GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF WHITE MAIZE (*Zea mays* L.)

GOUTOM ROY

DEPARTMENT OF GENETICS AND PLANT BREEDING
SHER-E-BANGLA AGRICULTURAL UNIVERSITY
DHAKA-1207

JUNE, 2018

GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF WHITE MAIZE (*Zea mays* L.)

BY

GOUTOM ROY

REGISTRATION NO. : 11-04658

A Thesis
submitted to the Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka,
in partial fulfilment of the requirements
for the degree of

MASTER OF SCIENCE (MS)

IN

GENETICS AND PLANT BREEDING

SEMESTER: JANUARY – JUNE, 2018

APPROVED BY:

(Prof. Dr. Jamilur Rahman)
Supervisor

(Prof. Dr. Md. Ashaduzzaman Siddikee)
Co-supervisor

(Prof. Dr. Jamilur Rahman)
Chairman
Examination Committee

Dr. Jamilur Rahman
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Dhaka-1207, Bangladesh
Email: jamilsau@gmail.com
Mobile: 01552323928

CERTIFICATE

This is to certify that the thesis entitled ***'GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF WHITE MAIZE (Zea mays L.)'*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bonafide research work carried out by* ***Goutom Roy****, Registration number:* ***11-04658*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated: June, 2018
Dhaka, Bangladesh

Prof. Dr. Jamilur Rahman
Supervisor

Acknowledgements

First of all, I express my best gratitude to Almighty for His never-ending blessing to complete this work successfully. It is a great pleasure to express profound thankfulness to my respected parents, who entitled much hardship inspiring for prosecuting my studies, thereby receiving a proper education.

I want to express my sincere respect, sincere appreciation and enormous indebtedness to my reverend Supervisor Prof. Dr. Jamilur Rahman, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his academic supervision, helpful commentary and unvarying inspiration throughout the research work and preparation of the thesis.

I wish to express my gratitude and best regards to my respected Co-supervisor, Dr. Md. Ashaduzzaman Siddikee, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his continuous direction, constructive criticism, encouragement and valuable suggestions in carrying out the research work and preparation of this thesis.

I am also profoundly grateful to my honorable teacher Prof. Dr. Jamilur Rahman, Chairman, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for his valuable teaching, direct and indirect advice and encouragement and cooperation during the whole study period.

I am profoundly grateful to my honorable teachers Prof. Dr. Md. Shahidur Rashid Bhuiyan, Prof. Dr. Naheed Zeba, Prof. Dr. Mohammad Saiful Islam, Prof. Dr. Sarowar Hossain and Prof. Dr. Firoz Mahmud, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, for their valuable teaching, direct and indirect advice, and encouragement and cooperation during the whole study period.

I want to thank my friend, Susmita Mondal for her help and inspiration in preparing my thesis. I am pleased to thank all stuffs and workers of Genetics and Plant Breeding Department and all farm labors of Sher-e-Bangla Agricultural University, Dhaka for their valuable and sincere help in carrying out the research work.

I also wish to extend sincere gratitude to the Ministry of Science and Technology, Government of the People's Republic of Bangladesh for providing me financial support to conduct the research.

I found no words to thank my father Bipin Chandra Roy, mother Manada Bala Roy, sister Jharna Rani Roy, Brother Uttam Roy for their unquantifiable love and continuous support, their never-ending sacrifice affection, immense strength and untiring efforts for bringing my dream to the proper shape. They were a constant source of inspiration, zeal and enthusiasm in the critical moment of my studies.

June, 2018 ***The Author***

SAU, Dhaka

GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS OF WHITE MAIZE (*Zea mays* L.)

BY

GOUTOM ROY

ABSTRACT

Seventeen white maize inbreed lines were collected from CIMMYT, Mexico and Bangladesh and laid out in Randomized Complete Block Design (RCBD) with three replications in the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during October, 2016 to April, 2017. Mean performance, variability, correlation matrix and path analysis on different yield contributing characters and yield of maize inbreed line were calculated. The mean performance of the maize inbreed lines showed that the maximum grain yield/plant (170.01 g) was recorded in the genotype of CLTHW15008, whereas the minimum grain yield/plant (44.52 g) was recorded in CLTHW15007. The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the yield contributing traits. In correlation study, significant positive association was recorded for grain yield/plant with base diameter of plant (1.00), leaf breadth (1.00), cob length (0.979), cob diameter (0.930), number of row per cob (0.979), number of grain per row (0.999), 100-grain weight (0.992). Path analysis revealed that plant height (0.412), leaf breadth (0.073), days to 50% flowering (0.280), number of rows per cob (0.462), number of grain per row (0.209) had positive direct effect on yield/plant. Base to cob distance (-0.214), base diameter (-0.614), leaf length (-0.467), days to maturity (-0.262), cob length (-0.725), cob diameter (-0.355), 100-grain weight (-0.472) had negative direct effect on grain yield. In diversity analysis the clustering pattern denoted that, cluster II was the largest cluster comprising of 6 genotypes and cluster III belonged to 4 genotypes of maize. The maximum inter-cluster divergence was observed between cluster I and V (58.22) followed by cluster I and III (48.35). Considering diversity pattern, genetic variability and other agronomic performance CLTHW15008 from cluster I; CLTHW15004, CLTHW15005, CLTHW15006, CLTHW15015 from cluster II might be considered as potential parents for hybridization program for further improvement of the crop.

Table of Contents

List of Tables

List of Figures

List of Plates

List of Appendices

Some commonly used abbreviations

Full word	Abbreviation
Agro-Ecological Zone	AEZ
And others	et al.
Accessions	ACC
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of Variation	CV
Etcetera	etc.
Figure	Fig.
Genotype	g
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	δ^2g
Gram	G
Heritability in broad sense	h^2b
International maize and wheat improvement centre	CIMMYT
Journal	j.
Kilogram	kg
Meter	m
Mean Sum of Square	MSS
Millimeter	mm
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	δ^2p
Randomized Complete Block Design	RCBD
Replication	r
Research	Res.
Sher-e-Bangla Agricultural University	SAU

CHAPTER I

INTRODUCTION

Maize or corn is one of the most important cereal crops providing the primary source of food in many countries of the world. It is grown as a fodder, feed and food crop. It is also used as raw material for manufacturing pharmaceutical and industrial products. Maize is known as “queen of cereal”. Globally, maize ranks third among the cereal crops next to rice and wheat. Rice is the major staple in Bangladesh; however, in a very recent year maize ranks the second position in respect of production and acreage of cultivation in Bangladesh (BBS, 2018).

Maize (*Zea mays* L.) is a tall, determinate annual C4 plant. It is mostly photo-insensitive, cross pollinated cereal crops. The Mesoamerican region is known to the center of origin for *Zea mays* (Matsuoka *et al.*, 2002). Maize is a versatile crop grown from 58º N to 40º S from below sea level to altitudes higher than 3000 m and in areas with (250–5000) mm of rainfall per year (Shaw, 1988) and with a growing cycle ranging from 3 to 13 months. In fact, worldwide the major maize production areas are located in temperate regions.

In Bangladesh, maize production has an increasing tendency with the introduction of hybrid maize varieties since 1993 (BBS, 2018). Area, production, and yield of maize have increased in Bangladesh by 17%, 33% and 16%, respectively (BBS, 2018), which reflects the effect of adopting improved technology. In Bangladesh, maize cultivated about 990 thousand acres of land, and total annual production is 3288 thousand metric tons with an average yield of 3.32 MTha^{-1} (BBS, 2018). Introduction of quality protein maize (QPM) in Bangladesh is a long aspiration to feed the million malnourished populations. Thus, maize should get priority considering the protein malnutrition of the people because it contains more digestible protein than the other cereals (Ahamed, 2010).

Maize is grown as grains as well as a fodder crop, although it has been cultivated in limited area ranking 2nd most important cereal crops in Bangladesh. As a food, it can be consumed directly as green cob, roasted cob or popped grain. Maize grain can be used for human consumption in various ways such as cornmeal, cooked grain and flour. Its grain has high nutritive value containing 66.2%, starch 11.1% protein, 7.12%

oil, and 1.5% minerals. Moreover, 100 g maize grains contain 90 mg carotene, 1.8 mg niacin, 0.8 mg thiamin, and 0.1 mg riboflavin (Chowdhury and Islam, 1993). Maize oil is used as the best quality edible oil. Green parts of the plant and grain are used as the feed of livestock and poultry. Stover and dry leaves are used as good fuel (Ahmed, 1994). The important industrial use of maize includes in the manufacture of starch and other products such as glucose, high fructose sugar, maize oil, alcohols, baby foods, and breakfast cereals (Kaul, 1985).

In Bangladesh, the cultivation of maize was started in the late 19th century, but the crop has started to gain the momentum as the requirement of maize grain is being increased as poultry industry flourishes in Bangladesh. Stem and foliage of maize plant can be used as livestock feed. Stalk, dry leave covering of cobs (husks) and shelled cobs can be used as fuel (Ahmed *et al.,* 2011). It can be grown all the year round in Bangladesh and fitted in the gap between the main cropping seasons without affecting the major crops. It can also be grown in flood prone areas under no tillage, and with no inputs (Efferson, 1982). With its multipurpose properties, it undoubtedly plays a vital role in reducing the food shortage around the world, especially in Bangladesh.

With the growing population and rising income, demand for food is on the increase in one hand and shrinking of agricultural land due to urbanization, industrialization, and infrastructure development on the other side. Therefore, growing food keeping pace with the demand faces unprecedented challenges while raising the yield and production of rice remains questionable (Dass, 2012). It is against the backdrop, introduction of white maize in Bangladesh as human food can be a viable alternative for sustaining food security given the productivity of maize much higher the rice and wheat (Ray, 2013).

Maize is well adapted to the climate and soils of Bangladesh. Since the early 1990s, the Bangladesh maize area has increased at an average rate of 20% per year to reach 990 thousand acres of land producing 32.88 lac MT tons of grains in 2017-2018 (BBS, 2018). Rice-maize cropping system has been expanded rapidly in the northern districts of Bangladesh (Timsina, 2010) mainly in response to increasing demand for poultry feed (Ali, 2009). Besides higher market of maize grains in the poultry industry has opened up an ample opportunity to cultivate hybrid maize throughout the whole country.

In Bangladesh, maize is being cultivated for a long time. Previously sporadic attempts were made to accelerate maize production. But few efforts were made to develop the improved and adapted variety of white maize. For example, till date, only two white maize hybrid verities viz., BARI White maize-12, and BARI white maize-13 have been released by BARI. White maize is generally considered as a food crop and there is enormous demand in the Bangladeshi market due to its diversified usage in food industries Market prices are usually higher for white maize compared to the yellow type. Besides, white maize has a medium GI (Glycemic Index), which help in reducing obesity.

For developing of the new and potential white maize hybrid varieties in Bangladesh, we have collected germplasms from CYMMIT and research institutions of Bangladersh. These germplasm needs to charaterize in view of genetic variability, heritability, and estimation of their genetic diversity among the collected germplasm. Knowledge of genetic diversity of germplasm is essential for long term success of the breeding program and maximizes the exploitation of these germplasm resources. Again, the selection criteria may be yield or one or more of the yield component characters, which is needed to be determined.

We, therefore having the above scheme and research goal in mind, the investigations were conducted to determine the genetic variability, character association, and diversity among the collected white maize germplasms the following objectives were addressed.

i. To study the genetic variability as well as genetic diverisity among the collected germplasms of white maize;
ii. To analyze the correlation and path coefficient analysis among the yield contributing traits; and
iii. To select the best and diverse inbred line(s) of white maize for future hybridization program.

CHAPTER II

REVIEW OF LITERATURE

Maize constitutes as third important cereal crop which has received much attention of research workers regarding improvement of maize through manipulations of qualitative and quantitative characters all over the world. Various investigators at home and abroad worked with different maize lines and studied their performance regarding the characterization and diversity of maize. Many studies on the growth, yield, variability, correlation, heritability and genetic advance have been carried out in many countries of the world. The work so far done in Bangladesh is not adequate and conclusive. Nevertheless, some of the important and informative works and research findings so far been done at home and abroad on this aspect have been reviewed in this chapter under the following headings:

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation co-efficient and path analysis

2.3 Genetic diversity

2.1 Genetic variability, heritability and genetic advance

Maize displays an orderly sequence of development of yield components namely number of ear per plant, number of grain per row, number of row per ear and hundred grain weights reported by Viola *et al*. (2004);

Babu *et al*. (1996); reported the performance of South African maize varieties Ksheeramrutha with Deccan 101, grown at Karnataka. Ksheeramrutha results fast growing, tall and high yielding, leafy compared with the other genotypes tested. Its fodder was good quality, higher protein content. Mixtures of black soya and cowpeas performed well. Finally it was released for cultivation in Karnataka in 1989.

Grzesiak (2001), observed considerable variability among maize genotypes for different traits. Ibsan *et al*. (2005) also reported significant genetic differences for morphological parameter for maize genotypes.

Naushad *et al*. (2007); conducted an experiment to observe the magnitude of genetic variability in maize genotypes for yield and yield components and significant variability was assessed for ear length, grains rows per cob, cob weight, grain moisture content, 300-grains weight and grain yield.

Shanthi *et al*. (2011); found that grain yield and its component characters viz., total anthers dehiscence period, total period of silk appearance, active pollination period, number of grains per cob, cob weight, protein yield and oil yield had expressed high estimates of GCV and PCV and high heritability (more than 85%) coupled with high genetic advance, indicating the genetic variances for these traits probably owing to their high additive gene effects. Hence, it was inferred that direct selection was a better scope for improvement of these traits.

Farhan *et al*. (2012); revealed that testcrosses differed significantly for all the characters studied except days to 50% anthesis, days to 50% silk emerging and ASI. The Genotype x environment interaction was also significant for all the traits except for cob length.

Praveen *et al*. (2014); revealed that the mean sum of squares due to genotypes showed significant variation for all the 12 characters studied. Traits yield per plant, plant height, ear height, number of grains per row, 100-grain weight were shown high heritability accompanied with high to moderate genotypic and phenotypic coefficient of variation and genetic advance which indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Whereas high to moderate heritability along with low estimates of genetic advance were observed for days to 50% tasseling, days to 50% silk emerge, shelling percentage, ear length and days to maturity ear girth and number of grain rows per cob.

Abel and Pollak (1991), evaluated test crosses of exotic maize accessions with several testers. In the experiment they found highly significant variations among test crosses for ear height. While Genter and Alexander (1965) results after testcross evaluation are in disagreement with this results. In their study test crosses of Va31xHy with CBS were not significantly different for ear height.

Rahman (2008); used 41 maize populations which were evaluated for plant height, ear height, number of tassel branches, days to 50% anthesis and days to 50% silk emergence. Significant amount of variability was observed among these populations for all the traits. A wide range of variability was found among these populations through cluster analysis that could be utilized in breeding programs.

Wannows *et al*. (2010); obtained that all estimates of additive (VA) and dominance (VD) variance were significant for all characteristics with exception of additive variance for specific leaf weight, And dominance variance for leaf area index, plant and cob height, cob length and number of grain per row. However the magnitude of VA was consistently larger than that of VD for all characteristics with exception of specific leaf weight, silk emergence date, stay green, 100- grain weight and grain yield where VD values were larger than VA values.

Amer and Mosa (2004),reported that heritability estimates in narrow sense were 44% for silk emergence date, 39% for plant height, 44% for ear height, 27% for ear length, 31% for ear circumference, 29% for number of rows per cob, 23% for number of grain per row and 36% for grain yield.

Breeders are interested in screening and development of open pollinated population in maize. Ishaq *et al*. (2015); showed highly significant differences ($P \leq 0.01$) for all the traits. The highest values for plant height (169.1 cm), ear height (75.13 cm), leaves per plant (11.33), flag leaf area (106.5 cm), grain rows per cob (13.67) and grain yield (5927 kg/ha) were recorded for Jalal-2003. Broad sense heritability (h2b) ranged from 0.29 to 0.95 for various traits. Among the tested populations Jalal-2003 proved to be superior for most of the traits studied. The study revealed a considerable amount of genetic variation and heritability estimates that could be manipulated for further improvement in maize breeding.

Number of grain-rows per cob is variable within and among the varieties of maize (Evans, l975). Begum and Roy (1987), reported that yield variation among the varieties were due to varietal characteristics.

Guaria 8045 gave significantly higher grain yield (5.15 t/ha), whereas Pirsabak 8146, LaMaquina and Khoibhutta produced grain yields of 4.50, 5.07 and 4.00 t/ha respectively (Anonymous 1987).

Pavlov *et al*. (2003); used a half diallel cross to evaluate combining abilities of six maize inbred lines and their hybrid combinations. General and specific combining ability (GCA and SCA) mean squares were significant for all traits. GCA/SCA ratios revealed that additive gene effects had larger importance of all investigated traits in inheritance than non-additive effects. The hybrid combinations those exhibited significant SCA effects involved low x high, average x high and high x high GCA parents.

