.25	14	29.45	34.39	1.12

4.3 Genetic parameters (variability, heritability, and genetic advance)

The estimates of genetic parameters viz. phenotypic and genotypic coefficient of variation (PCV and GCV), heritability in a broad sense, and genetic advance as percent of means were computed for eleven characters are discussed hereunder (Table 4.3.1) Heritability (broad-sense) and genetic advance as percent of the mean for eleven characters in maize (*Zea mays* L.) and in figure 4.3.1.

4.3.1 Days to 50% anthesis

Very low GCV (0.87%) and low value of PCV (2.26) were recorded for days to 50% anthesis. The low value of heritability (0.14%) with a very low value of genetic advance as a percent of the mean (0.69%) was observed for this trait.

4.3.2 Days to 50% silking

Very low GCV (0.71%) and low value of PCV (2.15%) were recorded for days to 50% silking. A low value of heritability (0.10%) with a very low value of genetic advance as a percent of the mean (0.48%) was recorded for this trait.

4.3.3 Anthesis-silking interval

The high values of GCV (23.79%) and PCV (33.14%) were recorded for the anthesis-silking interval. Heritability for this character was low (0.51%) but very high value of genetic advance as a percent of the mean (35.18%) was recorded for this character.

4.3.4 Plant height (cm)

Moderate GCV (14.79%) and high PCV (20.26%) were recorded for plant height. A low value of heritability (0.53%) with high genetic advance as a percent of the mean (22.25%) was observed for this trait.

4.3.5 Ear height (cm)

Moderate value of GCV (19.48%) and high value of PCV (27.44%) were recorded for ear height. Heritability value for this character was recorded low (0.50%) with a very high value of genetic advance as a percent of the mean (28.50%) was observed for this trait.

4.3.6 Ear length (cm)

Moderate values of both GCV (14.27%) and PCV (16.78%) were recorded for ear length. The low value of heritability (0.72%) along with the high value of genetic advance as a percent of the mean (25.00%) recorded for ear length.

4.3.7 Ear girth (cm)

The low value of GCV (9.30%) and moderate value of PCV (12.31%) were recorded for ear girth. Low-value heritability (0.57%) along with the moderate value of genetic advance as percent of the mean (14.49%) was recorded for this trait.

4.3.8 Number of kernel rows (days)

Moderate values for both GCV (14.06%) and PCV (18.99%) were recorded for the number of kernel rows. The heritability value for this trait is also low (0.54%) along with a high value of genetic advance as a percent of the mean (21.46%).

4.3.9 Number of kernels per row (days)

Moderate values for both GCV (14.88%) and PCV (16.87%) were recorded for the number of kernels per row. Heritability values for this trait are low (0.77%) along with very high-value genetic advance as a percent of the mean (27.05%).

4.3.10 100 seed weight (g)

Moderate values for both GCV (15.33%) and PCV (16.70%) were recorded for 100-grain weight. The heritability value recorded for this trait is low (0.84%) along with a very high value of genetic advance as a percent of the mean (28.99%).

4.3.11 Grain yield per plot (Kg)

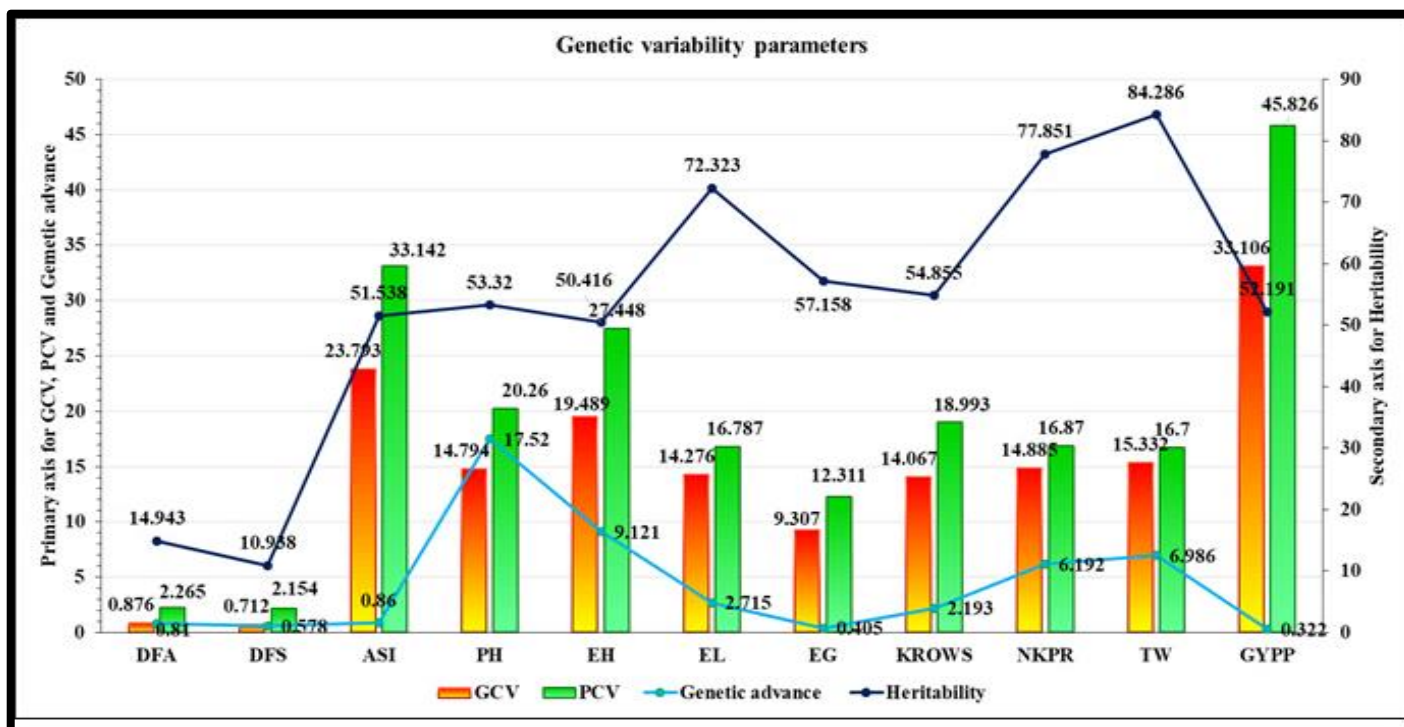
Very high values for both GCV (33.10%) and PCV (45.82%) were recorded for grain yield per plot. The heritability value observed for the trait is low (0.52%) along with a very high value of genetic advance as a percent of the mean (49.26%)

Table 4.3.1 Genetic variability parameters (GCV, PCV, Heritability, and Genetic advance) for yield and yield contributing characters in maize (*Zea mays* L.)

Parameters	Days to 50% anthesis (days)	Days to 50% silking (days)	Anthesis-silking interval	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows (No.)	Number of kernels per row (No.)	Test weight (g)	Grain yield per plot (Kg)
ECV	2.08	2.03	23.07	13.84	19.32	8.83	8.05	12.76	7.93	6.62	31.68
GCV	0.87	0.71	23.79	14.79	19.48	14.27	9.3	14.06	14.88	15.33	33.1
PCV	2.26	2.15	33.14	20.26	27.44	16.78	12.31	18.99	16.87	16.7	45.82
Heritability [$h^2_{(b)}$]	0.14	0.1	0.51	0.53	0.50	0.72	0.57	0.54	0.77	0.84	0.52
Gen. Adv as % of mean	0.69	0.48	35.18	22.25	28.5	25	14.49	21.46	27.05	28.99	49.26

ECV- Environmental coefficient of variation, GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, Heritability [$h^2_{(b)}$]- Heritability in broad sense, Gen. Adv as % of mean- Genetic Advancement as percent of mean.

Figure 4.3.1. Showing genetic variability parameters (GCV, PCV, Heritability and Genetic advance).



GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, DFA-Days to 50% anthesis, DFS-Days to 50% silking, ASI-Anthesis-silking interval, PH-Plant height, EL-Ear length, EG-Ear girth, KROWS- Number of kernel rows, NKPR- Number of kernels per row, TW- Test weight, GYPP- Grain yield per plot.

4.4 Correlation coefficient analysis

The study of correlation gives reliable information based on the degree and direction of the association between the characters, especially when the plant breeder needs to combine high yield potential with other desirable agronomic traits, correlation between these characters plays a vital role in breeding.

Character association of grain yield per plot with another character

The positive significant correlation of grain yield per plot was observed with characters such as, number of kernels per rows (0.336**), number of kernels per row (0.438**) and test weight (0.356**), which showed a strong positive correlation between these characters. The traits such as days to 50% anthesis (0.068), days to 50% silking (0.091), anthesis-silking interval (0.228), ear length (0.126) and ear girth (0.226) indicate a non-significant positive association with grain yield per plot. However, plant height (-0.027) and ear height (-0.171) showed a negative and non-significant correlation with grain yield per plot. Estimates of phenotypic correlation coefficients are presented in table 4.4.1.1 and figure 4.4.1.1 as corplot.

4.4.1 Phenotypic correlation coefficient

4.4.1.1 Days to 50% anthesis

Days to 50% anthesis showed a significant positive correlation with days to 50% flower silking (0.945**), plant height (0.258*), and a number of kernels per row (0.248*) indicated that these three traits are correlated significantly among themselves. However, it showed a nonsignificant positive correlation with anthesis silking interval (0.093), ear height (0.162), ear length (0.005), ear girth (0.189), number of kernel rows (0.167), and grain yield per plot (0.068). It also exhibited a negative and non-significant association with 100-grain weight (-0.15).

4.4.1.2 Days to 50% flower silking

Days to 50% flower silking showed a significant positive correlation with days to 50% anthesis (0.945**), plant height (0.258*) and the number of kernels per row (0.288*). It indicates that these traits correlated among themselves. It showed a non-significant positive correlation with anthesis-silking interval (0.123), ear height (0.152), ear length (0.036), ear girth (0.218), number of kernel rows (0.147), grain yield per plot (0.091). It also exhibited a negative non-significant correlation with 100-seed weight (-0.164).

4.4.1.3 Anthesis-silking interval

Anthesis-silking interval showed a positive and non-significant correlation with the days to 50% anthesis (0.093) and days to 50% silking (0.123), plant height (0.062), ear girth (0.106), number of kernels per row (0.001), 100-seed weight (0.105), grain yield per plot (0.228). It also showed a negative and non-significant correlation with ear height (-0.025), ear length (-0.001), number of kernel rows (-0.148).

4.4.1.4 Plant height

Plant height showed a positive and significant correlation with the days to 50% anthesis (0.258*), days to 50% silking (0.260*) and ear height(0.642**). It indicates that these traits are correlated significantly between themselves. However, it showed a non-significant and positive correlation with the anthesis-silking interval (0.062), ear length (0.094), ear girth (0.205), number of kernel rows (0.072), and number of kernels per row (0.116), test weight (0.094). Also, it showed a non-significant negative correlation with grain yield per plot (-0.027).