Ear length is an important yield component for maize and had a direct effect on grain yield (Sehata, 1975; Jha *et al*., 1979 and Subramanin *et al*., l98l). BARI (1990), reported that cv. Bamali gave more ear per plant than Khaibhutta.

Ogunniyan and Olakojo (2014), found significant variation existed in all the characters. The coefficients of variation were low except for ear weight and grain yield that were relatively higher. The anthesis silk emergence interval was highest in lines TZEI 124 and TZEI 16. The characters were less influenced by the environment thus the traits can be used for selection. Heritability was greater than 80% for all characters studied whereas expected genetic advance ranged from low (8.91) in days to silk emergence to high (72.03) in number of ear per plant. Days to anthesis and silk emergence, plant height and number of leaf per plant were positively correlated. Grain yield was positively correlated with ASI, plant and ear heights, number of leaf per plant and leaf area.

Studies were carried out by Umar *et al*. (2015); to estimate the extent of genetic variability in fifty six maize (*Zea mays* L.) genotypes (six drought tolerant inbred lines, seven other inbred lines, 42 crosses and a check) under non-stress and water stress at flowering. The genotypes were evaluated in 2012/2013 dry season across two locations to obtain more information on their genetic and morphological diversity. The experimental design was simple lattice design with two replications under each condition. Significant mean squares were obtained for the seven traits measured under non-stress and water stress in the combined analysis across locations.

Lee *et al*. (1986); analyzed data on maize yield (grain weight per plant) and eight agronomic traits from an 8×8 diallel cross. Significant heterosis and heterobeltosis were observed for all characters except days to harvest. Heterosis took the form of incomplete dominance (additive variation) for plant height and over dominance (non additive variation) for other characters.

Ganguli *et al*. (1989); got a total of 33 interoperation hybrids from crosses between 11 female and three male lines. Positive heterosis over the better parent was observed for grain yield, ear insertion height, plant height, days to maturity and days to silk emergence.

Debnath (1991a); studied heterosis over mild parent and better parent in a 36 hybrids involving nine maize inbred for grain yield, earliness (days to silk and grain moisture) plant height and ear height. Significant and positive heterosis over mid and better parent for yield was observed in thirteen and eight crosses respectively. For days to silk, significantly negative heterosis was exhibited by twelve crosses over mid parent and eight crosses over better parent. None of the crosses possessed negative and significant heterosis for rest of the characters studied.

Debnath (1992); studied heterosis in a 10×10 dialled cross of maize inbreeds and reported that heterobeltosis for grain yield varied from 38.56 to 71.60 percent. Positive and significant heterobeltosis were also observed in cob length, cob diameter, and grain rows per cob, number of grains per row and 1000-grain weight.

2.2 Correlation co-efficient and path analysis

Genotypic and phenotypic correlation determination is the basic step in the formulation and implementation of various breeding programs. The correlation among traits is also important for successful selections to be conducted in breeding activities. Again analysis of correlation coefficient is the most widely used one among several methods that can be used (Yagdi and Sozen, 2009).

Experiment conducted by Debnath (1991b); with 23 fourth generation lines of maize showed that grain yield was positively and significantly correlated with plant height, ear height, ear diameter and grain rows per cob, number of grains per row and 1000-grain weight.

Kumar *et al*. (2014); revealed that positive and significant phenotypic correlations were recorded for grain yield in association with plant and ear height, ear length and diameter, number of grains row per ear and grains per row and 100 grains weight except maturity traits which showed negative association with grain yield. The result obtained from path analysis showed that days to 50% tassel had highest magnitude directly effect on grain yield per plant followed by ear height, 100 grains weight and ear circumference.

When major yield characters are positively associated then breeding would be very effective. But when these characters are negatively associated, it would be difficult to practice simultaneous selection for them in developing a variety reported by Nemati *et al*. (2009).

AL-Ahmad (2004); Aydin *et al*. (2007) and Najeeb *et al*. (2009) found positive and significant correlation between grain yield and each of plant height, number of rows per cob, number of grain per row and 100-grain weight and emphasized the role of these traits in selection of high grain yield in corn also indicated that the correlation values were positive and significant between grain yield and each of ear circumference, ear length and number of grains per row. It also revealed that sources of variation in plant yield were the direct effects on both number of grains per row and ear circumference.

A field experiment was conducted by Begna *et al*. (2000); on clay loam soil at the E. A. lodes Agronomy Research Center, Ste. Anne de Bellevue, Quebec. Hybrids were set in a randomized complete block design including 11 newly developed leafy reduced stature (LRS), four non-leafy reduced-stature (LMBL) hybrids. One is conventional (Pioneer Brand 3979) and one late maturing big leaf (LMBL). Generally above-ground dry matter was greater for the taller LMBL and Pioneer Brand 3979 than for the shorter hybrids during both years. But greater grain yields were measured for both the tallest and five of the 11 LRS hybrids. Moreover grain yields averaged over canopy groups were not different. The shorter hybrids had greater assimilate allocation to the grain than the taller (especially LMBL) hybrids and this was evident in their harvest index values. However, within the LRS group, hybrids differed for both dry matter and grain yield with some being similar to the NLRS hybrids while others were similar to the taller pioneer Brand 3979 hybrid.

For better identification the required traits in some generations the selection was carried out by Virk *et al*. (2005); on a research farm under fertility levels that approximated farmers' practice. The improvement of the subpopulations resulted in several varieties that performed well in research station and on-farm trials. One of them BVM-2 was released in Jharkhand state of India. In multi-locational research station trials, it produced more than the control variety BM 1 but silk emergence was earlier. In the less favorable environments of on-farm trials, its yield superiority was higher in percentage. Farmers perceived BVM-2 to have better grain quality and stoves yield than the local varieties. BVM-2 was specifically bred to meet up the needs of the clients (resource-poor farmers with no access to irrigation) and conceived earlier maturity combined with higher grain yield. The outputs were higher from this highly client-oriented approach than by classical breeding. Uptake was faster as a result of research and extension being done in tandem beyond the reason.

It was found by Singh and Nigam (1977) that 1000-grain weight and grain rows per cob had positively direct effect on grain yield. Pande *et al*. (1971), observed that 100-grain weight was positively correlated with grain yield. Onn (1988), observed plant height significantly correlated with cultivar.

Field trials were initiated in 16 localities of Italy (of which three were conducted in Friuli-Venezia Giulia) to compare performance of 56 hybrids of FAO maturity groups 500, 600 and 700 by Barbiani *et al*. (2008). The final stage of the trials was conducted in 11 localities with medium late hybrids compared with 30 early hybrids of which 17 belonging to the maturity group

Information is gathered on soil characteristics, irrigation, cropping systems, use of fertilizers, herbicides and control of Pyralidae with Contest [alpha-cypermethrin]. Data are presented on plant height, grain humidity level at harvest, hectolitric weight and yield of hybrids belonging to maturity groups 300, 400, 500, 600 and 700 which ultimately showed significant differences.

Bikal and Deepika (2015), showed that traits plant height, cob height, cob length, cob girth, cob weight, number of grain row per cob, number of grain per row exhibited positive and highly significant correlation with grain yield per hectare and five hundred grain weight were given significant correlation. The analysis also indicated that days to 50% tasseling and days to 50% silk emergence explained negative and highly significant correlation with grain yield per hectare. Similarly, days to maturity showed negative and insignificant correlation with grain yield per hectare.

Bahoush and Abbasdokht (2008), showed that number of grains per cob and 100 grain weights had highly positive effects. Also cob length had positive and moderate direct effect on yield. Furthermore, ear height had low and negative direct effect on grain yield.

According to Kwaga (2014); maize grain yield correlated positive with plant height, cob length, cob diameter and 100 grains weight; but related negatively with days to 50% tasseling. The four characters that correlated positively to grain yield also associated positively to each other throughout the experiment.

Mohan *et al*. (2002); studied path analysis on corn cultivars (169 cultivars) for grain yield and oil content and resulted that number of grain per row, 100 grain weight, number of grain row and cob length had direct effect on grain yield. It was revealed that cob height, plant height and number of days until 50% tasseling had most minus direct effect on grain yield. Devi *et al*. (2001); reported that ear length, number of grain rows per cob, number of grains per row and 100-grain weight positively influenced the yield both directly and indirectly through several components.

Mohammadi *et al*. (2003); reported that 100-grain weight and total number of grains per cob revealed highest direct effects on total grain weight, while cob length, ear circumference, number of grain rows and number of grains per row were found to fit as second-order variables. Geetha and Jayaraman (2000), reported that number of grains per row exerted a maximum direct influence on grain yield. Hence, selection of number of grains per row will be highly effective for improvement of grain yield.

Khazaei *et al*. (2010); reported that 100-grains weight and number of grain had the highest direct effect on grain yield. However, the study carried out by Selvaraj and Nagarajan (2011) revealed that direct selection for ear length and numbers of rows per cob are effective for yield improvement. The same author stated that, the positive direct and indirect effects of a trait on grain yield make it possible for its exploitation in selection under specific conditions.

It was revealed by Mustafa *et al*. (2014); that the fresh shoot length had maximum direct effect on fresh root length followed by root density, dry shoot weight, leaf temperature and dry root weight. It may be concluded that fresh root length, dry shoot weight, root density, leaf temperature and dry root weight are the major contributing characters for the fresh shoot length of maize seedlings. These traits had reasonable heritability estimation. Thus selection could be made for high yielding maize genotypes on the basis of these traits.

In an experiment carried out by Bello *et al*. (2010) positive and significant phenotypic and genotypic correlations were found for days to 50% tasselling with plant and ear height and grain yield with plant height, number of grains per ear and ear weight. Positive and significant environmental correlation was also recorded for grain yield with plant and ear height and ear weight. The path analysis revealed that days to 50% silk emergence, ear weight and number of grains per cob had the highest direct effect on grain yield while number of grains per cob had the highest moderate indirect negative effects on grain yield. Days to flowering, plant and ear height, number of grains per ear and ear weight could be the important selection criteria for the improvement of open pollinated maize varieties and hybrids in terms of high grain yield.

Days to 50% tasselling and number of grain rows per cob showed negative indirect association with all traits towards grain yield. Study revealed that direct selection for these traits would be effective. Days to 50% silk exhibited negative direct effect on grain yield indicated that selection for high yield could be done by indirect selection through yield components. (Pavan *et al*., 2011; Venugopal *et al*., 2003)

2.3 Genetic diversity

The importance of genetic diversity in selecting genetically diverse parents either to exploit heterosis or getting desirable recombinants has been stressed upon by many researchers (Murthy, 1966; Joshi and Dhawan, l966). It is a powerful tool in quantifying the degree of divergence among biological population based on multiple characters. Genetic diversity is essential to meet the diverse goals of plant breeding such as producing cultivars with increased yield (Joshi and Dhawan, 1966), wider adaptation, desirable quality, pest and disease resistant (Nevo *et al*., 1982).To identify specific parents for realizing heterosis and recombination in breeding program mostly genetic divergence analysis is attempted so far.

Singh and Chaudhari (2001); evaluated fifty-five inbred lines for genetic divergence. The 55 inbred were grouped into 5 clusters. Among these, cluster had the maximum number of 16 inbred followed by clusters IV and V with 11 and 10 inbred respectively. Clusters I and II consisted of 9 inbred each. The highest inter-cluster distance was observed between clusters I and IV. As a consequence, it was indicating wide range of genetic diversity between them. The least inter-cluster distance was between clusters III and V that might be indicating the genetic closeness between the inbred of these clusters.

A study was conducted by Rafalski *et al*. (2001) with the help of PCR to evaluate the genetic diversity of maize germplasm. Twenty-two inbred lines representing early flint and dent types were evaluated for genetic distance based on analysis of 554 DNA fragments amplified using 25 primers from 10 to 18 bases in length. Cluster analysis based on above data resulted in a separate grouping of flint and dent inbred. Based on the result of cluster analysis five dent and four flint inbred were selected for evaluation of the performance of 36 single crosses.

Khumkar and Singh (2002); observed significant diversity among the inbred lines developed from the same or different source populations. The inbred lines were grouped into six clusters. The greatest intra-cluster distance was recorded for cluster IV whereas the greatest inter-cluster distance was observed between cluster III and V. Among the characters evaluated peduncle length, plant height and number of primary branches, 100-grain weight, ear circumference and number of grains per row had the greatest contribution towards genetic divergence.

Drinic *et al*. (2002); used twelve maize inbred lines by Simple Sequence Repeats (SSR) as molecular markers to analyze the genetic relationship among inbred lines and to predict heterosis in their respective crosses. Genetic distances for 66 crosses among l2 inbred lines ranged from 0.123 between pairs M017 and ZPL7O/9 up to 0.064 between B84 and LI55. The UPGMA clustering grouped the inbred into three clusters. Cluster I was consisted of inbred lines derived from BSSS germplasm or germplasm related to it. Cluster contained the Lancaster lines while cluster III included two independent lines. Data showed that inbred was closely related by their pedigree. They were also closely related based on marker intonations.

On the basis of D^2 statistics analysis the genotypes were grouped into 16 clusters by Singh *et al*. (2003). Cluster I comprised of the maximum number of genotypes (18) whereas cluster XIII to XVI comprised of a single genotype in each. It was indicating that there was wide range of variations amongst the genotypes. Clustering pattern indicated that the genetic diversity was due to genetic distance. As cluster XIII to XVI considered only genotypes in each, the intra-cluster distance of these groups was zero. The highest intra-cluster distance was observed in cluster II which had 6 genotypes. The inter-cluster distance was observed highest (26.4) between cluster V and IX and the lowest between III and XIV (5.3) respectively. The highest inter-cluster distance suggested that the genetic recombination between genotypes of these two clusters would result in considerable heterosis.

Brkic *et al*. (2003); used one hundred Simple Sequence Repeats (SSR) as molecular markers to analyze the genetic relationship among 9 maize inbred lines. Genetic variation was also examined between the inbred lines B73 and M017 obtained from two different sources. Genetic dissimilarity ranged from 8 (between the M017 lines obtained from different sources) to 92 (between M017 and Os438-95). Mean heterozygosity values within samples were relatively low (with an average of 2.18% across all samples). However, B73 from the Agro gene source showed a much higher level of within sample heterozygosity at 14%. The relationship among samples determined by the SSR markers and UPGMA clustering agreed with the pedigree of these lines. The results showed that different grain sources of the same inbred line did not vary considerably. Different sources of the same lines were tightly clustered in the UPGMA dendogram.

Li *et al*. (2004); showed that the accessions assessed could be clustered into a few groups. This was mostly in accordance with the heterotic groupings previously assigned based on conventional methods although some notable differences were detected. The results indicated that most of the Italian maize inbred used in the study were mainly related to the RYD background and most of the Chinese inbred were associated more with the Huangzaosi (HZS) background. In addition, the results supported the establishment of a new heterotic group. That is, the PN group derived from Pioneer hybrids in Chinese maize breeding programs. The study indicated that AFLP markers were suitable for the assessment of genetic diversity in maize germplasm because of its high polymorphism and for the identification of pedigrees of those germplasm with unknown or uncertain genetic background.

Characterization of genetic diversity of maize (*Zea mays* L.) germplasm is of great importance in hybrid maize breeding (Melchinger *et al*., 2005). Inbred included in the study were assayed with 79 SSR markers. The CIMMYT inbred lines originated from 35 mostly broad-based populations and pools with mixed origins. A total of 566 alleles were scored (averaging 7.2 and ranging from 2 to 16 alleles per locus).

An experiment was conducted by Singh *et al*. (2005) to study genetic divergence of 23 genotypes of maize using D^2 analysis. The genotypes fell into 6 clusters. The inter-cluster distances were higher than intra-cluster distances suggesting maximum genetic distance between clusters III and IV and the lowest distance between clusters I and IV. The cluster means were higher for 50% tasselling, 50% silk emergence, plant height, cob height, ear length, number of grains per row and 100- grain weight in cluster IV; for cob girth, days to maturity and number of rows per cob in cluster II; and for grain yield per plant in cluster III followed by cluster II. The genotypes of these clusters would offer a good scope for the improvement of this crop through selection and hybridization.

More *et al*. (2006); grouped forty five diverse genotypes into 7 clusters using Mahalanobis D^2 statistics. Cluster II was the largest with 25 genotypes followed by cluster III with eleven genotypes and cluster I with five genotypes. The clusters IV, V, VI and VII were mono-genotypic. The maximum inter-cluster distance was observed between clusters I and VI followed by distance between clusters I and IV and clusters I and V. Clusters V and VI exhibited the minimum inter-cluster distance.

Cluster analysis based on these quantitative characters assigned the test inbred lines into five major with minor grouping. Within the major clusters indicating the importance of phenotypic descriptors and were able to differentiate between them reported by Singh *et al*. (2005).

CHAPTER III

MATERIALS AND METHODS

The experiment was conducted to study the genetic variability, heritability, correlation and path co-efficient analysis for yield and its contributing factors and genetic diversity of seventeen (17) white maize inbred lines and varieties collected from CIMMYT and Bangladesh. The details of the materials and methods i.e. description of the experimental site, soil and climatic condition of the experimental plot, materials used, experimental design, data collection and procedure of data analysis that used or followed in this experiment has been presented below under the following points.