4.4.1.5 Ear height

Ear height showed a positive and significant correlation with the plant height (0.642). It indicated these traits are correlated significantly between themselves. However, it showed a non-significant positive correlation with days to 50% anthesis (0.162), days to 50% silking (0.152), ear girth (0.13), number of kernel rows (0.1) and 100 seed weight (0.035). It showed a non-significant negative correlation with anthesis-silking interval (-0.025), ear length (-0.013), number of kernels per row (-0.094) and grain yield per plot (-0.171).

4.4.1.6 Ear length

Ear length showed a significant positive association with ear girth (0.436*).It indicates that these traits are correlated significantly among themselves. It showed non-significant positive correlation with days to 50% anthesis (0.005),days to 50% silking (0.036), plant height (0.094), number of kernel rows (0.303), 100-seed weight (0.01) and grain yield per plot (0.126). It showed a negative and non-significant correlation with anthesis-silking interval (-0.001), ear length (-0.013) and number of kernels per row (-0.041).

4.4.1.7 Ear girth

It showed a positive and significant correlation with ear length (0.436**). It indicates that these traits are correlated significantly among themselves. However, it showed a non-significant positive correlation with days to 50% anthesis (0.189), days to 50% silking (0.218), anthesis-silking interval (0.106), plant height (0.205), ear height (0.13), number of kernel rows (0.182), 100-seed weight (0.153) and grain yield per plot (0.226). It showed a non-significant negative correlation with number of kernels per row (-0.083).

4.4.1.8 Number of kernel rows

A number of kernel rows showed a positive and significant correlation with number of kernels per row (0.327*) and grain yield per plot (0.336**). However, it showed a positive and non-significant correlation with correlation with days to 50% anthesis (0.167), days to 50% silking (0.147), plant height (0.072), ear height (0.1), ear length (0.303), ear girth (0.182), 100-seed weight (0.045). It also showed a non-significant and negative correlation with anthesis-silking interval (-0.148).

4.4.1.9 Number of kernels per row

The number of kernels per row showed a significant positive correlation with grain yield per plot (0.438**), days to 50% anthesis (0.248*), number of kernel rows (0.327**) and days to 50% silking (0.288*). It indicated that these three traits are correlated significantly among themselves. It also showed a non-significant and positive correlation with the days to anthesis-silking interval (0.001), plant height (0.116) and 100-seed weight (0.194). It also showed a non-significant and negative correlation with ear height (-0.094), ear length (-0.041) and ear girth (-0.083).

4.4.1.10 100-seed weight

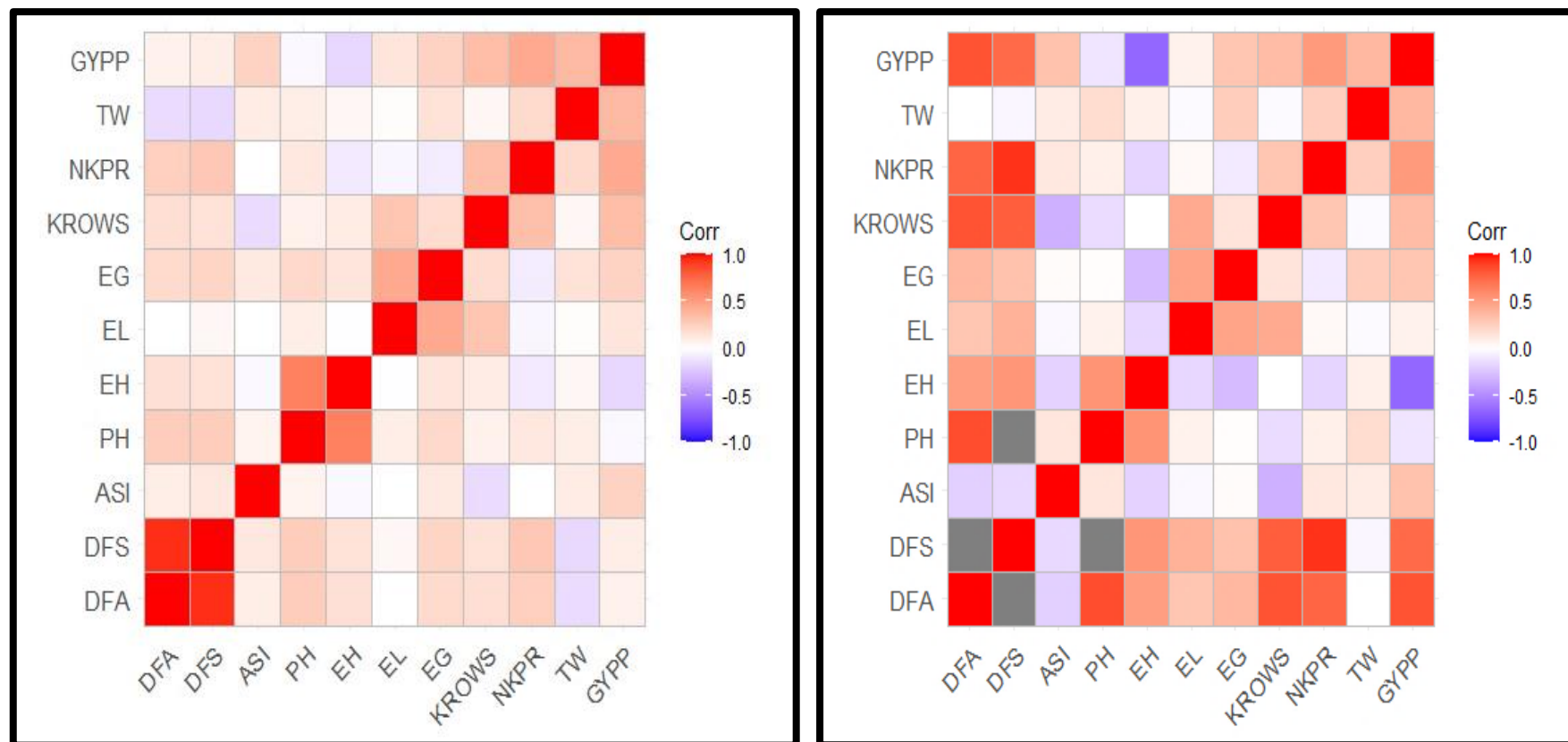
Test weight showed a positive and significant correlation with grain yield per plot (0.356**). However, it showed a positive and non-significant correlation with the days to anthesis-silking interval (0.105), plant height (0.094), ear height (0.035), ear length (0.01), ear girth (0.153), number of kernel rows (0.045) and number of kernels per row (0.194). It showed a non-significant negative correlation with the days to 50% anthesis (-0.15) and days to 50% silking (-0.164).

Experimental Result

Table 4.4.1.1 Phenotypic correlation between grain yield per plot (Kg/plot) and its component traits in 35 maize inbred lines.

	Days to 50% anthesis (days)	Days to 50% silking (days)	Anthesis-silking interval	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows (No.)	Number of kernels per row (No.)	Test weight (g)	Grain yield per plot (Kg)
Days to 50% anthesis	1.000										
Days to 50% silking	0.945**	1.000									
Anthesis- silking interval	0.093	0.123	1.000								
Plant height (cm)	0.258*	0.260*	0.062	1.000							
Ear height (cm)	0.162	0.152	-0.025	0.642**	1.000						
Ear length (cm)	0.005	0.036	-0.001	0.094	-0.013	1.000					
Ear girth (cm)	0.189	0.218	0.106	0.205	0.13	0.436**	1.000				
Number of kernel rows	0.167	0.147	-0.148	0.072	0.1	0.303*	0.182	1.000			
Number of kernels per row	0.248*	0.288*	0.001	0.116	-0.094	-0.041	-0.083	0.327**	1.000		
Test weight (g)	-0.15	-0.164	0.105	0.094	0.035	0.01	0.153	0.045	0.194	1.000	
Grain yield per plot (Kg)	<u>0.068</u>	<u>0.091</u>	<u>0.228</u>	<u>-0.027</u>	<u>-0.171</u>	<u>0.126</u>	<u>0.226</u>	<u>0.336**</u>	<u>0.438**</u>	<u>0.356**</u>	<u>1.000</u>

Figure 4.4.1.1 & 4.4.2.1 Correlation matrix of phenotypic and genotypic correlation of grain yield per plot (Kg/plot) in maize.



GYPP- Grain yield per plot, TW- Test weight, NKPR-Number of kernels per row, KROWS- Number of kernel rows, EG-Ear girth, EL-Ear length, PH-Plant height, ASI-Anthesis silking interval, DFS- Days to 50%silking, DFA-Days to 50% anthesis.

4.4.2 Genotypic correlation coefficient

Character association of grain yield per plot with other characters

The positive and significant correlation with grain yield per plot was observed with days to 50% anthesis (0.831**), days to 50% silking (0.740**), anthesis silking interval (0.323**), ear girth (0.303*), number of kernel rows (0.352**), number of kernels per row (0.516**), test weight (0.370**) which indicated a strong positive association between these characters. The characters such as plant height (-0.111) showed a non-significant and negative correlation with grain yield per plot. While ear height (-0.664**) showed a negative and significant association with grain yield per plot. Estimates of genotypic correlation coefficients are presented in table 4.4.2.1 and figure 4.4.2.1 as corplot.

4.4.2.1 Days to 50% anthesis

Days to 50% anthesis showed a positive and significant correlation with days to silking (0.997**), plant height (0.850**), ear height (0.502**), ear length (0.296**), ear girth (0.372**), number of kernel rows (0.827**), number of kernels per row (0.763**), and grain yield per plot (0.831**). It indicates that all these characters are highly correlated between themselves. It also exhibited a significant negative correlation with anthesis-silking interval (-0.201) and 100 seed weight (-0.005).

4.4.2.2 Days to 50% silking

Days to 50% silking showed a positive and significant association with days to 50% anthesis (0.997**), plant height (0.998**), ear height (0.539**), ear length (0.401**), ear girth (0.320**), number of kernel rows (0.788**), number of kernels per row (0.934**) and grain yield per plot (0.740**). It indicates that these characters are correlated among themselves. It also exhibited a non-significant negative correlation with 100 seed weight (-0.044) and anthesis-silking interval (-0.158).

4.4.2.3 Anthesis-silking interval

Anthesis-silking interval showed a significant positive correlation with grain yield per plot (0.323**). It indicated that these two characters are correlated among themselves. It showed a negative and significant correlation with a number of kernel rows (-0.337**). Also, it showed a positive non-significant correlation with plant height (0.127), ear girth (0.022), number of kernels per row (0.115), 100 seed weight (0.105). It exhibited a non-significant negative

correlation with days to 50% anthesis (-0.201), days to 50% silking (-0.158), ear height (-0.189) and ear length (-0.031).

4.4.2.4 Plant height

Plant height showed a significant positive correlation with days to 50% anthesis (0.850**), days to 50% silking (0.998**) and ear height (0.551**). It indicated that these three characters are highly correlated among themselves. It showed a non-significant positive correlation with anthesis-silking interval (0.127), ear length (0.072), ear girth (0.007), number of kernels per row (0.077), 100 seed weight (0.178). It also exhibited a non-significant negative correlation with the number of kernel rows (-0.154) and grain yield per plot (-0.111).

4.4.2.5 Ear height

Ear height showed a positive and significant correlation with days to 50% anthesis (0.502**), days to 50% silking (0.539**) and plant height (0.551**). It showed a negative significant correlation with ear girth (-0.294*) and grain yield per plot (-0.664**). However, it showed a negative and non-significant correlation with anthesis-silking interval (-0.189), ear length (-0.171) and number of kernels per row (-0.178). while test weight (0.081) and number of kernel rows (0.000) showed a non-significant positive correlation with ear height.

4.4.2.6 Ear length

Ear length showed a significant positive correlation with days to 50% anthesis (0.296*), days to 50% silking (0.401**) ear girth (0.469**), number of kernel rows (0.444**). It indicated that these traits are correlated among themselves. It showed a non-significant positive correlation with plant height (0.072) and number of kernels per row (0.028) and grain yield per plot (0.071). However, it also exhibited a negative and non-significant correlation with anthesis-silking interval (-0.031), ear height (-0.171) and 100 seed weight (-0.023).

4.4.2.7 Ear girth

Ear girth showed a significant positive correlation with days to 50% anthesis (0.372**), days to 50% silking (0.320**), ear length (0.469**), test weight (0.256*) and grain yield per plot (0.303*). It indicated that these traits are highly correlated with each other. However, it showed a positive non-significant correlation with anthesis-silking interval (0.022), plant height (0.007) a number of kernel rows (0.135). Also, it exhibited a negative and significant

correlation with the ear height (-0.294*). While it showed a negative and non-significant correlation with number of kernels per row (-0.089).

4.4.2.8 Number of kernel rows

A number of kernel rows showed a significant and positive correlation with the days to 50% anthesis (0.827**), days to 50% silking (0.788**), ear length (0.444*), number of kernels per row (0.303*) and grain yields per plot (0.352**). It indicated that these characters are correlated among themselves. However, it showed a non-significant positive correlation with the ear height (0.000) and ear girth (0.135). while it showed the negative non-significant correlation with plant height (-0.154) and 100 seed weight (-0.022). It also showed a significant negative correlation with anthesis-silking interval (-0.337**).

4.4.2.9 Number of kernels per row

A number of kernels per row showed a positive and significant correlation with days to 50% anthesis (0.763**), days to 50% silking (0.934**), number of kernel rows (0.303*), 100 seed weight (0.249*) and grain yield per plot (0.516**).It indicated that these characters are correlated among themselves. However, it showed a positive non-significant correlation with anthesis-silking interval (0.115), plant height (0.077) and ear length (0.028). while it showed a negative non-significant correlation with ear height (-0.178) and ear girth (-0.089).

4.4.2.10 100-seed weight

Test weight showed a positive and significant association with ear girth (0.256*), number of kernels per row (0.249*) and grain yield per plot (0.370**).It indicated that these characters are correlated among themselves. However, it showed a positive and non-significant correlation with anthesis-silking interval (0.105), plant height (0.178) and ear height (0.081). Also, it showed a negative and non-significant correlation with days to 50% anthesis (-0.005), days to 50% silking (-0.044), ear length (-0.023) and number of kernel rows (-0.022).

Experimental Result

Table 4.4.2.1 Genotypic correlation between grain yield per plot (Kg/plot) and its component characters in 35 inbred lines.

	Days to 50% anthesis (days)	Days to 50% silking (days)	Anthesis- silking interval	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows (No.)	Number of kernels per row (No.)	Test weight (g)	Grain yield per plot (Kg)
Days to 50% anthesis	1.000										
Days to 50% silking	0.997**	1.000									
Anthesis- silking interval	-0.201	-0.158	1.000								
Plant height (cm)	0.850**	0.998**	0.127	1.000							
Ear height (cm)	0.502**	0.539**	-0.189	0.551**	1.000						
Ear length (cm)	0.296*	0.401**	-0.031	0.072	-0.171	1.000					
Ear girth (cm)	0.372**	0.320**	0.022	0.007	-0.294*	0.469**	1.000				
Number of kernel rows	0.827**	0.788**	-0.337**	-0.154	0.000	0.444**	0.135	1.000			
Number of kernels per row	0.763**	0.934**	0.115	0.077	-0.178	0.028	-0.089	0.303*	1.000		
Test weight (g)	-0.005	-0.044	0.105	0.178	0.081	-0.023	0.256*	-0.022	0.249*	1.000	
Grain yield per plot (Kg)	<u>0.831**</u>	<u>0.740**</u>	<u>0.323**</u>	<u>-0.111</u>	<u>-0.664**</u>	<u>0.071</u>	<u>0.303*</u>	<u>0.352**</u>	<u>0.516**</u>	<u>0.370**</u>	<u>1.000</u>

4.5 Path coefficient analysis

The concept of path analysis was originally developed by **wright (1934)**. The path coefficient analysis is simply a standardized partial regression coefficient that split the correlation coefficient into the measures of direct and indirect effects. In another word, it measures the direct and indirect contribution of various independent characters on a dependent character. The path diagram may be explained in terms of the causes and effect relationship of different variables.

4.5.1 Phenotypic path coefficient

Path coefficient analysis among other characters

The traits such as days to 50% anthesis (0.068), days to 50% flower silking (0.091), anthesis silking interval (0.228), ear length (0.126) and ear girth (0.226) showed a positive non-significant direct effect on grain yield per plot. While the non-significant negative indirect effect was found for plant height (-0.027) and ear height (-0.171) on grain yield per plot. However, characters like number of kernel rows (0.336**), number of kernels per row (0.438**) and 100-seed weight (0.356**) showed a strong positive and significant direct effect on grain yield per plot. Estimates of direct and indirect effects are presented and shown in table 4.5.1.1. And figure 4.5.1.1 is a matrix plot.

4.5.1.1 Days to 50% anthesis

The direct effect of this character was shown negative on grain yield per plot (-0.070). This character displayed a positive indirect effect on grain yield per plot *via* days to 50% anthesis (0.031), days to 50% silking (0.020), ear length (0.000), ear girth (0.036), number of kernel rows (0.02) and number of kernels per row (0.081). Whereas it showed a negative indirect effect on grain yield per plot *via* plant height (-0.018), ear height (-0.011), ear height (-0.026) and test weight (-0.035).

4.5.1.2 Days to 50% flower silking

The direct effect of days to 50% flower silking on grain yield per plot was seen as positive (0.033). It displayed a positive indirect effect on grain yield per plot *via* anthesis-silking interval (0.027), ear girth (0.042), number of kernel rows (0.037) and number of kernels per row (0.093). However, it showed a negative indirect effect on grain per plot *via* days to 50% anthesis (-0.066), plant height (-0.011), ear height (-0.024), ear length (-0.001) and 100-seed weight (-0.038).

4.5.1.3 Anthesis-silking interval

The direct effect of the anthesis silking interval on grain yield per plot was positive (0.221). It displayed an indirect positive effect on grain yield per plot *via* days to 50% silking (0.004), ear height (0.004), ear length (0.000), ear girth (0.0021), number of kernels per row (0.000), test weight (0.024). Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis (-0.007), plant height (-0.003) and a number of kernel rows (-0.037).

4.5.1.4 Plant height

The direct effect of plant height on grain yield per plot was negative (-0.044). It displayed an indirect positive effect on grain yield per plot *via* day days to 50% flower silking (0.009), anthesis-silking interval (0.014), ear girth (0.040), number of kernel rows (0.018), number of kernels per row (0.037), and 100 seed weight (0.022). Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis (-0.018), ear height (-0.102), ear length (-0.002).

4.5.1.5 Ear height

The direct effect of ear height on grain yield per plot was seen as negative (-0.159). Displayed an indirect positive effect on grain yield per plot *via* days to 50% silking (0.005), ear length (0.000), ear girth (0.025), number of kernel rows (0.025) and test weight (0.008). However, it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis (-0.011), anthesis-silking interval (-0.005), plant height (-0.028) and number of kernels per row (-0.030).

4.5.1.6 Ear length

The direct effect of ear length on grain yield per plot was seen as negative (-0.021). Displayed a direct positive effect on dependent trait grain per plot *via* other traits such as days to 50% anthesis (0.000), days to 50% silking (0.001), anthesis silking interval (0.000), ear height (0.002), ear girth (0.084), number of kernel rows (0.076) and 100 seed weight (0.002). However, its negative indirect effect on grain yield per plot *via* plant height (-0.004) and number of kernels per row (-0.013).

4.5.1.7 Ear girth

The direct effect of ear diameter on grain-dependent character yield per plot was seen as positive (0.193). It displayed an indirect positive effect on days to 50% silking (0.007), anthesis silking interval (0.023), number of kernel rows (0.045) and 100 seed weight (0.036). However, it also showed an indirect negative effect on grain yield per plot *via* the days to 50% anthesis (-0.013), plant height (-0.009), ear height (-0.021), ear length (-0.009) and number of kernels per row (-0.027).

4.5.1.8 Number of kernel rows

The direct effect of the number of kernel rows on grain yield per plot was seen as positive (0.250). It displayed an indirect positive effect on grain yield per plot *via* the days to 50% silking (0.005), ear girth (0.035), number of kernels per row (0.106) and 100 seed weight (0.010). Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis (-0.012), anthesis-silking interval (-0.033), plant height (-0.003), ear height (-0.016) and ear length (-0.006).

4.5.1.9 Number of kernels per row

The direct effect of the number of kernels per row on the dependent character grain yield per plot was seen as positive (0.324). Whereas it displayed positive and indirect effects on grain yield per plot *via* other characters such as days to 50% flower silking (0.009), anthesis-silking interval (0.000), ear height (0.015), ear length (0.001), number of kernel rows (0.082) and 100 seed weight (0.045). Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis (-0.017), ear girth (-0.016) and plant height (-0.004).

4.5.1.10 100 seed weight

The direct effect of test weight on grain yield per plot was seen positive (0.234). And displayed a positive indirect effect on dependent character grain yield per plot *via* other traits such as days to 50% anthesis (0.011), anthesis-silking interval (0.023), ear length (0.000), ear diameter (0.030), number of kernel row (0.011), and number kernels per row (0.063). Whereas it showed an indirect effect on grain yield per plot *via* and days to 50% silking (-0.005), plant height (-0.005) and ear height (-0.006).