3.1 Description of the experimental site

3.1.1 Experimental period

The field experiment was conducted during the period of October to April, 2016-2017.

3.1.2 Location of the experiment

The present research work was conducted in the experimental area of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka. The location of the site is $23^{0}74^{/}$N latitude and $90^{0}35^{/}$E longitude with an elevation of 8.2 meter from sea level. Location of the experimental site presented in Appendix I.

3.1.3 Climatic condition

The geographical location of the experimental site was under the subtropical climate and its climatic conditions is characterized by three distinct seasons, namely winter season from the month of November to February and the pre-monsoon period or hot season from the month of March to April and monsoon period from the month of May to October (Edris *et al*., 1979). Details of the meteorological data of air temperature, relative humidity, rainfall and sunshine hour during the period of the experiment was collected from the Weather Station of Bangladesh, Sher-e-Bangla Nagar, Dhaka and details has been presented in Appendix II.

3.1.4 Soil characteristics of the experimental plot

The soil belonged to “The Modhupur Tract”, AEZ-28 (FAO, 1988). Top soil was silt clay in texture, olive-gray with common fine to medium distinct dark yellowish brown mottles. Soil pH was 5.6 and had organic carbon 0.45%. The experimental area was flat having available irrigation and drainage system and above flood level. The selected plot was medium high land. The details have been presented in Appendix III.

3.2 Experimental details

3.2.1 Planting materials

In this experiment Seventeen (17) white maize varieties (Table 1) were used as experimental materials which were collected form CYMMIT, Mexico and BARI, Gazipur. The purity and germination percentage of the collected were assessed as 94% and 91% respectively.

Table 1. Name and origin of the white maize (*Zea mays*) inbred lines and variety used in the present study

Sl.	**Code**	**Genotypes**	**Source of collection**
1.	G1	CLTHW15004	CIMMYT, Mexico
2.	G2	CLTHW15005	CIMMYT, Mexico
3.	G3	CLTHW15006	CIMMYT, Mexico
4.	G4	CLTHW15007	CIMMYT, Mexico
5.	G5	CLTHW15008	CIMMYT, Mexico
6.	G6	CLTHW15009	CIMMYT, Mexico
7	G7	CLTHW15003	CIMMYT, Mexico
8	G8	CLTHW15010	CIMMYT, Mexico
9	G9	CLTHW15011	CIMMYT, Mexico
10	G10	CLTHW15012	CIMMYT, Mexico
11	G11	CLTHW15001	CIMMYT, Mexico
12	G12	CLTHW15014	CIMMYT, Mexico
13	G13	CLTHW15015	CIMMYT, Mexico
14	G14	CLTHW14001	CIMMYT, Mexico
15	G15	CLTHW14003	CIMMYT, Mexico
16	G16	CLTHW13001	CIMMYT, Mexico
17	G17	Suvra	BARI, Gazipur

3.2.2 Experimental design and layout

The experiment was laid out in randomized complete block design (RCBD) with 3 replications. The field was divided into 3 blocks. The individual block size was 33.15 m × 2.5 m. Each plot was 2.5 m in length and 2 m in breadth containing three rows. The plant spacing provided was 65 cm between rows and 25 cm between plants of the same row. The experiment was laid out in a Randomized Complete Block Design (RCBD). Three replications were performed in this experiment.

Plate 1. Photograph Showing seed sowing at the experimental plot

3.3. Growing of crops

3.3.1 Preparation of the main field

The selected field for growing maize was first opened with power tiller and was exposed to the sun for a week. Then the land was prepared to obtain goodtilth by several ploughing, cross ploughing and laddering. Subsequent operations were done with harrow, spade and hammer. Weeds and stubbles were removed; larger clods were broken into small particles and finally attained into a desirable tilth to ensure proper growing conditions. The plot was partitioned into the unit blocks according to the experimental design as mentioned earlier. Recommended doses of well decomposed cow dung, manure and chemical fertilizers were applied and mixed well with the soil each blocks. Proper irrigation and drainage channels were also prepared around the blocks. The bed soil was made friable and the surface of the bed was leveled.

3.3.2 Application of manure and fertilizers

Generally cow dung, Urea, TSP and MP fertilizers are required for maize cultivation. The field was fertilized with 10 ton cow dung per ha. The field was also fertilized with 185-276-276-185-17-12 kg NPKSZn and B/ha, respectively. The entire amount of cow dung was applied seven days before sowing. TSP. MP, Gypsum and Boron were applied during final land preparation and incorporated into the soil. The total amount of urea was divided by three splits. One third of the urea was applied after 30 days of seed germination and the rest two splits of the urea applied after 50 and 70 days of seed germination (before flowering) of the plants, respectively.

Table 2. Dose and method of application of fertilizers in maize field

Sl.	Manures and Fertilizers	Dose/ha	Application (kg)			
			Basal	30 DAS	50 DAS	70DAS
1.	Cow dung	10 tons	10 tons	--	--	--
2.	Urea	185 kg	--	65 kg	60 kg	60 kg
3.	TSP	195 kg	195 kg	--	--	--
4.	MP	70 kg	70kg	--	--	--
5.	Zinc Sulphate	17 kg	17 kg	--	--	--
6.	Boric acid	12 kg	12 kg	--	--	--

3.3.3 Sowing of seeds in the field

The maize seeds were planted in lines each having a line to line distance of 75 cm and seed hill to hill 25 cm under direct planting in the well prepared plot on 16 November 2016.

3.3.4 Post care

When the seedlings started to emerge in the beds it was always kept under careful observation. After emergence of seedlings, various intercultural operations were accomplished for better growth and development of the maize seedlings.

3.3.4.1 Irrigation

Irrigation was provided at seedling stage, knee stage, pre-flowering stage and milking stage at 20, 45, 65 and 78 days after sowing (DAS) for four times for proper growth and development of the plants.

3.3.4.2 Thinning and gap filling

The seedling were first thinned from all of the plots at 25 days after sowing (DAS) 2nd thinning was carried out after seven days of 1st thinning for maintaining proper spacing the experimental plots. Gap filling was done within 10 days of sowing.

3.3.4.3 Weeding

Weeding were done to keep the plots free from weeds, easy aeration of soil and to conserve soil moisture, which ultimately ensured better growth and development. The newly emerged weeds were uprooted carefully after complete emergence of maize seedlings and whenever necessary. Breaking the crust of the soil, when needed was done through mulching.

3.3.4.4 Plant protection

Adult and larva of many insects were found in the crop during the vegetative and flowering stage of the plant. To control such insects Malathion-57 EC @2ml/litre and Diazinon 60 EC @ 2 ml/litre of water were sprayed at 70 and 90 DAS respectively. The insecticide was applied in the afternoon. Ridomil 2g per litre of water was sprayed three times in the plants as protective measures against fungal disease.

3.4 Harvesting

Different genotypes matured at different times. The crops were harvested when the husk cover was completely dried and straw color was formed of the husk of the mature cob. The five randomly selected plants of each line were separately harvested. Border plants were discarded to avoid border effect.

3.5 Data recording

3.5.1 Plant height (cm)

Plant height was measured in centimeters from the base of the plants up to the tassel base from where the tassel branching started at each of the five randomly selected plants from each line.

CLTHW15010 CLTHW 15006 CLTHW15009 CLTHW 15015 CLTHW 15007

CLTHW15004 CLTHW 14001 CLTHW15014 CLTHW 15005 CLTHW 15012

Plate 2. Photograph showing some cobs of white maize genotypes

3.5.2 Base to cob distance (cm)

The base to cob distances from randomly selected plants was measured from each unit plot in centimeters with a graduated measuring stick. Cob height was taken from the soil surface (ground level) to the node bearing the uppermost cob node. Base to cob distances were measured from the same plant from which plant heights were recorded.

3.5.3 Base diameter of plant

Base diameter of plant was calculated with calipers at randomly and average was done in centimeters.

3.5.4 Leaf length (cm)

It was measured in centimeter scale from the jointing point of leaf and to the tip point each of the five randomly selected plants in each line of leaf.

3.5.5 Leaf breadth (cm)

Breadth of leaf was measured in centimeter using scale at the middle of leaf from the randomly selected five plants and average the result.

3.5.6 Days to 50% flowering

Days of 50% flowering was recorded from the sowing date to the flowering of the 50% plants at every 3 replications for each line.

3.5.7 Days to maturity

Days to maturity was recorded from the sowing date to the maturity stage when cob was harvested for each of the three replications.

3.5.8 Cob length (cm)

It was measured in centimeter from the base to the tip of the cob with the help of a meter scale and average was recorded.

3.5.9 Cob diameter (cm)

Cob diameter measured in centimeter with the help of a slide calipers from the three position of cob and average was recorded.

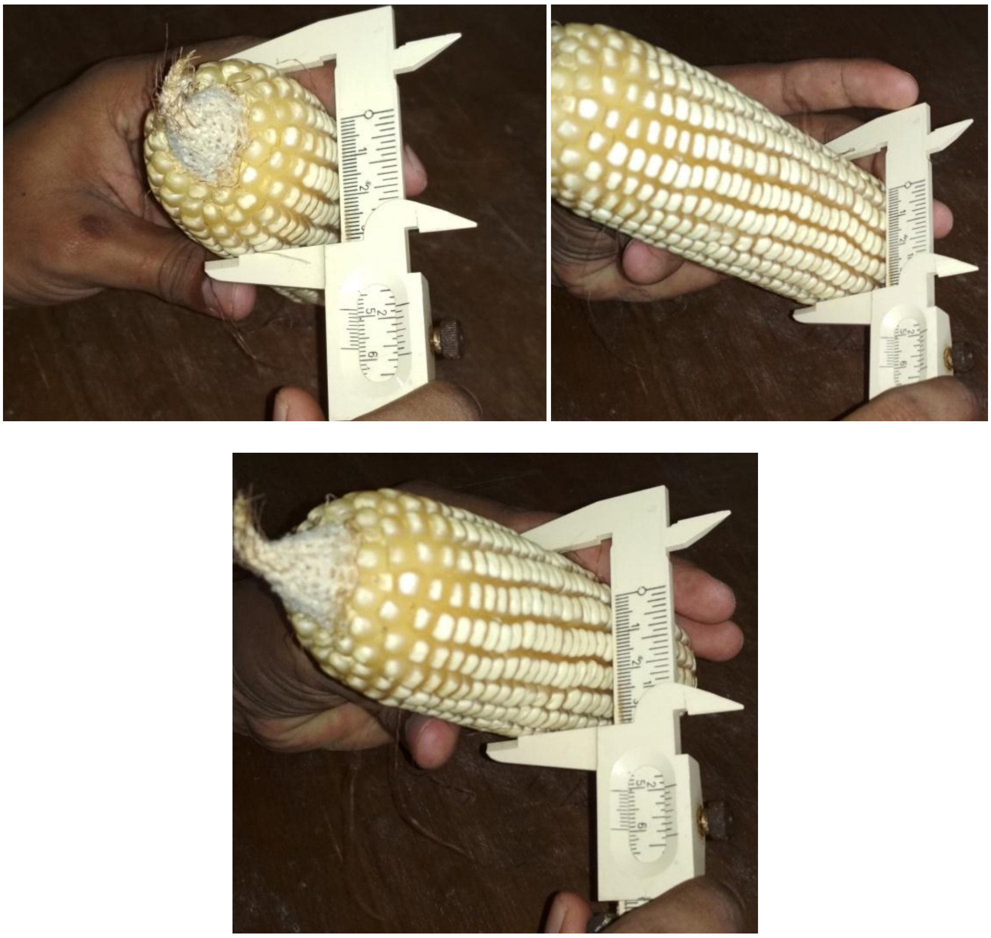


Plate 3. Photograph showing measuring cob length by a slide calipers

3.5.10 Number of row per cob

Number of rows per cob was counted in the central part of the ear and recorded for ten randomly selected ears and average value was taken.

3.5.11 Number of grains per row

Number of grains per row was counted and recorded for ten randomly selected cobs and average value was taken.

3.5.12 100 grain weight

A sample of 100 grains were taken at random and weighed to the nearest 1/10 gram.

3.5.13 Yield per plant

All cobs were shelled from selected plants and yield was measured as a bulk weight then average was calculated by dividing the number of selected plants to the nearest gram. Yield was measure as gram per plant.

3.6 Statistical analysis

The data obtained for different characters were statistically analyzed to find out the significance among the difference the white maize genotypes. The mean values of all the characters were evaluated and analysis of variance was performing by the ‘F’ test. The significance of the difference among the treatments means was estimated by the Duncan’s Multiple Range Test (DMRT) test at 5% level of probability (Gomez and Gomez, 1984).

3.7 Estimation of variability

Genotypic and phenotypic coefficient of variation and heritability were estimated by using the following formulae:

3.7.1 Estimation of components of variance from individual environment

Genotypic and phenotypic variances were estimated with the help of the following formula suggested by Johnson *et al*. (1955). The genotypic variance (σ^2_g) was estimated by subtracting error mean square (σ^2_e) from the genotypic mean square and dividing it by the number of replication (r) as per following formula –

Genotypic variance (σ^2_g) $= \frac{MS_V - MS_E}{r}$

MS_V = genotype mean square

MS_E = error mean square

r = number of replication

The phenotypic variance (σ^2_p) was derived by adding genotypic variances with the error variance, as given by the following formula – Phenotypic variance (σ^2_{ph}) $= \sigma^2_g + \sigma^2_e$

Where,

σ^2_{ph} = phenotypic variance

σ^2_g = genotypic variance

σ^2_e = error variance

3.7.2 Estimation of genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV)

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following formula as suggested by Burton (1952):

% Genotypic coefficient of variance=$\frac{\sigma_g}{\bar{x}} \times 100$

Where, σ_g= genotypic standard deviation;

$\bar{x}$= population mean

% phenotypic coefficient of variance=$\frac{\sigma_{p\square}}{\bar{x}} \times 100$

Where, σ_{ph}= genotypic standard deviation;

$\bar{x}$= population mean

3.7.3 Estimation of heritability

Heritability in broad sense was estimated following the formula as suggested by Johnson *et al*. (1955):

Heritability (%) =$\frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$

Where,

σ^2_g = genotypic variance and

σ^2_{ph} = phenotypic variance

3.7.4 Estimation of genetic advance

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960):

GA =$\frac{\sigma^2_g}{\sigma^2_{ph}} \times K.\, \sigma_{ph}$

Where,

GA = Genetic advance

σ^2_g = genotypic variance

σ^2_{ph} = phenotypic variance

σ_{ph}= phenotypic standard deviation

K = Selection differential which is equal to 2.64 at 5% selection intensity

3.7.5 Estimation of genetic advance in percentage of mean

Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952):

Benetic Advance in percentage of mean $= \frac{\text{Genetic advance}}{\bar{x}} \times 100$

3.8 Estimation of correlation

Simple correlation was estimated for different traits with the following formula (Singh and Chowdhury, 1985):

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{\left\{\sum x^2 - \frac{(\sum x)^2}{N}\right\}\left\{\sum y^2 - \frac{(\sum y)^2}{N}\right\}}}$$

Where,

∑= Summation x and y are the two variables

N = Number of observations

3.9 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chowdhury (1985), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect of independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say x_1, x_2, x_3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as given below:

$ryx_1 = Pyx_1 + Pyx_2rx_1x_2 + Pyx_3rx_1x_3$

$ryx_2 = Pyx_1rx_1x_2 + Pyx_2 + Pyx_3rx_2x_3$

$ryx_3 = Pyx_1rx_1x_3 + Pyx_2 rx_2x_3 + Pyx_3$

Where, r’s denotes simple correlation co-efficient and P’s denote path co-efficient (unknown). P’s in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows:

Pyx_1 = The direct effect of x_1 on y

$Pyx_1rx_1x_2$ = The indirect effect of x_1 via x_2 on y

$Pyx_1rx_1x_3$ = The indirect effect of x_1 via x_3 on y

After calculating the direct and indirect effect of the studied characters, residual effect (R) was calculated by using the formula given below according to the Singh and Chowdhury, 1985):

$$P^2RY = 1 - \sum Piy.riy$$

Where,

$P^2RY = (R^2)$; and hence residual effect,

$R = (P^2RY)^{1/2}$ Piy = Direct effect of the character on yield

riy = Correlation of the character with yield

3.10 Multivariate analysis

Mean data for each character was subjected to multivariate analysis methods viz, principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis (CLSA) using GENSTAT 4.2 program.

3.10.1 Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to know the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores obtained for the first component and succeeding components with latent roots greater than unity (Jager *et al.,* 1983).

3.10.2 Principal coordinates analysis (PCO)

Principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of p it gives the minimum distances between each pair of n points using similarity matrix (Digby *et al.,* 1989). Inter-distances between genotypes were studied by PCO.