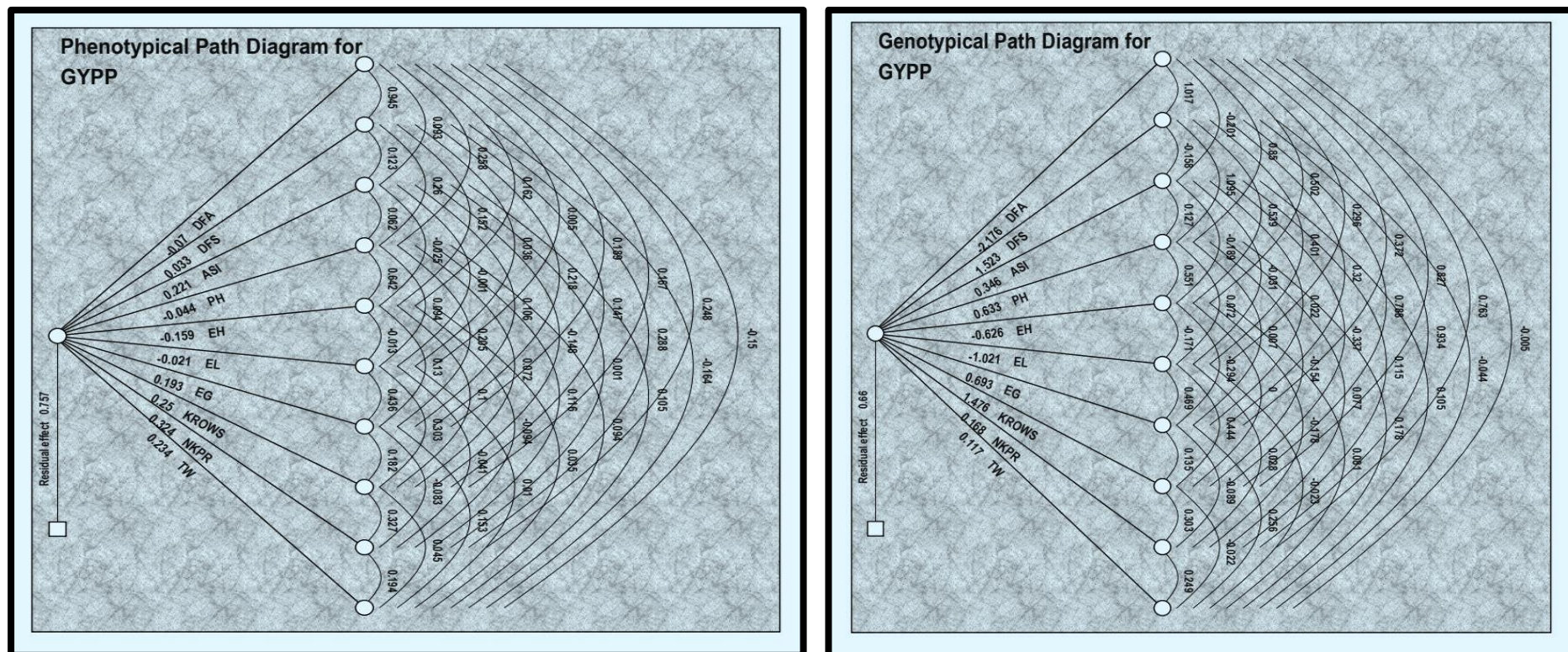
Experimental Result

Table 4.5.1.1 Direct and indirect effect of component characters attributing to grain yield per plot (Kg/plot) at the phenotypic level.

	Days to 50% anthesis (days)	Days to 50% silking (days)	Anthesis silking interval	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows (No.)	Number of kernels per row (No.)	Test weight (g)	Grain yield per plot (Kg)
Days to 50% anthesis	<u>-0.070</u>	0.031	0.020	-0.011	-0.026	0.000	0.036	0.02	0.081	-0.035	0.068
Days to 50% silking	-0.066	<u>0.033</u>	0.027	-0.011	-0.024	-0.001	0.042	0.037	0.093	-0.038	0.091
Anthesis- silking interval	-0.007	0.004	<u>0.221</u>	-0.003	0.004	0.000	0.0021	-0.037	0.000	0.024	0.228
Plant height (cm)	-0.018	0.009	0.014	<u>-0.044</u>	-0.102	-0.002	0.040	0.018	0.037	0.022	-0.027
Ear height (cm)	-0.011	0.005	-0.005	-0.028	<u>-0.159</u>	0.000	0.025	0.025	-0.030	0.008	-0.171
Ear length (cm)	0.000	0.001	0.000	-0.004	0.002	<u>-0.021</u>	0.084	0.076	-0.013	0.002	0.126
Ear girth (cm)	-0.013	0.007	0.023	-0.009	-0.021	-0.009	<u>0.193</u>	0.045	-0.027	0.036	0.226
Number of kernel rows	-0.012	0.005	-0.033	-0.003	-0.016	-0.006	0.035	<u>0.250</u>	0.106	0.010	0.336**
Number of kernels per row	-0.017	0.009	0.000	-0.004	0.015	0.001	-0.016	0.082	<u>0.324</u>	0.045	0.438**
Test weight (g)	0.011	-0.005	0.023	-0.005	-0.006	0.000	0.030	0.011	0.063	<u>0.234</u>	0.356**

Residual value 0.757

Figure 4.5.1.1 & 4.5.2.1 Path diagram showing estimates of the phenotypic and genotypic path for grain yield per plot (Kg/plot) in maize.



GYPP- Grain yield per plot, TW- Test weight, NKPR-Number of kernels per row, KROWS- Number of kernel rows, EG-Ear girth, EL- Ear length, PH-Plant height, ASI-Anthesis silking interval, DFS- Days to 50% flower silking, DFA-Days to 50% anthesis.

4.5.2 Genotypic path coefficient

Path coefficient analysis of grain yield per hectare with other characters

The traits such as days to 50% anthesis (0.831**), days to 50% silking (0.740**), anthesis silking interval (0.323**), ear girth (0.303*), number of kernel rows (0.352**), number of kernels per row (0.516**), and 100 seed weight (0.370**) showed a strong positive significant direct effect on grain yield per plot. While the non-significant positive indirect effect was found for ear length (0.071). However, ear height (-0.664**) showed direct negative and significant effect on grain yield per plot. Estimates of direct and indirect effects are presented and shown in table 4.5.2.1. And figure 4.5.2.1 is a matrix plot.

4.5.2.1 Days to 50% anthesis

The direct effect of days to 50% anthesis on grain yield per plot was seen as negative (-2.176). It displayed a positive indirect effect on grain yield per plot *via* characters days to 50% silking (1.548), plant height (0.538), ear girth (0.258), number of kernel rows (1.220) and number of kernels per row (0.128). Whereas it showed an indirect and negative effect on grain yield per plot *via* anthesis-silking interval (-0.070), ear height (-0.314), ear length (-0.302) and test weight (-0.001).

4.5.2.2 Days to 50% flower silking

The direct effect of days to 50% silking on grain yield per plot was seen as positive (1.523). It displayed a positive indirect effect on grain yield per plot *via* plant height (0.693), ear length (0.222) number of kernel rows (1.163) and number of kernels per row (0.157). Whereas it showed an indirect negative effect on grain yield per plot *via* days to 50% anthesis (-2.212), anthesis-silking interval (-0.055), ear height (-0.338), ear length (-0.409) and test weight (-0.005).

4.5.2.3 Anthesis silking interval

The direct effect of anthesis silking interval on grain yield per plot was seen positive (0.346). It displayed a positive indirect effect on grain yield per plot *via* days to 50% anthesis (0.437), plant height (0.081), ear height (0.118), ear length (0.032), ear girth (0.015), number of kernels per row (0.019) and test weight (0.012). Whereas it also showed an indirect negative effect on grain yield per plot *via* days to 50% silking (-0.020) and number of kernel rows (-0.498).

4.5.2.4 Plant height

The direct effect of plant height on grain yield per plot was seen as positive (0.633). It displayed a positive indirect effect on dependent character grain yield per plot *via* another character such as days to 50% silking (1.667), anthesis silking interval (0.044), ear girth (0.005), number of kernels per row (0.013), and test weight (0.021). Whereas it also showed an indirect negative effect on grain yield per plot *via* days to 50% anthesis (-1.894), ear height (-0.345), ear length (-0.073) and number of kernel rows (-0.227).

4.5.2.5 Ear height

The direct effect of ear height on grain yield per plot was seen as negative (-0.626). It displayed a positive indirect effect on dependent character grain yield per plot *via* another character such as days to 50% silking (0.821), plant height (0.349), ear length (0.175), number of kernel rows (0.000) and test weight (0.009). Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis (-1.092), anthesis-silking interval (-0.065), ear girth (-0.204) and number of kernels per row (-0.003).

4.5.2.6 Ear length

The direct effect of ear length on grain yield per plot was seen as negative (-1.021). It displayed a positive indirect effect on grain yield per plot *via* days to 50% silking (0.610), plant height (0.045), ear height (0.107), ear girth (0.325), number of kernel rows (0.656) and number of kernels per row (0.005). Whereas it showed an indirect negative effect on grain yield per plot *via* days to 50% anthesis (-0.643), anthesis-silking interval (-0.011) and test weight (-0.003).

4.5.2.7 Ear diameter

The direct effect of ear diameter on grain yield per plot was seen positive (0.693). It displayed an indirect positive effect on days to 50% silking (0.488), anthesis silking interval (0.008), plant height (0.004), ear length (0.184), number of kernel rows (0.199), 100 seed weight (0.030). Whereas it showed an indirect negative effect on grain yield per plot *via* days to 50% anthesis (-0.809), ear height (-0.479), and a number of kernels per row (-0.015).

4.5.2.8 Number of kernel rows

The direct effect of the number of kernel rows on grain yield per plot was seen as positive (1.476). It displayed a positive indirect effect on dependent character grain yield per plot *via* other characters days to 50% silking (1.200), ear height (0.000), ear girth (0.093) and a number of kernels per row (0.051). Whereas it showed a negative and indirect effect on grain yield per plot *via* days to 50% anthesis (-1.799), anthesis silking interval (-0.117), plant height (-0.097), ear length (-0.454) and test weight (-0.003).

4.5.2.9 Number of kernels per row

The direct effect of the number of kernels per row on grain yield per plot was seen as positive (0.168). It displayed a positive indirect effect on dependent character grain yield per plot *via* other character days to 50% silking (1.422), anthesis silking interval (0.040), plant height (0.049), ear height (0.112), number of kernel rows (0.447), and 100 seed weight (0.029). Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis (-1.660), ear length (-0.028) and ear girth (-0.062).

4.5.2.10 100 seed weight

The direct effect of test weight on grain yield per plot was seen positive (0.117). It displayed an indirect positive effect on days to 50% anthesis (0.012), anthesis silking interval (0.036), number of kernels per row (0.113), ear length (0.024), ear girth (0.177) and number of kernels per row (0.042). Whereas it displayed an indirect negative effect on days to 50% silking (-0.067), ear height (-0.051) and number of kernel rows (-0.003).

Experimental Result

4.5.2.1 Direct and indirect effect of component characters attributing to grain yield per plot (Kg/plot) at genotypic level.

	Days to 50% anthesis (days)	Days to 50% silking (days)	Anthesis silking interval	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows (No.)	Number of kernels per row (No.)	Test weight (g)	Grain yield per plot (Kg)
Days to 50% anthesis	<u>-2.176</u>	1.548	-0.070	0.538	-0.314	-0.302	0.258	1.220	0.128	-0.001	0.831**
Days to 50% silking	-2.212	<u>1.523</u>	-0.055	0.693	-0.338	-0.409	0.222	1.163	0.157	-0.005	0.740**
Anthesis- silking interval	0.437	-0.240	<u>0.346</u>	0.081	0.118	0.032	0.015	-0.498	0.019	0.012	0.323**
Plant height (cm)	-1.849	1.667	0.044	<u>0.633</u>	-0.345	-0.073	0.005	-0.227	0.013	0.021	-0.111
Ear height (cm)	-1.092	0.821	-0.065	0.349	<u>-0.626</u>	0.175	-0.204	0.000	-0.030	0.009	-0.664**
Ear length (cm)	-0.643	0.610	-0.011	0.045	0.107	<u>-1.021</u>	0.325	0.656	0.005	-0.003	0.071
Ear girth (cm)	-0.809	0.488	0.008	0.004	0.184	-0.479	<u>0.693</u>	0.199	-0.015	0.030	0.303*
Number of kernel rows	-1.799	1.200	-0.117	-0.097	0.000	-0.454	0.093	<u>1.476</u>	0.051	-0.003	0.352**
Number of kernels per row	-1.660	1.422	0.040	0.049	0.112	-0.028	-0.062	0.447	<u>0.168</u>	0.029	0.516**
Test weight (g)	0.012	-0.067	0.036	0.113	-0.051	0.024	0.177	-0.033	0.042	<u>0.117</u>	0.370**

Residual value 0.66

4.6 Genetic divergence

Detail study of genetic diversity of germplasm material is necessary to group into a cluster based on similarities and to select desirable inbred lines from two distantly related groups exploiting heterosis in F_1 generation and transgressive segregants from F_2 and later generations in all the breeding programs. Genetic divergence is mainly assessed using D^2 -statistics. The projection of diverse clusters is done through the analysis based on the inter-genetic distances, which specifies the presence of significantly diverse maize inbred lines in the experimental materials. The genetic diversity study on 35 inbred lines of maize was carried out considering eleven characters including yield and yield-related traits using Mahalanobi's D^2 statistic.

4.6.1 Wilk's criterion test

Wilk's 'v' (statistic) criterion was used in this analysis to test the significant differences between the clusters based on the pooled effects of all the characters. The highly significant 'v' statistic value was recorded in the analysis which indicates that the inbred lines significantly differ from each other. The analysis of variance for dispersion of 35 inbred lines. The significance of inbred lines indicated the significant pooled effect of all the characters between different inbred lines. Hence further analysis was made to estimate D^2 values.

4.6.2 Mahalanobis's D^2 values

The mean values of 35 inbred lines were transformed into standardized uncorrelated mean values using the pivotal condensation method ($y_1 - y_2$).

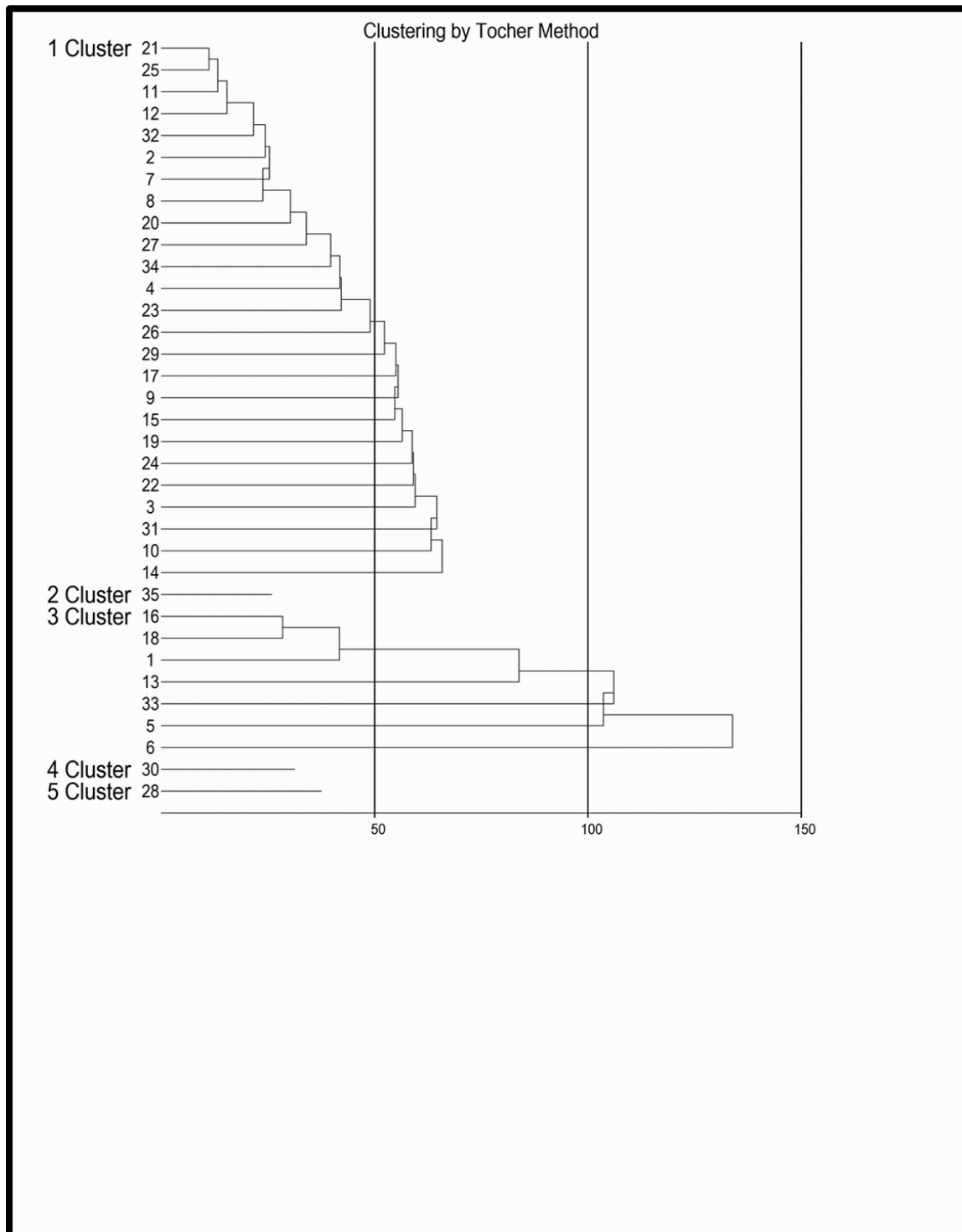
4.6.3 Cluster composition

All the 35 inbred lines were grouped into five clusters by using Tocher's method. The distribution of inbred lines into five clusters is presented in table 4.6.3.1 and illustrated in figure 4.6.3.1 Cluster I had 25 inbred lines, cluster ii had one inbred line, cluster III had seven inbred lines, and cluster IV had one inbred line, while a single inbred line was included in cluster V.

Table 4.6.3.1 Cluster composition of 35 maize inbred lines (Tocher's method)

Clust ers	Number included Inbred lines	Inbred lines
I	25	HUZH6, HUZH294, HUZH-1-13, HUZH328, SCFEMALE, HUZH68-1, HUZH256, HUZH484, HUZH642-1, HUZH-4-32, HUZH-44-111, HUZH491, HUZH9083A, MM-721-2, HUZH455, HUZH-405-1, HUZH1108-2, HUZH-22-4, HUZH-111-8, HUZH-3-2-1, HUZH72087, HUZH470, HUZH393, DMR-113, HUZH-2A-1
II	1	HUZH-88-3
III	7	HUZH-53-10, CML-163, LM-13, CML-41, HUZH-100-10, HUZH637-1, HUZH416
IV	1	HUZH451
V	1	HUZH489

Figure 4.6.3.1 Clustering of inbred lines by Tocher's Method



4.6.4 Intra and Inter-cluster average distance

The five cluster's intra type and inter-cluster distance is presented in Table 4.6.4.1 and illustrated in Figure 4.6.4.1 Intra-cluster average D^2 values ranged from 0 to 13.99. Among the clusters, cluster III the maximum intra-cluster distance (11.08) and the minimum was recorded for cluster I (7.43), while it was zero value for cluster II, IV, and V as they had only a single inbred line each. The minimum inter-cluster D^2 values were recorded between cluster IV and V (9.09) while the highest D^2 value was recorded in-between cluster II and cluster V (13.99) followed by cluster III and V (13.35) and cluster III and cluster IV (13.00).

Table 4.6.4.1 Average intra and inter-cluster distance among seven characters for 35 maize inbred lines

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	<u>7.43</u>	9.74	9.83	10.57	11.06
Cluster II	9.74	<u>0.00</u>	9.62	11.06	13.99
Cluster III	9.83	9.62	<u>11.08</u>	13.00	13.35
Cluster IV	10.57	11.06	13.00	<u>0.00</u>	9.09
Cluster V	11.06	13.99	13.35	9.09	<u>0.00</u>

Figure 4.6.4.1 Intra and inter-cluster distance between inbred lines by Tocher's Method (Not to the Scale)

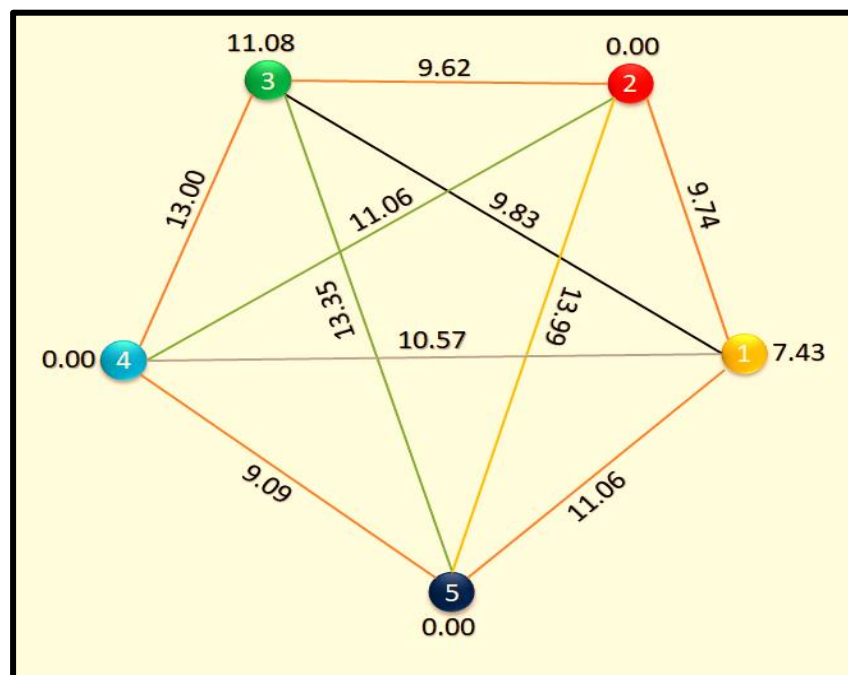
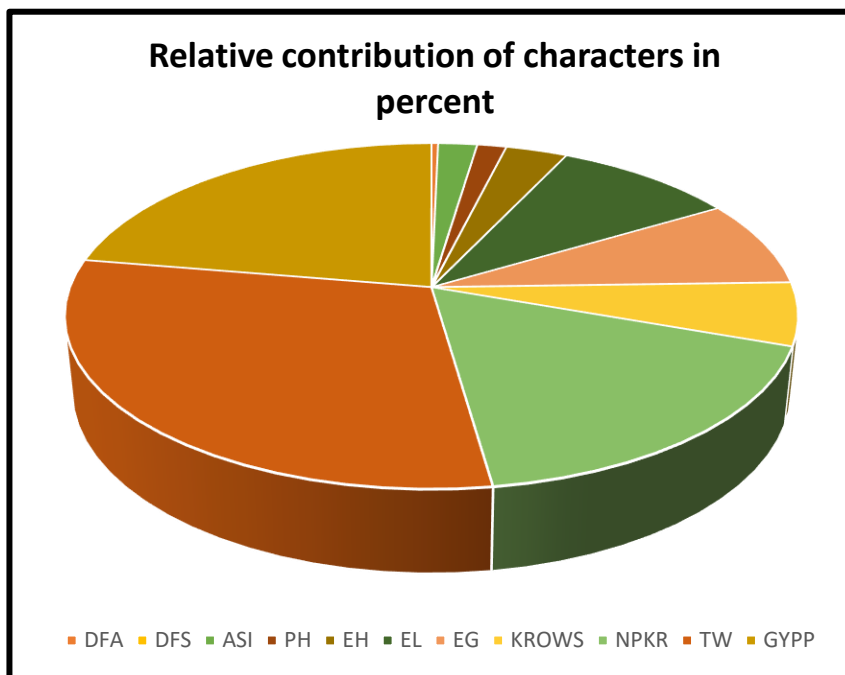