3.10.3 Canonical variate analysis (CVA)

The canonical variate analysis is based upon the roots and vectors of W-IB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix. It provides two-dimensional plots that helped in separating different populations involved.

3.10.4 Cluster analysis (CLSA)

Genotypes were divided into groups on the basis of a data set into some number of mutually exclusive groups. The clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optical values of the chosen criterion. The optimal values of the criteria followed by some initial classification of the genotypes into required number of groups, the algorithm repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to second stage that examine the effect of two genotypes of different classes and so on.

3.10.5 Computation of average intra-cluster distance

Computation of average intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters are formed. The formula utilized was $\Sigma D^2/n$, where ΣD^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

3.10.6 Computation of average inter-cluster distances

The procedures of calculating inter-cluster distance between cluster II and I and between cluster III and I and between I and IV, between II and IV and so on. The clusters were taken one by one and their distances from other clusters were calculated.

3.10.7 Cluster diagram

It was drawn using the values between and within clusters distances, which presents a momentary idea of the pattern of diversity among the genotypes included in a cluster.

3.11 Analysis of genetic divergence

Genetic divergences among the genotypes studied were assessed by using Mahalanobis' D^2 statistics and its auxiliary analysis. Both techniques estimate divergences among a set of genotypes on multivariate scale.

Mahalanobis' D^2 statistics

First the variation among the materials were tested by Wilkin's criteria '^'.

$$\text{`}\wedge\text{'} = \frac{|W|}{|S|} = \frac{|\text{Determination of error matrix}|}{|\text{Determenationoferror} + \text{varietymatrix}|}$$

Now, 'v' $_{(\text{stat})}$ = -m $\log_{e\wedge}$ = - {n-(p+q+1)/2} $\log_{e\wedge}$

Where,

m = n-(p+q+1)/2

p = number of variables or characters

q = number of varieties – 1 (or df for population)

n = df for error + varieties

e = 2.7183

Data were then analysed for D^2 statistics according to Rao (1952). Error variance and covariance matrix obtained from analysis of variance and covariance were inverted by pivotal condensation method. Using the pivotal elements the original means of the characters (X1, X2---------X8) were transformed into a set of uncorrelated variables (Y1, Y2---------Y8).

Now, the genetic divergence between two varieties/lines (suppose Vi and Vj) was calculated as

$_{k=1}^{8}D^2ij = \sum (\text{Vik} - \text{Vjk})^2$

Where,

D^2ij = Genetic divergence between 'i' th and 'j' th genotypes Vik = Transformed mean of the 'i' th genotype for 'k' th character

Vjk =Transformed mean of the 'j' th genotype for 'k' th character.

The D^2 values between all the studied genotypes were arranged in order of relative distances from each other and were used for clusters formation, as suggested by Rao, 1952.

Average intra-cluster $D^2 = \frac{D^2 i}{n}$

Where,

$\sum D^2 i$= Sum of distances between all possible combinations (n) of the genotypes included in a cluster.

n=All possible combinations.

Plate 4. Photograph showing experimental field at reproductive stage

CHAPTER IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The data on seventeen maize genotypes, as well as their yield and its contributing characters were computed, statistically analyzed, and the results thus obtained are discussed below under the following headings**.**

4.1 Analysis of variance

4.2 Genetic variability, heritability and genetic advance

4.3 Correlation analysis

4.4 Path coefficient analysis

4.5 Genetic diversity analysis

4.1 Analysis of variance

The analysis of variance indicated a significant amount of variability among the genotypes for all the characters studied *viz*., Plant height (cm), base to cob distance (cm), base diameter of plant (cm), leaf length (cm), leaf breadth (cm), days to 50% flowering, days to maturity, cob length (cm), cob diameter (cm), number of row per cob, number of grains per row, 100 grain weight (g), yield per plant (g) in Table 3.

4.2 Analysis of mean performance, genetic variability, heritability and genetic advance of white maize

The estimation of mean, range, genotypic and phenotypic co-efficient of variation, heritability, genetic advance and genetic advance as percent of the mean for all the characters were studied, and the results are presented in Table 4. The mean performance of white maize genotypes for various growth characters and yield components are presented in Appendix 4.

Table 3. Analysis of variance of different characters in white maize

Sources of variation	df	Mean sum square												
		Plant height	Distance between base to cob	Base diameter of plant	Leaf length	Leaf breadth	Days to 50% flowering	Days to maturity	Cob length (cm)	Cob diameter	No. of row per cob	No. of grains per row	100 grain weight	Yield per plant
Genotypes	16	604.78**	369.84**	0.82	63.47**	1.44	24.04**	96.45**	2.97**	0.13	3.93**	29.41**	34.57**	15505.68**
Replication	2	1079.99	181.02	1.31	177.36	0.74	12.50	55.90	0.09	0.01	0.03	2.01	115.01	300.23
Error	32	385.93	6.12	0.01	59.02	0.02	0.09	17.86	0.01	0.00	0.08	0.45	0.01	77.48

** Significant at 1% level of significance

* Significant at 5% level of significance

4.2.1 Plant height (cm)

Plant height is an essential agronomic character for selecting desirable genotype for the breeding program (Ali *et al*., 2012). Significant mean sum of the square for plant height indicated considerable difference among the genotypes studied in Table 3. Plant height ranged from 172.67 cm (G14) to 223.93 cm (G8) (Table 4 and Appendix 4).The phenotypic and genotypic variances for this trait was comparatively high (458.88 and 72.95) (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested the considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (10.48) was higher than the genotypic coefficient of variation (4.18) (Table 4) which indicated the environment has a significant role in the expression of this trait.

Heritability was low (15.90%) with low genetic advance (7.02) and low genetic advance in percent of the mean (3.43) in Table 4 was considerable for this trait indicating non-apparent variation was due to genotypes. So, selection based on this trait would not be effective. Similar findings were also reported by Alvi *et al.* (2003). Mihaljevic *et al.* (2005) obtained high heritability values (0.90) for plant height. The lower the heritability of a particular trait, the higher will be the environmental effect on its expression.

4.2.2 Base to cob distance (cm)

Maximum base to cob distance was noted in G4 (121.80 cm) while minimum in G5 (75.20 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 127.36 and 121.23 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested the considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (11.05) was higher than the genotypic coefficient of variation (10.78) (Table 4 and Figure 1). Heritability estimates was high (95.19%) with high genetic advance (22.13) and high genetic advance in percent of mean (21.66) (Table 4 and Figure 2) was considerable for this trait indicating apparent variation was due to genotypes.

4.2.3 Base diameter of plant (cm)

The maximum base diameter of the plant was noted in G5 (7.20 cm) while minimum in G4 (5.10 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 0.2822 and 0.2691 (Table 4). The phenotypic coefficient of variation (8.75) was higher than the genotypic coefficient of variation (8.55) (Table 4 and Figure 1). Heritability estimates were high (95.36%) with low genetic advance (1.04) and high genetic advance in percent of mean (17.19) (Table 4 and Figure 2) was considered for this trait indicating apparent variation was due to genotypes.

4.2.4 Leaf length (cm)

Maximum leaf length was noted in G8 (76.19 cm) followed by G12, G5, G6 and G16 while minimum in G13 (59.47 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 60.51 and 1.48 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (11.63) was higher than the genotypic coefficient of variation (1.82) (Table 4 and Figure 1).This analysis showed that leaf length was highly significant. with leaves per plant; leaf breadth and 100-grain weight. It's positively correlated with yield per plant. If length was increased then leaf area also was increased and consequently more photosynthesis will take place which lead to vigorous vegetative growth which resulted increased plant length and low grain yield.

4.2.5 Leaf breadth (cm)

Maximum cob length was recorded in G5 (9.39 cm) followed by G1, G9, G3, G13 and G2 while minimum in G4 (6.63 cm) (Appendix 4). The phenotypic and genotypic variances for this trait were 0.49 and 0.47 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (8.87) was higher than the genotypic coefficient of variation (8.72) (Table 4). Cob length was highly significant with plant height, leaf length, 100-grain weight and yield per plant.

4.2.6 Days to 50% flowering

Maximum days to 50% flowering was recorded in G9 (87.83) while minimum in G5 (78.13) (Appendix 4).The phenotypic and genotypic variances for this trait were 8.07 and 7.98 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (3.35) was higher than the genotypic coefficient of variation (3.33) (Table 4). Days to 50% flowering

Table 4. Estimation of genetic parameters in 13 characters of 17 inbreed lines in maize (*Zea mays*)

Parameter	Min	Max	Mean	CV (%)	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA	GA (% mean)
PH	172.67	223.93	204.40	9.61	72.95	385.91	458.88	4.18	9.61	10.48	15.90	7.02	3.43
DBC	75.20	121.80	102.15	2.42	121.24	6.12	127.36	10.78	2.42	11.05	95.19	22.13	21.66
BD	5.10	7.20	6.07	1.89	0.27	0.01	0.28	8.55	1.89	8.75	95.36	1.04	17.19
LL	59.47	76.19	66.89	11.49	1.48	59.02	60.51	1.82	11.49	11.63	2.45	0.39	0.59
LB	6.63	9.39	7.90	1.64	0.47	0.02	0.49	8.72	1.65	8.87	96.56	1.39	17.65
DFF	78.17	87.83	84.87	0.35	7.98	0.09	8.07	3.33	0.35	3.35	98.91	5.79	6.82
DM	129.00	151.67	133.78	3.16	26.20	17.86	44.06	3.83	3.16	4.96	59.46	8.13	6.08
CL	13.17	16.47	14.96	2.10	0.96	0.10	1.06	6.54	2.10	6.87	90.67	1.92	12.83
CD	4.06	4.85	4.59	1.10	0.04	0.003	0.04	4.50	1.09	4.63	94.47	0.41	9.02
RPC	12.11	16.57	14.55	2.00	1.28	0.08	1.37	7.78	2.00	8.04	93.80	2.26	15.53
GPR	17.89	30.14	23.54	2.85	9.65	0.45	10.10	13.20	2.85	13.50	95.54	6.26	26.58
HGW	20.54	34.10	27.15	0.37	11.52	0.01	11.53	12.50	0.37	12.51	99.91	6.99	25.74
YPP	44.52	170.01	96.24	2.87	994.45	7.65	1002.10	32.77	2.87	32.89	99.24	64.71	67.24

PH = Plant height (cm), DBC = Distance between base and cob (cm), BD= Base diameter of Plant, LL = Leaf length (cm), LB = Breadth of leaf (cm), DF= Days to 50% flowering, DM= Days to maturity, CL = Cob length (cm), CD = Cob diameter (cm), RPC = Number of row per cob, GPR = Number of grains per row and HGW = 100 grains weight (g), YPP= Yield per plant (g), Max= Maximum, Min=Minimum, CV (%)=Co-efficient of variance in percentage, σ^2_g=Genotypic standard deviation, σ^2_e =environmental standard deviation, σ^2_P =Phenotypic standard deviation, GCV=Coefficient of variance, ECV = Coefficient of variance, PCV= Coefficient of variance, h^2_b =Heritability, GA =Genetic advance, GA (% mean)= Genetic advance in percentage.

were highly significant and negatively correlated with plant height, leaf length, 100-grain weight and yield per plant.

4.2.7 Days to maturity

Maximum days to maturity was recorded in G12 (151.67) followed by G17, G13, G2, G16 and G15 while minimum in G10 (129.00) (Appendix 4).The phenotypic and genotypic variances for this trait were 44.05 and 26.20 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (4.96) was higher than the genotypic coefficient of variation (3.83) (Table 4 and Figure 1). Days to maturity was highly significant and positively correlated with plant height, leaf length, 100-grain weight and yield per plant.

4.2.8 Cob length (cm)

Maximum cob length was recorded in G5 (16.47 cm) followed by G1, G9, G13, G11 and G6 while minimum in G4 (13.17 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 1.0562 and 0.09577 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (6.87) was higher than the genotypic coefficient of variation (6.54) (Table 4 and Figure 1).Cob length was highly significant and positively correlated with plant height, leaf length, 100-grain weight and yield per plant.

4.2.9 Cob diameter (cm)

Maximum cob diameter was recorded in G5 (4.85 cm) followed by G1, G9, G13, G3 and G6 while minimum in G4 (7.37 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 0.04 and 0.04 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (4.63) was higher than the genotypic coefficient of variation (4.50) (Table 4). Cob diameter was highly significant with plant height, leaf length, 100-grain weight and yield per plant.

4.2.10 Number of row per cob

Significant differences among the genotypes were observed due to number of row per cob (Table 3). The highest number of grain row per cob was 16.57, produced by the G5 and the lowest number of grain row per cob was 12.11, produced by G4 (Appendix 4 and Table 4). The phenotypic variance (1.3673) was slightly higher than genotypic variance (1.2825) (Table 4 and Figure 1). Moderate genotypic coefficient of variation (8.04) and phenotypic coefficient of variation (7.78) (Table 4 and Figure 2) were found for this trait.

The heritability was very higher (93.80%) together with low genetic advance (2.26) and moderate genetic advance in percent of mean (15.53) indicating the selection for this character would be effective (Table 4 and Figure 2). Similar results were reported by Chen *et al*. (1996), Satyanarayan and Kumar (1995) and Ojo *et al*. (2006). High heritability accompanied with low GA, and genetic advance in percent of mean indicates that most likely the heritability is due to additive gene effects.

4.2.11 Number of grains per row

Significant differences among the genotypes were observed due to number of grains per row (Table 3). The maximum number of grain per row were found (30.14) in the genotype G5 and minimum number of grain per row were found (17.89) in the genotype G4 (Appendix 4). The phenotypic variance (10.10) was higher than genotypic variance (9.65) and the PCV (13.50) was also a little greater than GCV (13.20) (Table 4 and Figure 1) indicating the role of environment on the expression of this trait.

The genetic advance was moderate (6.26) with high genetic advance in percent of mean (26.58) for this trait (Table 4). Similar results were reported by Rather *et al.* (2003) and Rajesh *et al.* (2013). Heritability was found to be highest for this trait (95.54%) (Table 4 and Figure 2), which indicated this character was less influenced by environmental effects. High heritability accompanied with high to moderate GCV and high genetic advance in percent of mean indicated that most likely the heritability was due to additive gene effects and selection may be effective in early generations for these traits. High heritability estimates for number of grain per row were also reported by Abd El-Sattar (2003).

4.2.12 100 grain weight (g)

Significant differences among the genotypes were observed due to 100-grain weight (Table 3). Maximum number of 100-grain weight was found in G5 (34.10 g) and minimum in G4 (20.54 g) (Appendix 4). The phenotypic and genotypic variance was high and the difference between the phenotypic variance (11.53) and the genotypic variance (11.52) was not significant. Little influence of environment upon this trait was reported due to difference between the estimation of GCV (12.50) and PCV (12.51) which suggesting existing of sufficient variability and offers scope for selection (Table 4). High heritability (99.91%), high genetic advance (6.99) and high genetic advance in percent of mean (25.74) were found for this trait (Table 4 and Figure 2) which indicating very low or no influence of environment and apparent variability due to additive gene and selection may be effective in early generations for this trait 100-grain weight. Similar results were reported by Anshuman *et al.* (2013). Similar results of PCV and GCV values for this trait were reported by Abirami *et al*. (2005).

4.2.13 Yield per plant (g)

The genotypes varied significantly for yield per plant (Table 3). The highest yield per plant was observed in the genotype G5 (170.01g) and the lowest total yield per plant was observed in the genotype G3 (44.52g) (Appendix 4). The phenotypic variance (1002.10) differed slightly from genotypic variance (994.4548) for this trait. Moderate genotypic (32.77) and phenotypic (32.89) coefficient of variation and high heritability (99.24%) along with high genetic advance (64.71) and high genetic advance in percent mean (67.24) were estimated for this character (Table 4 and Figure 1and2). All these value of statistical analysis indicated that the characters were less influenced by environment and additive gene involved in the expression and selection may be effective in early generations for these traits. Similar results were reported by Chen *et al.* (1996), Ojo *et al*. (2006), Mahmood *et al*. (2004), Hemavathy *et al.* (2008) and Anshuman *et al.* (2013).

4.3 Correlation analysis

The study of yield components and the inter relationship with yield and their direct and indirect contribution to yield is of immense importance. Yield is the resultant of combined effect of several component characters and environment. Understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. Correlation studies provide information on the nature and extent of association between only two pairs of metric characters. From this it would be possible to bring about genetic improvement in one character by selection of the other of a pair. Obviously, knowledge character associations will surely help to identify the characters to make selection for higher yield with a view to determining the extent and nature of relationship prevailing among yield contributing characters. Genotypic and phenotypic correlations between pairs of characters are presented in Table 5a and 5b. The genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the cases indicating the association is largely due to genetic reason. The results are discussed character wise as follows:

4.3.1 Plant height

Plant height showed highly significant negative correlation with leaf length (-.98) at the genotypic level 1% (Table 5a and 5b). It showed non-significant positive correlation with base to cob, days to 50% flowering, cob length, number of grains per row for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with base diameter, leaf length, leaf breadth, days to maturity, cob diameter, number of row per cob, 100-grain weight (Table 5a and5b). Mohammadi *etal.* (2003); Ojo *et al.* (2006); Sadek *et al.* (2006) and Abou-Deif (2007) reportedthat plant height was significantly and positively correlated with each of number of rows per cob and cob diameter. However, Srekove *et al.* (2011) reported negative correlation between grain yield and plant height.