Figure 4.6.6.2 Relative contribution of yield and its contributing characters in percent.



DFS-Days to 50% silking, ASI-Anthesis-silking interval, PH-Plant height, EL-Ear length, EG-Ear girth, KROWS- Number of kernel rows, NPKR-Number of kernels per row, TW- Test weight, GYYP- Grain yield per plot.

4.6.5 Cluster means for various characters

The cluster means for each of eleven characters were furnished in table 4.6.5.1. The cluster mean for days to 50% anthesis ranged from cluster IV (15.00) to cluster II (119.00). Days to 50% flower silking ranged from cluster I (119.04) to cluster II (122.50). Anthesis-silking interval ranged from cluster II (1.50) to cluster IV (3.50). For plant height, cluster means grouped from cluster IV (57.55) to cluster V (112.50). Similarly, for ear height ranged from cluster IV (20.00) to cluster II (41.42). Whereas the ear length ranged from cluster IV (8.34) to cluster V (12.40) and ear girth ranged from cluster III (2.62) to cluster V (3.22). The cluster means for the number of kernel rows ranged from cluster IV (8.00) to cluster II (12.20). The cluster mean for the number of kernels per row ranged from cluster I (21.67) to cluster II (29.27). and for 100 seed weight it ranged from cluster I (23.58) to cluster IV (30.00). Likewise, the cluster means for grain yield per plot ranged from cluster III (0.56) to cluster IV (1.14).

Table 4.6.5.1 Cluster mean for yield and yield contributing characters in 35 inbred lines of maize (Tocher's Method)

	Days to 50% anthesis (days)	Days to 50% flower silking (days)	Anthesis silking interval	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows (No.)	Number of kernels per row (No.)	Test weight (g)	Grain yield per plot (Kg)
Cluster I	116.16	119.04	2.58	77.82	32.15	10.70	2.80	10.09	21.67	23.58	0.64
Cluster II	119.00	122.50	1.50	69.57	41.42	11.08	3.15	12.20	29.27	26.54	0.92
Cluster III	115.39	118.79	1.93	81.48	32.45	11.51	2.62	10.86	25.29	24.65	0.56
Cluster IV	115.00	118.50	3.50	57.55	20.00	8.34	3.00	8.00	26.50	30.00	1.14
Cluster V	118.00	121.00	2.50	112.50	27.50	12.40	3.22	9.00	26.50	24.56	0.97

4.6.6 Relative contribution of characters towards diversity

The relative contribution of eleven characters towards diversity is presented in table 4.6.6.1. and figure 4.6.6.2.

Table 4.6.6.1 The relative contribution of yield and its contributing characters to genetic diversity in 35 inbred of maize

Source	Times ranked first	Contribution %
Days to 50% anthesis (days)	2	0.34%
Days to 50% silking (days)	0	0.00%
Anthesis silking interval	12	2.02%
Plant height (cm)	9	1.51%
Ear height (cm)	19	3.19%
Ear length (cm)	56	9.41%
Ear girth (cm)	48	8.07%
No. of Kernel rows (No.)	35	5.88%
No. of kernel per row (No.)	103	17.31%
Test weight (g)	178	29.92%
Grain yield/plot(Kg)	133	22.35%

The characters appeared in the first rank more to contribute towards diversity. Among all the characters, test weight contributed the maximum (29.92%) to the diversity by taking the first rank 178 times, followed by grain yield per plot (22.35%) with 133 times ranked first, a number of kernels per row (17.31%) with 103 times ranked first, ear length (9.41%) with 56 times ranked first, ear girth (8.07%) with 48 times ranked first, and a number of kernel rows (5.88%) with 35 times ranked first.

Other characters viz., ear height, anthesis-silking interval, plant height, days to 50% flower anthesis, and days to 50% flower silking contributed 3.19, 2.02, 1.51, 0.34, 0.00 percent, respectively to the total genetic diversity.



DISCUSSION

In the present investigation, work has been made to accomplish information on hereditary variation, correlation coefficient, path analysis, and genetic diversity in 35 inbred lines of maize. The information about variation is needed to begin any crop improvement program. As phenotypic change contains both genotypic and environmental variances, it doesn't give a dependable estimate of plausible gain through the selection and thus it is important to separate phenotypic variance to get the heritable part of variance and considering this for outlining crop improvement methodologies to understand a marked improvement in crop yield. To upgrade grain yield is the basic aim of the vast majority of the crop improvement programs. But the yield is a complex character influenced by different ascribing characters. Along these lines, information on the relationship of yield ascribes and their direct and indirect consequences for grain yield is of fundamental significance. Genetic divergence between the inbred lines is pre-essential for their use in the hybridization program. The greatest variation within the segregating generation can be achieved distinctly through the hybridization of diverse parents. In the current study, the genetic divergence was assessed in a set of 35 inbred lines by utilizing Mahalanobis' D^2 -statistics to identify the variety among maize inbred lines. The outcomes acquired from the research work directed with 35 maize inbred lines with eleven characters have been discussed herein references of observations given by previous works on maize.

5.1 Analysis of variance and mean performance of 35 inbred lines

From the analysis of variance, it was obtained that all the 35 inbred lines differed significantly for all the eleven characters which were understudies and are presented in table 4.4.1. Many scientists also demonstrated that the presence of variability for different quantitative characters in and amongst the maize inbred lines. Those investigations are in favor of the findings of **Sravanthi *et al.*, (2017); Sesay *et al.*, (2016), and Bello *et al.*, (2012).**

The inbred lines HUZM68-1, HUZM470, HUZM416, HUZM-2A-1 and LM-13 (112 days) had taken fewer days to 50% anthesis and inbred lines HUZM68-1, HUZM470 and HUZM-

2A-1 (115 days) had taken minimum days to 50% silking along with this HUZM68-1, HUZM491, HUZM-1-13, HUZM-328, CML-163, HUZM642-1, HUZM72087, HUZM9043A, HUZM-3-2-1, HUZM-94, MM-721-2, HUZM-4-32, HUZM455 and HUZM-44-111 had taken minimum days (2 days) to anthesis-silking interval suggesting the potential of these inbred lines to be used for early flowering in a breeding program. HUZM-44-111 (38.94 cm) and HUZM498 (112.5 cm) are the shortest and tallest inbred lines respectively.

Ear length was highest in inbred lines HUZM-22-4 (14.84 cm), HUZM637-1(13.64 cm) and smallest in inbred lines HUZM9043A (7.30 cm) and CML-41 (7.805 cm). The maximum and minimum ear diameter was exhibited by DMR-113-1 (2.2 cm), HUZM470 (2.3 cm), HUZM-1-13(2.3 cm), HUZM-100-10 (2.3cm) and HUZM-22-4 (3.25 cm), HUZM-3-2-1 (3.25 cm) respectively. The maximum mean performance for ear height was observed in inbred line HUZM-4-32 (48.4 cm), HUZM-88-3 (41.415 cm) and HUZM256 (41 cm). The inbred lines CML-163 and HUZM642-1 recorded the highest number of kernel rows per cob, and the inbred lines also for the highest number of kernels per row. The highest mean performance for 100 seed weight was recorded by inbred lines LM-13(34.39), HUZM451(29.99), HUZM470 (28.55). Grain yield per plot was found to be highest for inbred lines HUZM451 (1.12 Kg), HUZM470 (0.94 Kg), HUZM455 (0.94 Kg) and HUZM-100-10 (0.94 Kg) with a capacity to yield per plot. The sufficient number of variations in different yield contributing character were also observed by many researchers namely **Thapa Magar *et al.*, (2021)** and **Bal Krishna *et al.*, (2021)**.

5.2 Genetic variability, heritability, and genetic advance

The presence of variability among the inbred lines is the primary criterion, for any crop improvement program because the viability of selection is determined by the extent of genetic variation which is heritable. Subsequently, parameters like PCV, GCV, heritability and genetic advance will be useful for assessing heritable genetic variation and for outlining better breeding programs.

In the present investigation, the values of the phenotypic coefficient of variation are higher than their corresponding genotypic coefficient of variation for the characters viz. days to 50% anthesis, days to 50% silking, anthesis silking interval, plant height, ear height, ear length, ear diameter, number of kernel rows, number of kernels per row, and 100 seed weight along with

grain yield per plot. These discoveries were like the result of **Chauhan *et al.*, (2010); Dar *et al.* (2018); Shanthi *et al.* (2011), and Bartula *et al.* (2019)**. The characters grain yield per plot followed by anthesis silking interval, ear height, plant height, number of kernel rows, number of kernels per row, 100 seed weight, number of parts per line, and plant stature recorded highest values of PCV esteems. The characters *viz.* grain yield per plot, anthesis silking interval recorded the maximum values of GCV. Similar discoveries were accounted for by **Shanthi *et al.* (2011) and Bartula *et al.* (2019)**. Though the characters like days to 50% flower anthesis, days to 50% flower silking had low values of PCV and traits *viz.* days to 50% flower anthesis, days to 50% silking, ear diameter showed low GCV exhibiting that selection for these traits will be somewhat less viable. Some of these discoveries are by the investigations of **Chauhan *et al.*, (2010) and Dar *et al.* (2018)**.

Almost all the characters considered in the experiment showed the less difference between the PCV and GCV values indicating that there is less impact on the environment in the expression of these characters suggesting selection of these character should be rewarding. And also, other variability parameters like heritability and genetic advance showed moderate to high value provided same result as discussed earlier by **Sandeep *et al.*, (2015)**. So that in these characters other variability parameters like heritability may also be taken into consideration.