4.3.2 Base to cob distance

Base to cob distance showed highly significant positive correlation with base diameter of plant, number of grains per row, 100-grain weight, yield per plant at the genotypic level (Table 5a) and highly significant positive correlation with leaf breadth(cm), cob length(cm), number of grain per row, 100-grain weight and yield per plant(g) at the phenotypic level (Table 5b). It showed non-significant positive correlation with days to 50% flowering, days to maturity for both genotypic and phenotypic levels. Non-significant negative phenotypic correlation was also observed with leaf length(cm) (Table 5a and5b).

4.3.3 Base diameter of plant

Base diameter of plant showed highly significant positive correlation with leaf length(cm), cob length(cm), cob diameter(cm), number of row per cob, number of grains per row, 100-grain weight, yield per plant at the both genotypic and phenotypic level (Table 5a and 5b). It showed non-significant positive correlation with leaf length(cm) and leaf breadth(cm) for both genotypic and phenotypic levels. Non-significant negative phenotypic correlation was also observed with leaf length (cm) (Table 5a and 5b).

4.3.4 Leaf length

Highly significant positive association was recorded for base diameter, days to 50% flowering, days to maturity, cob diameter (cm), number of grain per row, 100-grain weight for the genotypic and for distance between base to cob, base diameter of plant for the phenotypic level. The insignificant positive association of leaf length cm) was recorded with leaf breadth (cm), cob length (cm), number of row per cob (Table 5a and 5b). On the other hand, significant negative association was observed for base to cob distance as well as insignificant negative association was not also observed (Table 5a and 5b).

4.3.5 Leaf breadth

Highly significant positive association was recorded for breadth of leaf of maize inbreeds lines with cob length (cm) for both genotypic and phenotypic level (Table 5a and 5b). The insignificant positive association was recorded for grain per row, cob breadth(cm) and cob weight (Table 5a and 5b). On the other hand, significant negative association was observed with row per cob for genotypic significant level as well as insignificant negative association was also observed in grain per cob, 100-grain weight and total yield per plant (Table 5a and 5b).

4.3.6 Days to 50% flowering

Highly significant positive association was recorded for days to 50% flowering of maize varieties with cob length (cm), cob diameter (cm), number of rows, and number of seed per row, 100-grain weight and yield per plant for genotypic level (Table 5a). The insignificant positive association was recorded for plant height (cm), ear height (cm) (Table 5a and 5b).

4.3.7 Days to maturity

Highly significant positive correlation was recorded for days to maturity of maize inbreed lines with leaf length (cm) for the genotypic level (Table5a). The insignificant positive association was recorded for base to cob distance and days to 50% flowering.

4.3.8 Cob length (cm)

Highly significant positive correlation was recorded for cob length of maize inbreed lines with cob breadth(cm), grain per row, grain per cob, cob weight, 100- grain weight and total yield per plant for both the genotypic and phenotypic level (Table 5a and 5b). The insignificant positive association was recorded for row per cob. On the other hand, significant negative association was not found for any significant level.

4.3.9 Cob diameter

Significant positive association was recorded for cob diameter of maize inbreed lines with base to cob distance, base diameter (cm), leaf breadth (cm), cob length(cm), number of row per cob, number of grain per row, 100-grain weight and yield per plant (g) for both significant level (Table 5a and 5b). The insignificant positive association was recorded for leaf length and days to 50% flowering. On the other hand, insignificant negative association was recorded for grain per row at phenotypic level (Table 5a and 5b).

4.3.10 Number of row per cob

Number of row per cob showed highly significant positive correlation with base diameter (cm), leaf breadth (cm), cob length (cm), cob diameter (cm), number of grain per row, 100-grain weight and yield per plant (g) at the genotypic level. It showed non-significant positive correlation with leaf length (0.234), days to 50% flowering at genotypic level. It showed highly significant negative correlation with base to cob distance (-0.989) at genotypic level and (-0.966) at phenotypic level. Our results disagree with EL-Hosary *et al.* (1989); Amin *et al.* (2003); EL-Beially (2003) and Mohammadi *et al.*(2003) who found number of rows per cob showed significant and negative correlations with 100-grain weights and number of grain per row.

Table 5a. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different varieties of white maize

Parameters	**DBC**	**BD**	**LL**	**LB**	**DFF**	**DM**	**CL**	**CD**	**RPC**	**GPR**	**HGW**	**YPP**
PH	0.013	-0.022	-0.968**	-0.129	0.010	-0.391	0.031	-0.048	-0.028	0.013	-0.044	-0.025
DBC		-0.999**	-0.570*	-0.986**	0.093	0.273	-0.990**	-0.931**	-0.989**	-0.986**	-0.992**	-0.966**
BD			0.241	0.988**	-0.087	-0.332	0.994**	0.945**	0.986**	0.986**	0.999**	0.985**
LL				0.259	0.500*	0.779**	0.211	0.502*	0.234	0.608**	0.546*	0.410
LB					-0.067	-0.239	0.979**	0.962**	0.976**	0.986**	0.998**	0.985**
DFF						0.232	-0.002	0.181	0.042	-0.048	-0.060	-0.125
DM							-0.299	-0.264	-0.346	-0.300	-0.310	-0.308
CL								0.989**	0.986**	0.993**	0.986**	0.979**
CD									0.986**	0.969**	0.965**	0.930**
RPC										0.986**	0.989**	0.979**
GPR											0.986**	0.999**
HGW												0.992**

**5% = 2.131; *1% = 2.947

PH = Plant height (cm), DBC = Distance between base and cob (cm), BD= Base diameter of Plant, LL = Leaf length (cm), LB = Breadth of leaf (cm), DF= Days to 50% flowering, DM= Days to maturity, CL = Cob length (cm), CD = Cob diameter (cm), RPC = Number of row per cob, GPR = Number of grains per row and HGW = 100 grains weight (g)

Table 5b. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different inbreed lines of white maize

Parameters	DBC	BD	LL	LB	DFF	DM	CL	CD	RPC	GPR	HGW	YPP
PH	0.041	-0.030	-0.066	-0.069	0.004	-0.285	0.040	-0.046	0.031	-0.020	-0.032	-0.026
DBC		-0.986**	-0.160	-0.990**	0.093	0.226	-0.948**	-0.924**	-0.966**	-0.993**	-0.985**	-0.995**
BD			0.088	0.993**	-0.087	-0.284	0.962**	0.932**	0.967**	0.989**	0.991**	0.993**
LL				0.079	0.127	0.172	0.013	0.140	0.123	0.111	0.113	0.100**
LB					-0.065	-0.220	0.961**	0.941**	0.967**	0.993**	0.991**	0.993**
DFF						0.207	0.000	0.178	0.044	-0.047	-0.060	-0.124
DM							-0.280	-0.225	-0.309	-0.258	-0.280	-0.271
CL								0.953**	0.976**	0.973**	0.968**	0.961**
CD									0.977**	0.952**	0.956**	0.921**
RPC										0.982**	0.977**	0.966**
GPR											0.995**	0.995**
HGW												0.991**

**1% = 2.947; *5% = 2.131

PH = Plant height (cm), DBC = Distance between base and cob (cm), BD= Base diameter of Plant, LL = Leaf length (cm), LB = Breadth of leaf (cm), DF= Days to 50% flowering, DM= Days to maturity, CL = Cob length (cm), CD = Cob diameter (cm), RPC = Number of row per cob, GPR = Number of grains per row and HGW = 100 grains weight (g), YPP=Yield per plant(g)

4.3.11 Number of grains per row

Number of grain per row showed highly significant positive correlation with base to cob distance (cm), base diameter (cm), leaf length (cm), leaf breadth (cm), cob length (cm), cob diameter cm), number of row per cob, 100-grain weight and yield per plant at both the genotypic and phenotypic level (Table 5a and 5b). It showed non-significant positive correlation with plant height for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with days to 50% flowering, and days to maturity (Table 5a and 5b). Amin *et al.* (2003) indicated that number of grains per row and 100- grain weight (g) were the highest contributors to variation in grain yield directly or indirectly.

4.3.12 100-grain weight

Highly significant positive correlation were observed between 100-grain weight with base diameter of plant, leaf breadth (cm), cob length (cm), cob diameter (cm), number of row per cob, number of grain per row total yield per plant (g) at both the genotypic and phenotypic level (Table 5a and 5b). It showed non-significant positive correlation with leaf length for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with plant height, days to 50% flowering, days to maturity (Table 5a and 5b). Grain yield is considered to have positive correlation with plant height (cm) and hundred grain weight (Ajmal *et al*., 2000). Sumathi *et al.* (2005) also found medium strong correlative relation between these two traits, but that relation was negative, while the majority of authors (Alvi *et al.* 2003; Sofi and Rather 2005; Bocanski *et al.* 2009) who studied relation between these two traits established strong correlations between grain yield and 100-grain weight.

4.4 Path coefficient analysis

Though correlation analysis indicates the association pattern of components traits with yield, the analysis simply represents the overall influence of a particular trait on yield rather than providing cause and effect relationship. The technique of path coefficient analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

Path co-efficient analysis denotes the components of correlation co-efficient within different traits into the direct and indirect effects and indicates the relationship in more meaningful way. The results of the path co-efficient analysis are presented in Table 6.

4.4.1 Direct effects

Five out of twelve characters had positive direct effect on grain yield per plant. The characters which had positive direct effect are plant height (0.412), leaf breadth (0.073), days to 50% flowering (0.280), number of row per cob (0.461) and number of grains per row (0.209). However, character *viz.*, distance between base to cob (-0.214), base diameter of plant (-0.614), leaf length (-0.467), days to maturity (-0.262), cob length (-0.725), cob diameter (-0.355) and 100-grain weight (-0.472) had negative direct effect on grain yield (Table 6). Path coefficient analysis revealed that grain yield per plant was directly influenced by plant height(cm), leaf breadth(cm), days to 50% flowering, number of row per cob and number of grains per row. Hence, selection for any of these independent traits leads to improving the varieties for grain yield per plant.

4.4.2 Indirect effects

Plant height had negative indirect effect through base to cob distance (0.03), base diameter of plant (0.204), leaf breadth (0.005), days to 50% flowering (0.052), days to maturity (0.005), cob length (0.025), cob diameter (0.067), number of row per cob (0.120), number of grains per row (0.078) (Table 6). However, its positive indirect effects through leaf length (0.031), 100 grains weight (0.01).The effect of distance between base to cob to grain yield per plant through 100 grain weight (0.174) was remarkable, its contribution through other traits was low. Base diameter influenced the grain yield per plant indirectly through plant height (0.234), distance between base to cob (0.108), leaf length (0.079) leaf breadth (0.122), days to 50% flowering (0.085), days to maturity (0.235), cob length (0.221), cob diameter (0.073), number of row per cob (0.120), number of grains per row (0.125), 100-grain weight (0.212). Leaf length influenced the grain yield per plant indirectly through plant height

Table 6. Path coefficient analysis showing direct and indirect effects of different characters on yield of white maize

Characters	Direct effect	Indirect effect												Genotypic correlation with yield
		PH	DBC	BD	LL	LB	DF	DM	CL	CD	RPC	GPR	HGW	
PH	0.412		-0.030	-0.204	0.031	-0.005	-0.052	-0.005	-0.023	-0.067	-0.120	-0.078	0.116	-0.025
DBC	-0.214	-0.023		-0.153	-0.122	-0.068	-0.210	-0.037	-0.113	-0.067	-0.066	-0.099	0.174	-1.000**
BD	-0.614	0.234	0.108		0.079	0.122	0.085	0.235	0.221	0.073	0.120	0.125	0.212	1.000**
LL	-0.467	0.007	0.030	-0.021		0.042	0.094	0.073	0.427	0.081	0.057	0.050	0.037	0.410
LB	0.073	-0.120	0.111	-0.002	0.049		0.110	0.067	0.181	0.294	0.073	0.106	0.059	1.000**
DF	0.280	-0.072	0.051	0.081	-0.103	-0.018		-0.029	-0.095	0.021	-0.163	-0.028	-0.050	-0.125
DM	-0.262	-0.054	-0.014	0.325	0.031	-0.038	-0.020		-0.088	-0.087	-0.060	-0.086	0.045	-0.308
CL	-0.725	0.107	0.095	0.189	0.339	0.105	0.131	0.088		0.046	0.181	0.091	0.330	0.979**
CD	-0.355	0.165	0.119	0.038	0.158	0.126	0.094	0.093	0.019		0.155	0.135	0.183	0.930**
RPC	0.462	-0.027	0.093	0.103	0.077	0.096	-0.023	0.110	-0.083	0.048		0.109	0.015	0.979**
GPR	0.209	-0.132	0.116	0.080	0.061	0.082	0.058	0.176	0.157	0.019	0.123		0.052	0.999**
HGW	-0.472	-0.020	0.144	0.197	0.074	0.079	0.098	0.113	0.421	0.136	0.134	0.088		0.992**

Residual Effect = 0.13512, **1% level of significance, * 5% level of significance

PH = Plant height (cm), DBC = Distance between base and cob (cm), BD= Base diameter of Plant, LL = Leaf length (cm), LB = Breadth of leaf (cm), DF= Days to 50% flowering, DM= Days to maturity, CL = Cob length (cm), CD = Cob diameter (cm), RPC = Number of row per cob, GPR = Number of grains per row and HGW = 100 grains weight (g), YPP=Yield per plant (g)

(0.007), base to cob distance (0.030), leaf breadth (0.042), days to 50% flowering (0.094), days to maturity (0.073), cob length (0.427), cob diameter (0.081), number of row per cob (0.057), number of grains per row (0.050), 100-grain weight (0.037) (Table 6).

The indirect and positive effect on grain yield per plant was exhibited by leaf breadth via base to cob distance (0.111), leaf length (0.049), days to 50% flowering (0.110), days to maturity (0.067), cob length (0.181), cob diameter (0.294), number of row per cob (0.073), number of grains per row (0.106), 100-grain weight (0.059) Whereas, through other traits it had also negative indirect effects. Days to 50% flowering showed positive indirect effects to yield per plant through base to cob distance (0.051), base diameter of plant (0.081), cob diameter (0.021). Days to maturity showed positive indirect effects to yield per plant via base diameter of plant (0.325), leaf length (0.031) and100-grain weight (0.045). Cob length showed positive indirect effect to grain yield per plant via plant height (0.107), base to cob distance (0.095), base diameter of plant (0.189), leaf length (0.339), leaf breadth (0.105), days to 50% flowering (0.131), days to maturity (0.088), cob diameter (0.046), number of row per cob (0.181), number of grains per row (0.091), 100-grain weight (0.330) (Table 6). Cob diameter showed indirect effect on grain yield per plant had positive through plant height (0.165), base to cob distance (0.119), base diameter of plant (0.038), leaf length (0.158), leaf breadth (0.126), days to 50% flowering (0.094), days to maturity (0.093), cob length (0.019), number of row per cob (0.155), number of grains per row (0.135), 100-grain weight (0.183) (Table 6).

Number of row per cob had positive indirect effect through base to cob distance (0.093), base diameter of plant (0.103), leaf length (0.077), leaf breadth (0.096), days to maturity (0.110), cob diameter (0.048), number of grains per row (0.109), 100-grain weight (0.015) (table 6). This trait showed negative indirect effect via plant height (-0.027), days to 50% flowering (-0.023) and cob length (-0.083) (Table 8).

Number of grains per row showed indirect positive effects on grain yield per plant by base to cob distance (0.116), base diameter of plant (0.080), leaf length (0.061), leaf breadth (0.082), days to 50% flowering (0.058), days to maturity (0.176), cob length (0.157), cob diameter (0.019), number of row per cob (0.123), 100-grain weight (0.052) (Table 6). It showed indirect negative effect on grain yield per plant through plant height (-0.132) (Table 6). 100-grain weight showed indirect positive effects on grain yield per plant by base to cob distance (0.144), base diameter of plant (0.197), leaf length (0.074), leaf breadth (0.079), days to 50% flowering (0.098), days to maturity (0.113), cob length (0.421), cob diameter (0.136), number of row per cob (0.134), number of grains per row (0.088) (Table 6). It showed indirect negative effect on grain yield per plant through plant height (-0.020) (Table 6).

4.5 Genetic diversity analysis

The knowledge of genetic diversity is an important factor for any heritable improvement and its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding program. There is still much scope for improving of genetic architecture desirable for hybrid through heterosis breeding. Its magnitude in desirable direction is preferable. The success of hybridization depends upon the selection of suitable parental inbreed lines and performance of their cross combinations.

4.5.1 Principal component analysis (PCA)

Eigen values of principal component axis, percent of total variation and cumulative variation accounted for them obtained from principal component analysis (PCA) are presented in Table 7. The results showed that the first principal axis, plant height (cm) largely accounted for the variation among the lines which alone contributed 68.21% of the total variation among the lines.

The first five characters viz. plant height, base to cob distance, base diameter of plant, leaf length, leaf breadth of the principal component axes with eigen values above unity accounted for 97.89% of the total variation among the thirteen characters. The rest eight characters viz. days to 50% flowering, days to maturity, cob length, cob diameter, number of rows per cob, number of grain per row, 100-grain weight and yield per plant contributed remaining 2.11% of total variation. Based on principal component scores I and II obtained from the principal component analysis, a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed which has been presented in figure 3.

Table 7. Eigen values and yield percent contribution of 13 characters of seventeen (17) germplasm of white maize

Principal Component Axes	Eigen values	Percent variation	Cumulative of Percent variation
PH	8.87	68.21	68.21
DBC	1.46	11.20	79.41
BD	1.07	8.23	87.64
LL	0.88	6.79	94.43
LB	0.61	4.65	99.08
DFF	0.07	0.50	99.58
DM	0.02	0.19	99.77
CL	0.02	0.13	99.90
CD	0.01	0.07	99.97
RPC	0.00	0.02	99.99
GPR	0.00	0.01	100.00
HGW	0.00	0.00	100.00
YPP	0.00	0.00	100.00

PH = Plant height (cm), DBC = Distance between base and cob(cm), BD= Base diameter of Plant, LL = Leaf length (cm), LB = Breadth of leaf (cm), DF= Days to 50% flowering, DM= Days to maturity, CL = Cob length (cm), CD = Cob diameter (cm), RPC = Number of row per cob, GPR = Number of grains per row, HGW = 100 grains weight (g) and YPP= Yield per plant (g)

Table 8. Distribution of lines in different clusters

Cluster	Number of population	Inbreed lines
I	1	G5
II	6	G1,G2, G3, G9, G11 and G13
III	4	G6, G7, G8 and G10
IV	3	G4, G15 and G17
V	3	G12, G14 and G16

4.5.2 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, seventeen (17) maize lines were grouped into five different clusters. It is stated that highest 35% lines were included in cluster II and it was followed by 23% in cluster III, 17% lines in both cluster IV and V and the remaining 8% lines were in cluster I. The composition of clusters with different lines is presented in Table 8. From Table 8 cluster II had the maximum 6 lines (G1, G2, G3, G9, G11, G13) followed by cluster III which had 4 lines (G6, G7, G8, G10), cluster IV (G4, G15, G17) and V (G12, G14, G16) also had 6 lines and cluster I had 1 lines (G5).

4.5.3 Inter cluster distance

The inter cluster D^2 values are given in Table 9 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 10. The inter cluster D^2 values were maximum (14.57) between the cluster I and II, followed by I and IV (13.09) and II and V (10.53). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and II indicated the lines in these clusters were diverged than those clusters. Cluster II was the most diverse as many other clusters showed the maximum inter cluster distance with it (Table 10). The minimum distance observed between clusters II and III (3.30) indicated close relationship among the lines investigated here.

4.5.4 Intra cluster distance

The intra cluster D^2 values were given in Table 9. The intra cluster distance was observed in the clusters I, II, III, IV, V and VI. The intra cluster distance was higher in cluster I (0.654) followed by cluster II (0.456), cluster V (0.221),cluster IV (0.132), cluster III (0.087) and lowest in cluster IV (0.065). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that lines within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the lines of different groups.

Table 9. Intra and inter cluster distances (D^2) for 17 lines of white maize.

	I	II	III	IV	V
I	0	44.91	48.35	35.73	58.22
II		0	9.18	17.44	19.84
III			0	14.87	11.35
IV				0	22.81
V					0

Table 10. Nearest and farthest clusters from each cluster between D^2 vaues of white maize

Cluster	Nearest with D^2 values	Farthest with D^2 values
I	IV (35.73)	V (58.22)
II	III (9.18)	I (44.91)
III	II (9.18)	I (48.35)
IV	III (14.87)	I (35.73)
V	III (11.35)	I (58.22)

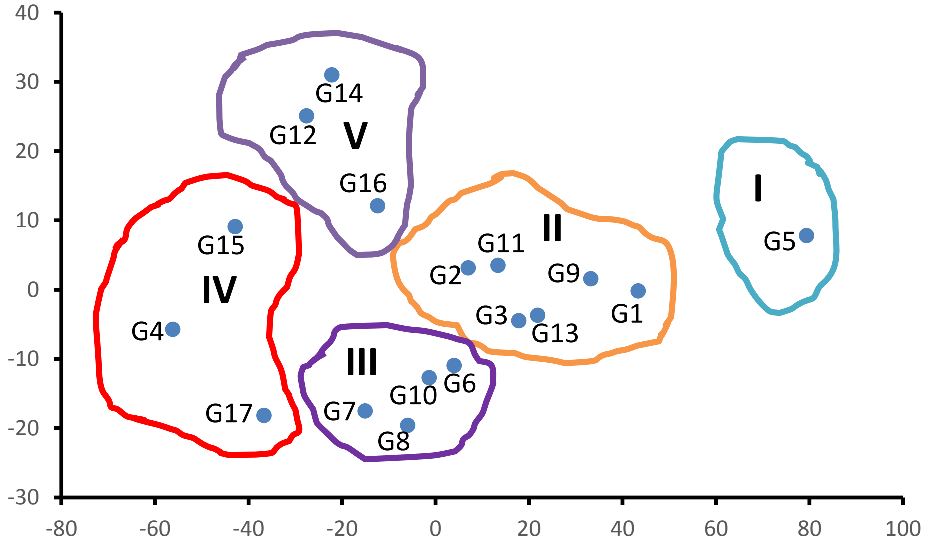


Figure 1. Intra and inter cluster distance among the 17 lines of white maize

4.5.5 Cluster diagram

The positions of the lines in the scatter diagram were apparently distributed into five groups, which indicated that considerable diversity existed among the lines (Fig 4).

4.5.6 Cluster mean analysis

The cluster means of 13 different characters (Table 11) were compared and indicated considerable differences between clusters for all the characters studied. Maximum plant height was observed in cluster III (219.29), whereas minimum plant height was observed in cluster V (182.36). Maximum (117.11) and minimum (75.2) distance between base to cob were observed in cluster IV and I respectively. lines in cluster IV showed the lowest base diameter (5.38) and cluster I had the highest mean (7.2). Maximum (72.21) and minimum (64.4) leaf length were observed in cluster I and II respectively. Maximum (9.39) and minimum (6.95) leaf breadth were observed in cluster I and VI respectively. Maximum cob length was observed in cluster I (16.47), whereas minimum cob length was observed in cluster IV (13.58). Cluster I had the maximum cob diameter (4.85), cluster IV had the minimum cob diameter (4.23). Days to 50% flowering were the highest in cluster V with a mean value of (86.83) and it was least in lines belongs to the cluster I (78.17). Days to maturity were observed in cluster V (138.67), whereas minimum cob weight was observed in cluster III (129.58). The maximum row per cob (16.57) was observed in the cluster I, whereas minimum row per cob (12.78) was observed in cluster VI. Number of grains per row was the highest in cluster I with a mean value of (30.14) and it was least in lines belongs to the cluster IV (19.02). Maximum 100-grain weight was observed in cluster I (34.1), whereas minimum 100-grain weight was observed in cluster IV (22.16). Highest yield per plant was recorded by the cluster I (170.01) while cluster IV (54.28) showed the least yield per plant.

Table 11. Cluster mean values of 13 different characters of 17 inbreed lines

Sl	Characters	I	II	III	IV	V
1	**Plant height**	195.81	204.17	219.29	209.93	182.36
2	**Distance between base to cob**	75.2	95.04	103.72	117.11	108.27
3	**Base diameter of plant**	7.2	6.43	5.99	5.38	5.75
4	**Leaf length**	72.21	64.4	69.2	64.47	69.44
5	**Leaf breadth**	9.39	8.41	7.74	6.95	7.54
6	**Days to 50% flowering**	78.17	85.67	85.58	82.61	86.83
7	**Days to maturity**	131.67	133.5	129.58	135.78	138.67
8	**Cob length (cm)**	16.47	15.84	14.87	13.58	14.21
9	**Cob diameter**	4.85	4.75	4.59	4.23	4.52
10	**No. of row per cob**	16.57	15.37	14.64	12.78	13.91
11	**No. of grains per row**	30.14	25.8	23.25	19.02	21.74
12	**100 grain weight**	34.1	29.57	26.94	22.16	25.27
13	**Yield per plant**	170.01	117.66	91.89	54.28	76.55

4.5.7 Contribution of characters towards divergence

Contribution of characters towards the divergence obtained from canonical variates analysis is presented in Table 12. The character, which gave high absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If the same characters given equal magnitude for both the vectors than the character was considered as responsible for primary as well as secondary differentiation.

In vector (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were leaf length (0.4669), leaf breadth (0.0281), days to 50% flowering (0.4394), days to maturity (0.5996), cob diameter (0.1178), number of rows per cob (0.009), number of grains per row (0.0136), 100 grains weight (0.0054) were important because all these characters had positive signs.

On the other hand, plant height, base to cob distance, base diameter of plant, cob length (cm), yield per plant possessed the negative sign in the first axis of differentiation and base diameter of plant (cm), leaf length (cm), leaf breadth cob length (cm), cob diameter (cm), number of row per cob, number. of grains per row, 100 grain weight (g), yield per plant (g) possessed negative signs in the second axis of differentiation that means it had minor role in the genetic diverse. Days to 50% flowering, days to maturity had positive signs in both the vectors, which indicated they were the important component characters having higher contribution to the genetic divergence among the materials studied.

Table 12. Relative contributions of the thirteen characters of seventeen lines to the total divergence

Sl. No.	Parameters	Vector-1	Vector-2
1	**Plant height** (cm)	0.0051	-0.46
2	**Distance between base to cob**	0.3318	-0.0335
3	**Base diameter of plant** (cm)	-0.333	-0.0151
4	**Leaf length** (cm)	-0.0366	0.4669
5	**Leaf breadth** (cm)	-0.3329	0.0281
6	**Days to 50% flowering**	0.013	0.4394
7	**Days to maturity**	0.0985	0.5996
8	**Cob length** (cm)	-0.3283	-0.034
9	**Cob diameter** (cm)	-0.3221	0.1178
10	**No. of row per cob**	-0.3319	0.009
11	**No. of grains per row**	-0.335	0.0136
12	**100 grain weight** (g)	-0.3346	0.0054
13	**Yield per plant** (g)	-0.3331	-0.0187

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted in the experimental area of Sher-e-Bangla Agricultural University, Dhaka during October, 2016 to April, 2017 to study the genetic diversity, correlation and path co-efficient analysis for yield and yield contributing characters of white maize lines collected from CIMMYT and Bangladesh. In this experiment seventeen maize lines were used as experimental materials. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Mean performance, variability, correlation and path analysis on different yield contributing characters and yield of maize lines were estimated.

Analysis of variance revealed highly significant difference among the accessions for all the characters. The maximum plant height was 223.93 cm recorded in the line CLTHW15010 and minimum was 172.67 cm recorded in the line CLTHW14001. The maximum distance between cob to base was recorded in CLTHW15007 (121.80 cm) and minimum in CLTHW15008 (75.20 cm). Maximum base diameter was noted in CLTHW15008 (7.20 cm) while minimum in CLTHW15007 (5.10 cm). The minimum and maximum leaf length was observed in the line CLTHW15015 (59.47 cm) and CLTHW15010 (76.19 cm) respectively. The minimum leaf breadth was in CLTHW15007 (6.63 cm) and maximum cob length was for CLTHW15008 (9.39 cm). Maximum days to 50% flowering was recorded in line CLTHW15011 (87.83 cm) while minimum was CLTHW15008 (78.17 cm).Maximum days to maturity were recorded in line CLTHW15014 (151.67 days) while minimum was CLTHW14001 (129.33days). Maximum cob length was recorded in line CLTHW15008 (16.47 cm) while minimum was CLTHW15007 (13.17 cm). Maximum cob diameter was recorded in line CLTHW15008 (4.85 cm) while minimum was CLTHW15007 (4.06 cm).The lowest number of row per cob was observed in line CLTHW15007 (12.11) while highest was CLTHW15008 (16.57). The lowest number of grain per row was observed in line CLTHW15007 (17.89) while highest was CLTHW15008 (30.14).100-grain weight ranged from 20.54 g to 34.10 g which was observed in CLTHW15007 and CLTHW15008 respectively. The highest total yield per plant was observed in the line CLTHW15008 (170.01 g). The lowest total yield per plant was observed in the line CLTHW15008 (44.52 g).

Characters like plant height (cm), base to cob distance (cm), base diameter of plant (cm), leaf breadth (cm), number of row per cob, number of grain per row, 100-grain weight (g) and yield per exhibited high (g) genotypic and phenotypic co-efficient of variation. The phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all characters which indicated greater influence of environment for the expression of these characters. The maximum differences between phenotypic and genotypic co-efficient of variation were 32.89 and 32.77 respectively, which indicated that yield per plant was mostly dependent on the environment condition. Amongst the characters, the highest genotypic co-efficient of variation was recorded for total yield per plant (33.77 g) followed by number of grain per row (13.20) and 100-grain weight (12.50 g). The maximum genotypic and phenotypic variations were 994.4548 and 1002.1035 respectively in yield per plant.

The highest estimated heritability amongst 13 characters of maize was 99.91% for 100-grain weight and the lowest was 2.42% for leaf length. The highest genetic advance amongst 13 characters was found in yield per plant is 64.71 and the lowest genetic advance was carried out in leaf length (0.39). The maximum genetic advance in percent of mean was observed for total yield per plant (67.24), followed by number of grain per row (26.58), 100-grain weight (25.74) and leaf breadth (17.65). High heritability accompanied with high to moderate GCV and genetic advance indicates that most likely the heritability is due to additive gene effects.

Again, considering both genotypic and phenotypic correlation co-efficient among thirteen yields contributing characters of 17 maize lines, total yield per plant was positively and significantly correlated with base diameter of plant (1.00), leaf breadth (1.00), cob length (0.979), cob diameter (0.930), number of row per cob (0.979), number of grain per row(0.999), 100-grain weight(0.992). Path analysis revealed that plant height (0.412), leaf breadth (0.073), days to 50% flowering (0.280), number of rows per cob (0.462), number of grain per row (0.209) had positive direct effect on yield/plant. Base to cob distance (-0.214), base diameter (-0.614), leaf length (-0.467), days to maturity (-0.262), cob length (-0.725), cob diameter (-0.355), 100-grain weight (-0.472) had negative direct effect on grain yield.

Clustering pattern denoted that, cluster II was the largest cluster comprising of 6 lines and cluster III belonged to 4 lines of maize. The maximum inter-cluster divergence was observed between cluster I and V (58.22) followed by cluster I and III (48.35).The maximum values of inter-cluster distance indicated that the lines belonging to cluster I was far diverged from those of cluster V. The distance was minimum between cluster II and III (9.18) followed by cluster III and V (11.35). The highest intra-cluster distance was computed for cluster II (0.316) composed of 6 lines followed by the cluster V (0.220) composed of three lines. However, the lowest value (0.172) of intra-cluster distance in cluster I indicated 4 lines constituted this cluster might have diverged characters.

In respect of cluster mean performances of different cluster revealed that cluster I can be selected for cob length (cm), cob breadth (cm), grain per row, cob weight, 100-grain weight (g) and yield per plant (g). Cluster II was remarkable due to lowest plant height, leaf length, diameter of leaf, cob length, row per cob, grain per row, grain per cob, 100-grain weight and total yield per.

Considering diversity pattern, genetic status and other agronomic performance, CLTHW15008 from cluster I; CLTHW15004, CLTHW15005, CLTHW15006, CLTHW15011, CLTHW15001 and CLTHW15015 from cluster II might be considered as better parents for efficient hybridization program to get heterotic effect to develop potential white maize hybrid lines. Result of present study revealed that the characters; plant height, base to cob distance, base diameter, leaf length, leaf breadth, number of grain per row and 100-grain weight contributed maximum divergence among the maize lines. Involvement of such diverse lines in crossing program may produce desirable sergeants. So, these divergent lines are recommended to use as parent in hybridization program.

Recommendations:

Considering the above findings of the present experiment, the following recommendations and suggestions may be made: Considering diversity pattern, genetic variability and other agronomic performance CLTHW15008 from cluster I; CLTHW15004, CLTHW15005, CLTHW15006, CLTHW15015 from cluster II might be selected as potential parents for hybridization program for further improvement of the crop.

Reference

Abayi, I.K., Ojo, A.A., Kalu, B.A. and Adeyemo, M.O. (2004). Genetic variability, heritability and genetic variance in S1 progenies of extra-early and early maize (*Zea mays* L.) population. *J. Sustain. Agric. Environ*. **6**: 179-184.