GCV, explained by **Burton (1952)**, is an index for estimating genotypic variation present in the population. The broad sense heritability is the ratio between genotypic and phenotypic variation for the characters and subsequently, it is significantly much more reliable and helpful in deciding selection strategies.

In the current study low broad sense heritability along with low genetic advance as percent of mean has been recorded for the characters under investigation *viz.*, days to 50% anthesis, days to 50% silking. Similar reports were also made by **Yanhua *et al.*, (1999) and Bartula *et al.*, (2019)**

5.3 Correlation coefficient analysis

Correlation coefficient analysis gives the idea regarding the degree and direction of the relationship between the different traits and between component character and grain yield. Characters display association due to pleiotropic or linkage, if the linkage is between two

desirable traits it will be useful for the plant breeder since selection for one character prompts the improvement of the other trait simultaneously. As grain yield is a complex trait governed by many genes and relies upon many factors for its expression, selection for yield isn't always efficient and productive. Hence, it is highly desirable to incorporate the yield contributing attributes that show a positive and significant relationship with grain yield for yield improvement.

The correlation analysis showed that the grain yield per plot had a positive and significant correlation with the number of kernel rows, number of kernels per row and 100 seed weight. However, it showed a negative and non-significant correlation with plant height, ear height. Also, positive and non-significant relation with days to 50% anthesis, days to 50% silking, anthesis-silking interval, ear length and ear girth. At the genotypic level the positive and significant correlation with grain yield per plot was observed with days to 50% anthesis, days to 50% silking, anthesis silking interval, ear girth, number of kernel rows, number of kernels per row, and test weight while ear length showed a non-significant positive correlation. The other characteristics such as plant height showed a negative non-significant association. However, ear height showed a significant negative correlation with grain yield per plot. A similar result was found in the works of **Reddy and Jabeen (2016); Raghu *et al.*, (2005) and Amini *et al.*, (2013).**

At phenotypic level days to 50% anthesis, days to 50% silking showed, anthesis-silking interval and ear girth showed a positive and non-significant correlation with plant height, ear height, ear length, ear girth, number of kernel rows, number of kernels per row, and grain yield per plot. However, a non-significant negative correlation with grain yield per plot was showed by plant height and ear height. a significant positive correlation with number of kernel rows, number of kernels per row. Similar results were found in the work of **Xio *et al.*, (2015) and Rafiq *et al.*, (2014).**

5.4 Path coefficient analysis

Path coefficient analysis differentiates the correlation coefficient into direct and indirect effects and therefore gives accurate information about whether the association of traits with grain yield per plot is because of direct effect or due to indirect effect through other component character and hence beneficial in indirect selection. This analysis was first

discovered by **Wright (1921)** and first applied for plant selection in crested wheatgrass by **Dewey and Lu (1959)**. It measures the direct and indirect contribution of the independent variable on the dependent variable and helps the breeder in determining the yield components.

The path coefficient analysis was employed to work out direct and indirect effects. At the phenotypic level traits such as days to 50% anthesis (0.068), days to 50% flower silking (0.091), anthesis silking interval (0.228), ear length (0.126) and ear girth (0.226) showed a positive non-significant direct effect on grain yield per plot. While the non-significant negative indirect effect was found for plant height (-0.027) and ear height (-0.171) on grain yield per plot. However, characters like number of kernel rows (0.336**), number of kernels per row (0.438**) and 100-seed weight (0.356**) showed a strong positive and significant direct effect on grain yield per plot. While, at the genotypic level traits such as days to 50% anthesis (0.831**), days to 50% silking (0.740**), anthesis silking interval (0.323**), ear girth (0.303*), number of kernel rows (0.352**), number of kernels per row (0.516**), and 100 seed weight (0.370**) showed a strong positive significant direct effect on grain yield per plot. While the non-significant positive indirect effect was found for ear length (0.071). However, ear height (-0.664**) showed direct negative and significant effect on grain yield per plot **Pavan et al., (2011); Nemati et al., (2009) and Rani et al., (2017)**.

Days to 50% anthesis showed indirect positive effect on grain yield per plot via days to 50% silking, anthesis-silking interval, ear length, ear girth, number of kernel rows, number of kernels per row and indirect negative via days plant height, ear girth and test weight. Days to 50% silking showed indirect positive effect on grain yield per plot via anthesis-silking interval, ear girth, number of kernel rows and number of kernels per row and indirect negative via days to 50% anthesis, plant height, ear height, ear length and test weight. Anthesis-silking interval showed indirect and positive effect on grain yield per plot via days to 50% silking, ear height, ear girth, ear length and test weight and indirect negative via traits like days to 50% anthesis, plant height, number of kernel rows. Plant height and ear height showed positive indirect effect on grain yield per plot via days to 50% silking, ear girth and number of kernel rows. It also showed a negative indirect effect on grain yield per plot via days to 50% anthesis. Similar reports were made by **Hepziba et al., (2013); Beiragi et al., (2011) and Saidaiah et al., (2008)**.

Ear girth showed positive indirect effect on grain yield per plot *via* traits like days to 50% silking, anthesis-silking interval, number of kernel rows and test weight. And negative and indirect effect days to 50% anthesis, plant height, ear height, ear length and number of kernels per row. Number of kernel rows and number of kernels per row positive indirect effect on grain yield per plot *via* days to 50% silking, ear girth, number of kernels per row, test weight and days to 50% silking, anthesis silking interval, ear height, ear length number of kernel rows and test weight respectively. Test weight showed indirect and positive effect on grain yield per plot *via* traits like days to 50% anthesis, anthesis-silking interval, ear girth, number of kernel rows, number of kernels per row and negative indirect effect on days to 50% silking plant height and ear height. Similar reports were made by **Wannows *et al.*, (2010); Saleem *et al.*, (2007), and rani *et al.*, (2017).**

Days to 50% anthesis showed a positive indirect effect on grain yield per plot *via* traits like days to 50% silking, plant height, ear girth, number of kernel rows, number of kernels per row and negative indirect on anthesis-silking interval, ear height, ear length, and test weight. Days to 50% silking showed an indirect positive effect *via* plant height, ear girth, number of kernel rows and number of kernels per row. While indirect negative effect *via* traits like days to 50% anthesis, ear height, ear length and test weight. Anthesis-silking interval showed a positive indirect effect on grain yield per plot *via* traits like days to 50% anthesis, plant height, ear length, ear girth, number of kernels per row and negative indirect on days to 50% silking and , number of kernel rows. Plant height showed a positive indirect effect *via* characters like days to 50% silking, anthesis-silking interval, ear length, test weight and number of kernels per row. While indirect negative effect *via* traits like days to 50% anthesis, ear height, ear length and number of kernel rows. Ear height displayed a positive indirect effect on dependent character grain yield per plot *via* another character such as days to 50% silking, plant height, ear length, number of kernel rows and test weight. Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis, anthesis-silking interval, ear girth and number of kernels per row. Ear length displayed a positive indirect effect on grain yield per plot *via* days to 50% silking, plant height, ear height, ear girth, number of kernel rows and number of kernels per row. Whereas it showed an indirect negative effect on grain yield per plot *via* days to 50% anthesis (-0.643), anthesis-silking interval and test weight. **Nataraj *et al.*, (2014); Cheng *et al.*, (2002), and Pavan *et al.*, (2011).**

Ear girth displayed an indirect positive effect on days to 50% silking, anthesis silking interval, plant height, ear length, number of kernel rows, 100 seed weight. Whereas it showed an indirect negative effect on grain yield per plot *via* days to 50% anthesis, ear height, and a number of kernels per row. Number of kernel rows displayed a positive indirect effect on dependent character grain yield per plot *via* other characters days to 50% silking, ear height, ear girth and a number of kernels per row. Whereas it showed a negative and indirect effect on grain yield per plot *via* days to 50% anthesis, anthesis silking interval, plant height, ear length and test weight. Number of kernels per row displayed a positive indirect effect on dependent character grain yield per plot *via* other character days to 50% silking, anthesis silking interval, plant height, ear height, number of kernel rows, and 100 seed weight. Whereas it showed a negative indirect effect on grain yield per plot *via* days to 50% anthesis, ear length and ear girth. Test weight displayed an indirect positive effect on days to 50% anthesis, anthesis silking interval, number of kernels per row, ear length, ear girth and number of kernels per row. Whereas it displayed an indirect negative effect on days to 50% silking, ear height and number of kernel rows. These outcomes were in concurrence with the discoveries of **Pallabi Rani Roy *et al.*, (2021)**.

Residual value 0.757(Indicates in this study we were taken ten characters which shows 75% total variation towards grain yield per plot so some missing characters showed the rest of the variation that should be incorporated during the future study.) and **Residual value 0.66** (Indicates in this study we were taken ten characters which shows 66% total variation towards grain yield per plot so some missing characters showed the rest of the variation that should be incorporated during the future study.) in phenotypic and genotypic path coefficient analysis for yield and yield contributing traits.

5.5 Genetic diversity analysis

The evaluation of inbred lines or variety is the first step in any breeding program. D^2 -analysis from Mahalanobis should be sufficient to assess this. It collects information on character contributing towards diversity and assesses the degree of diversification. As a result, Mahalanobis' D^2 -analysis encourages the selection of parents for hybridization from hereditarily distinct groups in various crop improvement programs.

In the current assessment, the D² investigation uncovered the presence of generous diversity in the group of 35 inbred lines of maize. Based on their degree of dissimilarity, the inbred lines were categorized into five distinct bunches. The intra-group distances for clusters II, IV, and V were observed to be zero as it contains just a single inbred line each. Group I showed the most extreme intra-cluster distance with 25 inbred lines followed by group 3 with 7 inbred lines. The inbred lines which are comparable and have a close relationship with others fall into similar groups and the inbred lines which are different and show somewhat more divergence were contained in the various clusters. Along these lines, it very well may be likely that inbred lines gathered together in one cluster were less assorted than those which are situated in the various clusters. Cluster II and V showed the most extreme between-group distance followed by clusters III and V implying that the hybridization between the inbred lines falls in divergent groups would yield better heterosis and positive response in F₂ with the accumulation of desired traits in the subsequent generation.

The greater the distance between two clusters, the higher is the expected genetic advancement between them. Along these lines, the clustering pattern gives the legitimate image of the diversity among the inbred lines and is useful in selecting diverse parents for hybridization programs. In any case, while selecting parents for hybridization programs their yield potential ought not to be disregarded.

An investigation of a cluster means implies uncovered the presence of extensive contrasts in the mean values of various characters. In such manner, Test weight contributed the greatest (29.92%) to the variety by taking the first position in quite a while, trailed by Grain yield per plot (22.35%) with 133 times positioned first, Number of kernels per row (17.31%) with 103 times positioned first and ear length (9.41%) with 56 times positioned first. Ear girth (8.07%) with 48 times positioned first, Number of kernel rows (5.88%) with 35 times positioned first, anthesis-silking interval (2.02%) with 12 times positioned first, Days to 50% anthesis (0.34%) with 02 times positioned first. These outcomes were in concurrence with the discoveries of **Maruthi *et al.*, (2015); Singh *et al.*, (2007); S.B. Singh *et al.*, (2019) and Mamud Aman (2021)** who have likewise researched work on diversity in rice utilizing 43 and 101 inbred lines, respectively.