Abd El-Sattar, A.A. (2003). Genetic parameters estimation from design-1 and S1 lines in maize. *Minufiya J. Agric. Res*. **28**(5): 1387-1402.

Abel, B.C. and Pollak, L.M. (1991). Rank comparisons of unadapted maize populations by testers and per se evaluation. *Crop Sci*. **31**: 650-656.

Abirami, S., Vanniarajan, C and Armugachamy, S. (2005). Genetic variability studies in maize (*Zea mays* L.) germplasm. *Plant Archeives*. **5**(1): 105-108.

Abou-Deif, M.H. (2007). Estimation of gene effects on some agronomic characters in five hybrids and six population of maize (*Zea mays* L.). *World J. Agric. Sci.* **3**(1): 86-90.

Agrawal, K.B. (2002).Characters association and heriatability. *Revista Brasileira de Milhoe Sorgo*. **1**(3): 59-67.

Ahamed, K.U. (2010). Efficacy of indigenous mulches on maize–pulse association. A. Ph.D. Thesis, Department of Crop Botany, Bangladesh Agricultural University, Mymensingh. p. 1–202.

Ahmed, F. (1994). Maize Production Technology (in Bengali). Published by International Fertilizer Development Centre. Consultant of Ministry of Agriculture, Bangladesh. p. 13-15.

Ahmed, M., Mian, M.A. and Chowdhury, M.A. (2011). Correlation study in maize. *J. Agric. Res.* **16**: 399-405.

AL-Ahmad, A.S. (2004). Genetic parameters for yield and its components in some new yellow maize crosses. Ph.D. Thesis, *Faculty of Agriculture*, Ain Shams Univ., Egypt.

Ali F., Shah, I.A., Rahman, H., Noor, M., Durrishahwar, Khan, M.Y., Ullah, I. and Yan, J.B. (2012). Heterosis for yield and agronomic attributes in diverse maize germplasm. *Australian J. Crop Sci*. **6**: 455-462.

Ali, M. Y., S. R. Waddington, J. Timsina, D. Hodson and J. Dixon (2009). Maize-rice cropping system in Bangladesh: Status and research needs. J. of Agric. Sci. Technol. 3(6): 35-53.

Allard, R.W. (1960). Principles of Plant Breeding, John Wiley and Sons. Inc., New York. p. 43.

Alvi, M.B., Rafique, M., Shafique, M., Hussain, A., Mohommad, T. and Sarwar, M. (2003). Characters association and path analysis of grain yield and yield components in maize. *Pakstan J. Biol. Sci*. **6**(2): 136-138.

Amer, E.A. and Mosa, H.E. (2004). Gene effects of some plant and yield traits in four maize crosses. *Minofiya J. Agric. Res*. 1(29): 181-192.

Amin, A.Z., Khalil, H.A. and Hassan, R.K. (2003). Correlation studies and relative importance of some plant characters and grain yield in maize single crosses. *Arab Univ. J. Agric. Sci*. **11**(1): 181-190.

Anonymous. (1987). Annual Report. Plant Breeding Division, Maize Section Bangladesh Agril. Res. Inst. Joydevpur. Gazipur.

Anshuman, V., Dixit, N.N., Sharma, S.K and Marker, S. (2013). Studies on heritability and genetic advance estimates in Maize genotypes. *Bioscience Discovery*. **4**(2):165-168.

Aydin, N., Gökmen, S., Yildirim, A., Öz, A., Figliuolo, G. and Budak, H. (2007). Estimating genetic variation among dent corn inbred lines and top crosses using multivariate analysis. *J. Appl. Bio. Sci*. **1**(2): 63-70.

Babu, R., Gumaste, S., Patil, S.J., Jayanna, M. and Patil, T.C. (1996). Performance of Ksheeramrutha-a high yielding forage maize variety for Karantaka. Karantaka J. Agril Sci. **9**(1): 1-6.

Bahoush, M. and Abbasdokht, H. (2008). Correlation coefficient analysis between grain yield and its components in corn (*Zea mays* L.) hybrids. International meeting on soil fertility land management and Agroclimatology. Turkey. pp: 263-265

Barbiani, G., Signor, M. and Snidaro, M. (2008). Good results with maize hybrids in 2007. Notiziario ERSA. **22**(1): 28-36.

BARI, (1990). A Decade of agronomic research (1978-88). Div. Agron. Bangladesh Agril. Res. lnst. Gazipur. pp. 29-34.

BBS. (2018). Statistical Year Book Bangladesh, Bangladesh Bureau of Statistics, Statistic Division, Ministry of Planning, Government people's Republic of Bangladesh, Dhaka, p. 141.

Begna, S.H., Hamilton, R.I., Dwyer, L.M., Stewart, D.W. and Smith, D.L. (2000). Variability among maize hybrids differing in Canopy architecture for above-ground dry matter and grain Yield. Maydica. **45**(2): 135-141.

Begum, S.N. and Roy, A.K. (1987). Proc. 12"'Bangladesh Sci. Conf. Sec. l. p. 58.

Bello, O.B., Abdulmaliq, S.Y., Afolabi, M.S., and Ige, S.A. (2010). Correlation and path coefficient analysis of yield and agronomic characters among open pollinated maize varieties and their F1 hybrids in a diallel cross. *African J. Biot.* **9**(18): 2633-2639.

Bikal, G. and Deepika, T. (2015). Analysis of yield and yield attributing traits of maize genotypes in Chitwan, Nepal. *World J. Agril. Res*. **3**(5): 153-162.

Brkic, I., Simic, D., Jambrovic, A., Zdunic, Z. and Ledencan, T. (2003). Genetic diversity among and within maize inbreds as revealed by 100 SSR markers. Sjemenarstvo. **20**(l and 2): 5-14.

Burton, G.W. (1952). Quantitative inheritance in Grasses. Proc. 6th Intl. Grassland Cong. **1**: 277-283.

Chen, L., Cui, A.P and Sun, Y.B. (1996). Analysis of the gene effect on ear characters in maize. ActaAgril. Bareli Sinica. **11**(2): 28-32.

Chowdhury, N.K. and Islam, M.A. (1993). Production and uses Maize (In Bengali). Pub. By on Farm Res. Div. Bangladesh Agril. Inst. Joydebpur, Gazipur. p. 1-189.

CIMMYT (International Maize and Wheat Improvement Centre). (2008). Achievement of the Bangladesh CIMMYT partnership for agricultural research and development. pp. 1-9.

Comstock, R.E. and Robinson, H.F. (1952). Genetic parameters, their estimate and significance, Proc. 6th *Intl. Grassland Cong*. 1: 284-291.

DAE. (2012). Department of Agriculture Extension. Annual Report for 2011-12. Bangladesh Agricultural University, Mymensingh.

Dass, S., A. Kumar, S. L. Jat, C. M. Parihar, A. K. Singh, G. K. Chikkappa, and M. L. Jat (2012). Maize holds potential for diversification and livelihood security. Indian J. Agron. (Special Issue) 57:86-91.

Debnath, S.C. (1991a). Analysis of heterosis in a 10×10 diallel crosses of maize. *Bangladesh J. Agril. Sci*. **19**: 161-164.

Debnath, S.C. (1991b). Variability and character association in forth generation selfed lines of maize. *Bangladesh J. Agril. Sci.* **18**: 187-190.

Debnath, S.C. (1992). Variability and character association in forth generation selfed lines of maize. *Bangladesh J. Agril. Sci*. **18**: 187-190.

Devi, K.T., Mayo, M.A., Reddy, G., Emmanuel, K.E., Larondelle, Y. and Reddy, D.V.R. (2001). Occurrence of Ochratoxin A inblack pepper, coriander, ginger and turmeric in India. Food Additives Contamination. **18**: 830-835.

Deway, D.R. and Lu, K.N. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J* .**51** : 515-518.

Dewey, D.R. and Lu, K.H. (1959). A correlation and path coefficient analysis of components of creast wheat grass seed production. *Agron. J. Hort*. **57**(4): 342-346.

Digby, P., Galway, N. and Lane, P. (1989). Genstat 5: A second course. *Oxford*.

Dijak, M., Modarres, A.M. and Hamilton, R.I. (1999). Leafy reduced-stature maize hybrids for short-season environments. *Crop Sci*. **39**: 1106-1110.

Drinic, S.M., Trifunovic, S., Drinic, G. and Konstantinov, K. (2002). Genetic divergence and its correlation to heterosis in maize as revealed by SSR-based markers. Maydica. **47**(1): 1-8.

Edris, K.M., Islam, A.T.M.T., Chowdhury, M. S. and Haque, A.K.M.M. (1979). Detailed Soil Survey of Bangladesh, Dept. Soil Survey, BAU and Govt. People’s Republic of Bangladesh. p. 118.

Efferson, K.J. (1982). Comparing farmers and breeders rankings in varietal selection for 1ow-input environments: a case study of rainfed rice in eastern India. *Euphytica*. **122**(3): 537-550.

El-Beially, I.E.M.A. (2003). Genetic analysis of yield characters in yellow maize inbred lines. *Zagazig. J. Agric. Res.* **30**(3): 677-689.

El-Hosary, A.A., Sedhom, S.A. and Mohamed, S.A. (1989). Correlation and path coefficient studies in maize. *Ann. Agric. Sci*. **27**(3): 1517-1525.

Evans, L.T. (1975). The physiological basis of crop yield. In: Crop Physiology. Camb. Univ. Press. Cambridge. pp. 327-355.

FAO. (1988). Production Year Book. Food and Agricultural Organizations of the United Nations. Rome, Italy. p. 190-193.

Farhan, A., Muneer, M., Hassan, W., Rahman, H.U., Noor, M.,Tariq Shah, T., Ullah, I., Iqbal, M., Afridi, K. and Ullah, H. (2012). Heritability estimates for maturity and morphological traits based on testcross progeny performance of maize. *ARPN J. Agric. Bio. Sci*. **7**(5).

Fetahu, S.h., Aliu, S. and Kaçiu, S. (2005). Variability and genetic erosion of white landrace of Maize (*Zea mays* L.) in Kosova. Eucarpia, Proceedings of the XVII Eucarpia Genetic Resources Section Meeting. Plant Genetics Resources of Geographical and “other” Island. Conservation, evaluation and use for plant breeding. Pp: 265-269.

Ganguli, D.K., Haque, M.F. and Sinha, P.K. (1989). Heterosis in inter population crosses in maize. *J. Res.***3**: 59-63.

Geetha, K. and Jayaraman, N. (2000). Path analysis in maize (*Zea mays* L.). *Agric. Sci. Digest.* **20**:60-106.

Genter, C.F. and Alexander, M.W. (1965). Test cross variability of samples from a broad based population of maize. *Crop Sci*. **5**: 355-358.

Gomez, K.A. and Gomez, A.A. (1984). Statistical Procedure for Agricultural Research (2nd edn.). Int. Rice Res. Inst., A Willey Int. Sci., Pub., p. 28-192.

Grzesiak, S. (2001). Genotypic variation between maize (*Zea mays* L.) single-cross hybrids in response to drought stress. Act a Phys. Plant., **23**(4): 443-456.

Hallauer, A.R. and Miranda, J.B. (1995). Quantitative genetics in maize breeding. 2nd edn. Ames: Iowa State and University press, p. 468.

Helm, T.C., Hallauer, A.R. and Smith, O.S. (1989). Genetic variability estimate in improved and unimproved Iowa Stiff Stalk Synthetics maize population. *Crop Sci*. **29**: 259-962.

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

Hoisington, D., Khairallah, M., Reeves, T. and Ribaut, J.M. (1999). Plant genetic resources: what can they contribute toward increased crop productivity.*Proc. Natl. Acad. Sci. USA*. **96**: 5937-5943.

Ilarslan, R., Kaya, Z., Kandemir, I. and Bretting, P.K. (2002). Genetic variability among Turkish populations, Flint and dent corn (*Zea mays spp. Mays*) races; morphological and agronomic traits. *Euphytica*, **128**: 173-182.

Ishaq, M., Rahman, H., Hassan, G., Iqbal, M., Khalil, I.A., Khan, S.A., Khan, S.A., Rafiullah, M. and Hussain, J. (2015). Genetic potential, variability and heritability of various morphological and yield traits among maize synthetics. *Elect. J. Bio.* **11**(4): 187-191.

Jager, M.I., Gerethojones, D. and Griffiths, E. (1983). Components of partial resistance of wheat seedlings to Seporianodrom. *Euhpytica*. **32**: 575-585.

Jha, P.B., Singh, T.P. and Aktar, S.A. (1979). Analysis of yield components in early maize germplasm complexes. *The Madras Agril. J.* **66**(9): 56l-564.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybeans. *Agron. J*.**3**: 314-318.

Joshi, A.B. and Dhawan, N.L. (1966). Genetic improvement of yield with special reference to self-fertilizing crops. *Indian J. Genet*. **26**: 101-113.

Kaul, M.L.M. (1985). Genetic divergence analysis in rice. *Annals of Biol*. **16**(1): 41-44.

Khazaei, F., Alikhani, M.A., Yari, L. and Khandan, A. (2010). Study the correlation, regression and path coefficient analysis in sweet corn (*Zea mays* var.

saccharata) under different levels of plant density and nitrogen rate. *ARPN J. Agric. Biol. Sci.* **5**: 14-19.

Khumkar, M.S. and Singh, R.D. (2002). Divergence analysis of elite inbred lines of maize (*Zea mays* L.). *Ann. Agril. Res*. **23**(4): 595-601.

Kumar, P.G., Prashanth, Y., Kumar, S.S., Reddy, N.V., and Rao, V.P. (2014). Character association and path coefficient analysis in maize (*Zea mays* L.). *Int. J. Appl. Bio. Pharm. Tech*. **5**(1): 257-260

Kwaga, Y.M., (2014). Correlation coefficients between grain yield and other characters of maize (*Zea mays* L.) grown at Mubi in Northern Savanna, Nigeria. *Int. J. Farm Alli. Sci*. **3**(2): 220-224.

Lee, T.C., Shieh, G.J., Ho, C.L. and Juang, J.R. (1986). Analysis of diallel sets of dent and flint maize inbreeds for combining ability and heterosis. *J. Agril. Res. China*. **35**: 145-164.

Li, Y., Shi, Y.S., Song, Y.C., Du, J.Y., Tuberosa, R. and Wang, T.Y. (2004). Analysis of genetic diversity in maize inbred lines based on AFLP markers. Maydica. **49**(2): 89-95.

Mahmood, Z., Mailk, S.R., Akthar, R. and Rafique, T. (2004). Heritability and genetic advance estimates from maize genotypes in ShishiLusht a valley of Krakurm. *Int. J. Agri. Bio*. **2**(2): 253-257.

Matsuoka, Y., Vigouriux, Y., Goodman, M.M., Sanchez, G.J. Buckler, E. and Doebley, J. (2002). A single domestication for maize shown by multilocus microsatellite genotyping. Proceeding of the national academy of sciences. **99**: 6080-6084.

Melchinger, A.E., Reif, J.C., Frisch, M., Hoisington, D.A., Beck, D., Pixley, K. and Warbunon, M.L. (2005). Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers. *Crop Sci*. **44**(6): 2230-2237.

Mihaljevic, R.C., Schoon, C.C., Utz, H.F. and Melchinger, A.E. (2005). Correlation and QTL correspondence between line per se and test cross performance for agronomic traits in four populations of European maize. *Crop Sci*. **45**: 114-112.

Mohammadi, S.A., Prasanna, B.M. and Singh, N.N. (2003). Sequential path model for determining inter-relationships among grain yield and related characters in maize. *Crop Sci*. **43**: 1690–1697.

Mohan, Y.C., Singh, D.K. and Rao, N.V. (2002). Path coefficient analysis for oil and grain yield in maize (*Zea mays* L.) genotypes. *National J. Plant Improvement*. **4** (1): 75-76.

More, A.J., Bhoite, K.D. and Pardeshi, S.R. (2006). Genetic diversity studies in forage maize (ZeamuysL.). *Res. Crops.* **7**(3): 728-730.

Murthy, R. (1966). Heterosis and combining ability in relation to genetic divergence in flue cured tobacco. *lndian J. Genet*. **25**: 46-56.

Mustafa, H.S.B., Aslam, M., Ejaz-ul-Hasan., Hussain, F. and Farooq, J. (2014) Genetic variability and path coefficient in maize (*Zea mays* L.) genotypes. *J. Agric. Sci.* **9**:1

Najeeb, S., Rather, A.G., Parray, G.A., Sheikh, F.A. and Razvi, S.M. (2009). Studies on genetic variability, genotypic correlation and path coefficient analysis in maize under high altitude temperate ecology of Kashmir.Maize Genetics Cooperation Newsletter. **83**: 46-47.

Naushad, A.T., Shah, S.S., Ali, S., Rahman, H., Ali, T. and Sajjad, M. (2007). Genetic variability for yield parameters in maize (*zea mays* l.) genotypes. *J. Agri. Bio. Sci*. **2**: 4-5.