SUMMARY AND CONCLUSION

Maize (*Zea mays* L.) is a diploid ($2n=20$) and cross-pollinated plant from the Poaceae family (monoecious crop). After wheat and rice, it is the most significant cereal crop. Maize is known as the "Queen of Cereals" because of its great genetic yielding potential, ability to be produced all year in nearly any suitable agro-climatic condition, and has multidimensional utility in our nutritional proportions. Maize has a lot of potential for increased grain yield. For small-holder farmer's maize crop production is critical in generating money, alleviating poverty, and contributing to the local and national economies. It is vitally important for human and animal nutrition as it is a staple food in a lot of industrialized and emerging countries.

In the present study, titled "Assessment of variability, correlation, path analysis, and genetic diversity among inbred lines of maize (*Zea mays* L.)," used 35 maize inbred lines to assess direct selection parameters (variability, heritability, and genetic advance), indirect selection parameters (correlation and path coefficient analysis and genetic diversity) estimation using Mahalanobis' method and other statistical tools. During the *Rabi* season of the year 2020, the research work was carried out at the Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi with two replications, the experiment was carried out in a complete randomized block design. The following characters *i.e.*, Days to 50% anthesis, days to 50% silking, anthesis silking interval, plant height, ear height, ear length, ear diameter, number of kernel rows, number of kernels per row, 100 seed weight, field weight, grain yield per plot were all observed and summarized below:-

- ❖ The analysis of variance revealed that inbred lines differed considerably for each of the eleven characters studied. From the bulk of traits, the inbred lines showed a wide range of variability. This indicated that there is plenty of scope for selecting good inbred lines in grain production improvement. From the current collection of inbred lines. Based on the performance of all inbred lines in two replications, it's noted that inbred line HUZM451 recorded the highest mean performance for grain yield per plot followed by HUZM470, HUZM642-1 and HUZM-100-10 indicating that these inbred lines can be used in hybridization program to achieve desirable increment in yield.

Summary and Conclusion

The earliest flowering was exhibited by inbred lines HUZM68-1 and HUZM-470 and HUZM-2A-1 for both anthesis and silking, suggesting the potential of these inbred lines to be utilized for developing early maturing variety. SCFEMALE and HUZM489 are the tallest and shortest inbred lines respectively, suggesting these inbred lines can be used to develop varieties/hybrids with long and short height. HUZM-22-4, HUZM-3-2-1, and HUZM-22-4, exhibited the highest mean performance for ear girth, ear length. For the both traits number of kernel rows and number of kernels per row HUZM-22-4 and for 100-seed weight LM-13 showed highest mean performance indicating the usefulness of this inbred lines in enhancing grain yield.

- ❖ For the character under study, days to 50% anthesis, days to 50% silking, ear height, ear length, the differences between the PCV and GCV estimates were low, indicating less effect of environment in expression of these characters, suggesting that phenotypic difference may be considered genotypic difference among the inbred lines for selection. While characters like number of kernel rows, number of kernels per row, and test weight showed moderate differences whereas the anthesis silking interval and grain yield per plot showed a large difference between PCV and GCV indicating both inbred lines and environment contribution for the expression of character. Further, low heritability coupled with moderate to high genetic advance as percent of mean of 5% was reported for an anthesis-silking interval, plant height, the height of the ear, ear length, ear girth, number of kernel rows, number of kernels per row, test weight indicating the effectiveness of selection for the improvement of traits. From the study, it is clear that the traits like grain yield per plot, test weight showed the highest value of PCV, GCV, and genetic advance. It is highly suggested to select these traits to attain increased yield. Days to 50% anthesis and days to 50% silking, revealed low PCV, GCV, heritability, genetic advance demonstrating that it is controlled by dominance and epistasis genetic variance which is present in moderate to high magnitude.
- ❖ The correlation analysis indicated that the grain yield per plot displayed a positive and significant association with the following traits number of kernel rows, number of kernels per row and test weight at phenotypic level. days to 50% anthesis, days to

Summary and Conclusion

50% silking, anthesis-silking interval, ear girth, number of kernel rows, number of kernels per row, and test weight at genotypic level. The correlation studied, indicated that maize grain yield can be increased by selecting inbred lines having higher mean values for the above-mentioned traits.

- ❖ The path-coefficient analysis was employed to work out direct and indirect effects. The traits like days to 50% silking, anthesis-silking interval, ear girth, number of kernel rows, number of kernels per row and test weight displayed a strong positive direct effect on grain yield per plot at phenotypic level. However, traits like days to 50% anthesis, days to 50% silking, anthesis-silking interval, plant height, ear girth, number of kernel rows, number of kernels per row and test weight showed a strong positive direct effect on grain yield per plot at genotypic level. While the indirect effect on grain yield per plot was found for days to 50% anthesis, plant height, ear height, ear length and days to 50% anthesis, ear height and ear length at phenotypic and genotypic level respectively.
- ❖ D^2 analysis was carried out to evaluate genetic divergence amongst the inbred lines. Based on the inter-cluster genetic distance, 35 maize inbred lines have been grouped into five different clusters. Cluster I was the biggest comprising 25 inbred lines followed by cluster III had 7 inbred lines, and a single inbred lines was included in cluster II, cluster IV, cluster V each. Cluster III showed the maximum intra-cluster distance followed by cluster I. The inbred lines with close relationships fall in the same cluster and the inbred lines which show relatively more divergence were contained in the different clusters. Cluster II and cluster V showed maximum inter-cluster distance followed by cluster III and cluster V signifying that the hybridization between the inbred lines fall in diverse clusters would yield desirable segregants with the accumulation of favorable genes in the segregating generations.
- ❖ When individual trait contribution towards divergence is concerned, test weight contributes highest towards divergence followed by grain yield per plot, number of kernels per row, ear length, ear girth, number of kernel rows. In the present group of maize inbred lines considered, based on the information obtained from the squared analysis, inbred lines belonging to the more diverse group with higher mean values

Summary and Conclusion

and with desirable traits can be utilized for hybridization program to accumulate favorable alleles and desirable traits into the single background and hence effective in developing improved cultivars.

In conclusion from the present research work, it's uncovered that valuable information on different yield traits in maize improvement. Inbred lines HUZM451, HUZM470, HUZM642-1, HUZM455, and HUZM-100-10 were found to be promising and desirable inbred lines for yield and yield attributing traits and fitting into different genetic clusters (HUZM470, HUZM642-1, HUZM455 in cluster I), (HUZM-100-10 in cluster 3) and (HUZM451 in cluster 4). Hence, these inbred lines can be used as parents in the hybridization program to develop hybrids with better heterosis in F_1 or to obtain potential progressive segregants in later segregating generations. The earliest to anthesis and silking was registered by inbred lines HUZM68-1, HUZM470, HUZM416, HUZM-2A-1 and LM-13 and HUZM68-1, HUZM470 and HUZM-2A-1 respectively. Suggesting that these inbred lines have the potential for evolving as early maturity variety.



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APPENDIX

WEEKLY METEOROLOGICAL DATA: VARANASI, YEAR- 2020-2021

Week No.	Month & Date	Rainfall mm	Temperature °C		R.H. %		Sunshine hours	Evaporation mm
			MAX	MIN	Morn.	Even		
49	Dec 03-09	0.0	27.7	12	93	53	0.9	1.2
50	10-16	0.0	23.9	14.8	93	64	1.8	1.4
51	17-23	3.6	20.5	7.5	91	59	-	1.3
52	24-31	0.0	22.3	7.8	94	49	-	1.2
1	Jan 1-7	0.0	25.4	12.3	90	54	3.3	1.1
2	8-14	0.0	21.7	13.0	92	59	2.3	1.6
3	15-21	0.0	19.4	8.1	95	65	0.2	1.0
4	22-28	0.0	17.5	9.2	95	71	2.2	1.0
5	29-04	0.0	22.3	7.3	96	46	4.5	1.25
6	Feb05-11	0.6	24.6	10.8	91	50	6.5	1.7
7	12-18	0.0	28.4	12.4	90	37	7.6	1.9
8	19-25	0.0	29.0	13.7	85	41	7.3	2.6
9	26-04	0.0	30.7	15.4	79	34	9.1	3.8
10	March 05-11	0.0	32.7	17.0	88	36	6.5	4.5
11	12-18	0.0	32.3	17.7	87	39	4.7	6.3
12	19-25	0.0	34.5	20.7	64	40	4.4	5.1
13	26-01	0.0	36.0	17.8	73	23	5.6	5.6

Appendix

14	April 02-08	0.0	38.8	18.9	74	20	6.5	6.3
15	09-15	0.0	35.3	20.2	60	25	2.9	6.9
16	16-22	0.0	37.3	22.1	58	38	6.0	6.4
17	23-29	0.0	40.7	20.7	-	-	9.8	4.9
18	30-06	0.0	38.9	23.7	54	46	5.2	6.7
19	May 07-13	10.2	36.1	24.5	80	60	6.4	6.3
20	14-20	77.3	37.0	23.7	65	65	4.1	6.3
21	21-27	4.2	33.9	24.1	-	-	6.2	6.0
22	28-03	48.6	33.8	23.8	-	-	4.8	4.2
23	June 04-10	1.6	36.9	27.0	71	55	6.2	4.6
24	11-17	196.6	34.2	25.8	91	71	0.0	2.9
25	18-24	456.7	32.9	25.3	94	86	1.2	2.4
26	25-01	16.4	34.6	26.8	87	71	2.7	3.3
11	12-18	0.0	32.3	17.7	87	39	3.3	1.1
12	19-25	0.0	34.5	20.7	64	40	2.3	1.6
13	26-01	0.0	36.0	17.8	73	23	0.2	1.0
14	April 02-08	0.0	38.8	18.9	74	20	2.2	1.0
15	09-15	0.0	35.3	20.2	60	25	4.5	1.25
16	16-22	0.0	37.3	22.1	58	38	6.5	1.7
17	23-29	0.0	40.7	20.7	-	-	7.6	1.9
18	30-06	0.0	38.9	23.7	54	46	7.3	2.6
19	May 07-13	10.2	36.1	24.5	80	60	9.1	3.8

Appendix

20	14-20	77.3	37.0	23.7	65	65	6.5	4.5
21	21-27	4.2	33.9	24.1	-	-	4.7	6.3
22	28-03	48.6	33.8	23.8	-	-	4.4	5.1
23	June 04-10	1.6	36.9	27.0	71	55	5.6	5.6
24	11-17	196.6	34.2	25.8	91	71	6.5	6.3
25	18-24	456.7	32.9	25.3	94	86	2.9	6.9
26	25-01	16.4	34.6	26.8	87	71	6.0	6.4

Source – Dept. of Agronomy, IAS, BHU.