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

Nevo, E., Golenberg, E., Beilies, A., Brown, A.H.D. and Zohary, D. (1982). Genetic diversity and environmental association of wild wheat, *Tritium*: in Israel. *Theory Appl. Genet*. **62**: 241-254.

Ogunniyan, D.J. and Olakojo, S.A. (2014). Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (*Zea mays* L.). *Nigerian J. Genet*. **28**: 24-28.

Ojo, D.K., Omikunle, O.A., Oduwaye, O.A. Ajala, M.O. and Ogunbayo, S.A. (2006). Heritability, character correlation and path coefficient analysis among six inbred- lines of maize (*Zea mays* L.). *World. J. Agric. Sci*. **2**(3): 352-358.

Onn, L.C. (1988). Maximum yield research towards predicting high yields of maize in Malaysia. Proc. Symposium on maximum yield research Nov. 16-18. New Delhi. India. *Field Crop Abst*. **43**(4): 305-990.

Oz, A. (2012). Comparison of hybrid maize obtained from inbred lines that are selected via top-crossing and discriminant analysis. J. Agric. *Forest*. **36**: 659-667.

Pande, R.C., Rajput, U.S., and Tawari, R.C. (1971). Studies on the yield and yield components in different hybrids, composites and local variety of maize (*Zea mays* L). *Mysore J. Agri. Sci.* **5**(2): 181-186.

Pavan, R., Lohithaswa, H.C, Wali, M.C., Prakash, G. and Shekara, B.G. (2011). Correlation and path analysis of grain yield and yield contributing traits in single cross hybrids of maize (*Zea mays* L.). *Electron J. Plant Breed*. **2**: 253-257.

Pavlov, J., Delic, N., Stevanovic, M., Camdzija, Z and Grcic, N. (2003).

Population in high altitude temperate conditions in Kashmir. *Indian J. Agric. Sci*. **79**(3): 179-180.

Praveen, K.G., Reddy, V.N., Kumar, S.S. and Rao, P.V. (2014). Genetic variability, heritability and genetic advance studies in newly developed maize genotypes (*Zea mays* L.). *Int. J. Pure Appl. Biosci*. **2**(1): 272-275.

Prodhan, H.S. and RAI, R. (1997). Genetic variability in popcorn. *Indian J. Agric*. **41**: 287-290.

Rafalski, A., Wisniewska, J., Adamczyk, M., and Krolikowski, Z. (2001). Molecular analysis of genetic diversity among maize inbred lines. Biuletyn-1nstytutu-Hodowli-i- Aklimatyzacji-Roslin. **217**: 127-137.

Rahman, M. (2008). Variability, correlation and path analysis in maize. *Indian J. Agric.* **41**: 287-290.

Rahman, M.M., Ali, M.R., Islam, M.K., Sultan, M.S. and Mitra, B. (1995). Correlation and path coefficient studies in maize (*Zea mays* L.) composites. *Bangladesh J. Sci. Indust. Res*. **30**: 87-92.

Rajesh, V., Kumar, S., Reddy, N.V. and Sanker, S.A. (2013). Studies on genetic variability, heritability and genetic advance estimates in newly developed maize genotypes (*Zea mays* L.). Int. *J. Appl. Bio. Pharm. Tech*. **4**(4): 242-245.

Rao, C.R. (1952). Advanced statistical methods in Biometrics Research, John Wiley and Sons, New York, p. 357-369.

Rather, A.G., Bhatt, M.A. and Zargar, M.A. (2003). Genetic variation in maize (*Zea mays* L.) population,in high altitude temperate conditions in Kashmir. *Indian J. Agril. Sci.* **79**(3): 179-180.

Ray, D. K., N. D. Mueller, P.C. West and J. A. Foley (2013). YYield trends are insufficient to double global crop production by 2050. PLoS ONE 8, e66428.

Sadek, S.E., Ahmed, M.A. and Abd El-Ghaney, H.M. (2006). Correlation and path coefficient analysis in five parents inbred lines and their six white maize (*Zea mays* L.) single crosses developed and grown in Egypt. *J. Appl. Sci. Res.* **2**(3): 159-167.

Salillari, A., Hyso, M., Faslia, N., Rusinovci, I. (2007). Resurset Gjenetike. ESHFF, .Tiranë. Pp.269-276.

Satyanarayana, E. and Kumar, R.S. (1995). Genetic variability and per se performance of non-conventional hybrids in maize. *Mysore J. Agric. Sci*. **29**(3): 213-218

Sehata, A.H. (1975). Association among metric attributes in varietial maize populations in relation to their future improvement. *Egyptian J. Genet. Cytol.* **4**(1): 66-89.

Selvaraj, C.I., Nagarajan, P. (2011). Inter-relationship and path coefficient studies for qualitative traits, grain yield and other yield related attributed among maize (*Zea mays* L.). *Int. J. Plant Breed. Genet*. (In Press).

Shanthi, P.E., Satyanarayana, G., Babu, S. and Kumar, R.S. (2011). Studies on genetic variability for phenological, yield and quality parameters in quality protein maize (QPM) (*Zea mays* L.). *Crop Res.* **41**(1, 2 and 3): 188-191.

Shaw, R.H. (1988). Climate requirement. In: Sprague G.F., Dudly J.W eds.Corn and Corn Improvement. 3rd ed. Madism, WI: ASA p.609.

Singh, P., Sain, D., Dwivedi, V.K., Kumar, Y and Sangwan, O. (2005). Genetic divergence studies in maize (*Zea mays* L.). *Ann. Agric. Biol. Res*. **10**: 43-46.

Singh, P.K. and Chaudhari, L.B. (2001). Genetic divergence in maize (*Zea mays* L.). J. Res. Birsa Agricultural University. **13**(2): 193-195.

Singh, P.K., Jha, P.B. and Kumar, P. (2003). Genetic divergence in fodder maize. *J. Appl. Biol.* **13**(1-2): 24-28.

Singh, R.K. and Chaudhury, B.D. (1985). Biometrical Method in Quantitative Genetics Analysis (rev. ed.). Kalyain Publishers, New Delhi, India, p. 78-85.

Singh, S.P. and Nigam, H.K. (1977). Path co-efficient analysis for yield components in maize. Allahabad Farmer. **48**: 163-165.

Sofi, P. and Rather, A.G. (2007). Studies on genetic variability, correlation and path analysis in maize (*Zea mays* L.). MNL. 81: 27.

Subramanian, P.S., Kolandaiswamy, S. and Subramanian, S. (1981). Path co-efiicient study in maize. *The Madras Agril. J.* **68**: 61-64.

Tabanao, D.A. and Bernardo, R. (2005). Genetic variation in maize breeding population with different numbers of parents. *Crop Sci*. 45: 2301-2306.

Triveni, S.A. Kumar, S.C. and Dwivedi, R.P. (2014). Traits based on testcross progeny performance of maize. *ARPN J. Agril. Biol. Sci*. **7**: 5.

Umar, U.U., Ado, S.G., Aba, D.A. and Bugaje, S.M. (2015). Studies on genetic variability in maize (*Zea mays* L.) under stress and non-stress environmental conditions. *Intl. J. Agril. Res*. **7**(1): 70-77.

Venugopal, M., Ansari, N.A. and Rajani, K.T. (2003) Correlation and path analysis in maize. *Crop Res. Hisar* **25**: 525-529.

Viola, G., Reddy, S.S. and Kumar, C.V. (2004). Study on heritability and genetic advances in elite baby corn (*Zea mays* L.) lines. *Prog. Agril.* **3**(2): 127-128.

Virk, D.S., Chakraborty, M., Ghosh, J., Prasad, S.C. and Witcombe, J.R. (2005). Increasing the client orientation of maize breeding using farmer participation in Eastern India. *Expt. Agric*. **41**(4): 413-426.

Wannows, A.K., Azzam, H.K. and AL-Ahmad, S.A. (2010). Genetic variances, heritability, correlation and path coefficient analysis in yellow maize crosses (*Zea mays* L.). *Agric. Biol. J. N. Am*. **1**(4): 630-637.

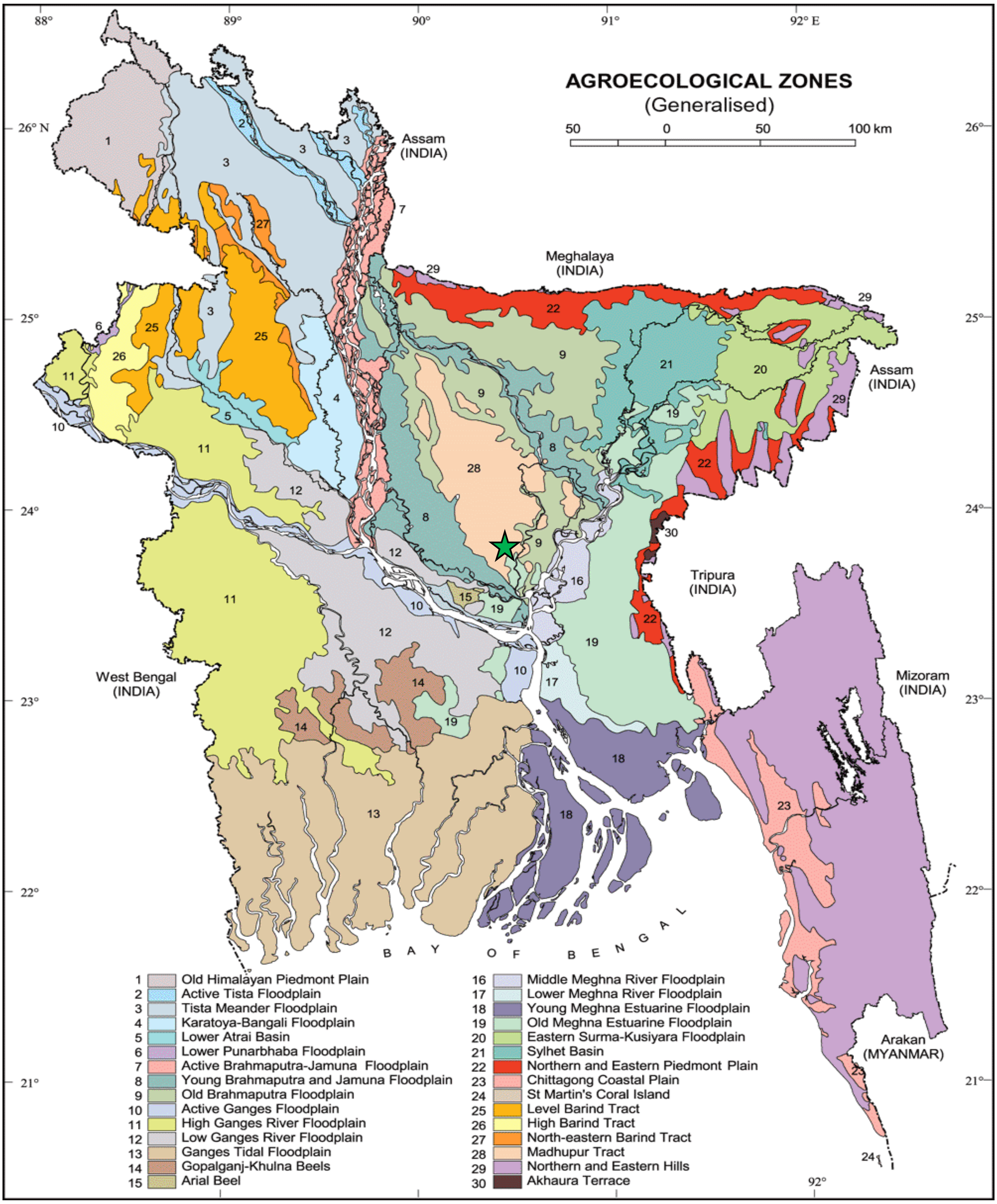
Wright, S. (1921). Correlation and Causation. *J. Agric. Res*. **20** : 202-209.

Yagdi, K. and Sozen, E. (2009). Heritability, variance components and correlations of yield and quality traits in durum wheat (Triticum durum Desf.). *Pakstan J. Bot.* **41**(2): 753-759.

Zdunic, Z, Mijic, A., Dugalic, K., Simic, D., Brkic, J. and Marjanovic-Jeromela, A. (2008). Genetic analysis of grain yield and starch content in nine maize populations. *Turkish J. Agric. Forest*. **32**: 495-500.

Appendices

Appendix 1. Map showing the experimental site under the study



★ The experimental site under the study

Appendix 2. Morphological, Physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

Soil separates	%	Methods employed
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

C. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (me/100 g soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Farmgate, Dhaka

Appendix 3. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from November, 2017 to February, 2018.

Month	**Air temperature (ºc)**		**Relative humidity (%)**	**Rainfall (mm) (total)**	**Sunshine (hr)**
	Maximum	**Minimum**			
November, 2017		18.0	77	227	**5.8**
December, 2017	32.4	16.3	69	0	**7.9**
January, 2018	29.1	13.0	79	0	**3.9**
February, 2018	**28.1**	**11.1**	**72**	**1**	**5.7**

Source: Bangladesh Meteorological Department (Climate and Weather Division), Agargoan, Dhaka – 1212

Appendix 4. Mean performance of various growth parameter and yield components

Parameters Genotypes	Plant height	Distance between base to cob	Base diameter of plant	Leaf length	Leaf breadth	Days to 50% flowering	Days to maturity	Cob length (cm)	Cob diameter	No. of row per cob	No. of grains per row	100 grain weight	Yield per plant
G1	203.73	89.80	6.90	63.53	8.90	86.17	130.33	16.23	4.82	15.73	27.40	31.85	137.30
G2	201.53	99.00	6.19	67.00	8.09	87.17	136.00	15.40	4.67	15.00	24.53	27.85	102.57
G3	208.27	97.40	6.33	60.60	8.31	81.17	131.33	15.73	4.72	15.20	25.43	29.25	113.23
G4	210.53	121.80	5.10	60.00	6.63	82.17	134.67	13.17	4.06	12.11	17.89	20.54	44.52
G5	195.81	75.20	7.20	72.21	9.39	78.17	131.67	16.47	4.85	16.57	30.14	34.10	170.01
G6	215.03	100.60	6.13	68.21	7.94	86.17	130.33	15.23	4.65	15.00	24.22	27.45	99.80
G7	221.60	106.67	5.81	66.26	7.59	86.17	129.33	14.22	4.53	14.07	22.27	26.14	82.00
G8	223.93	104.67	5.95	76.19	7.66	84.17	129.67	14.96	4.58	14.62	23.05	26.94	90.77
G9	202.68	90.73	6.53	69.83	8.51	87.83	133.67	16.15	4.81	15.70	26.77	30.25	127.08
G10	216.60	102.93	6.08	66.13	7.78	85.83	129.00	15.08	4.62	14.85	23.47	27.25	95.00
G11	200.27	97.93	6.23	66.00	8.20	85.83	130.33	15.55	4.70	15.07	24.97	28.85	108.54
G12	181.93	109.67	5.61	73.78	7.44	86.83	151.67	13.98	4.48	13.43	21.20	24.74	70.39
G13	208.53	95.40	6.39	59.47	8.43	85.83	139.33	15.98	4.77	15.53	25.70	29.35	117.23
G14	172.67	109.33	5.75	66.87	7.53	85.83	129.33	14.21	4.51	14.00	21.47	24.94	74.86
G15	195.40	117.20	5.47	64.47	6.98	79.83	133.33	13.75	4.28	12.84	19.10	22.94	56.46
G16	192.47	105.80	5.90	67.68	7.65	87.83	135.00	14.45	4.58	14.30	22.55	26.14	84.40
G17	223.87	112.33	5.57	68.94	7.23	85.83	139.33	13.83	4.35	13.40	20.07	22.99	61.85
Min	**172.67**	**75.20**	**5.10**	**59.47**	**6.63**	**78.17**	**129.00**	**13.17**	**4.06**	**12.11**	**17.89**	**20.54**	**44.52**
Max	**223.93**	**121.80**	**7.20**	**76.19**	**9.39**	**87.83**	**151.67**	**16.47**	**4.85**	**16.57**	**30.14**	**34.10**	**170.01**
Avg.	**204.40**	**102.15**	**6.07**	**66.89**	**7.90**	**84.87**	**133.78**	**14.96**	**4.59**	**14.55**	**23.54**	**27.15**	**96.24**

Appendix 5. Principal component score of 1 and 2.

Genotypes	PC1	PC2
G1	43.37	-0.22
G2	7.04	3.11
G3	17.84	-4.48
G4	-56.2	-5.75
G5	79.42	7.81
G6	3.97	-10.98
G7	-15.06	-17.53
G8	-5.92	-19.62
G9	33.23	1.54
G10	-1.36	-12.74
G11	13.38	3.51
G12	-27.54	25.07
G13	21.85	-3.7
G14	-22.14	30.99
G15	-42.81	9.08
G16	-12.37	12.1
G17	-36.71	-18.2