CHARACTER ASSOCIATION AND GENETIC DIVERSITY ANALYSIS OF MAIZE (*Zea mays* L.) VARIETIES IN BANGLADESH

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DHAKA-1207

JUNE, 2015

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By

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REGISTRATION NO.:- 09-03450

A Thesis
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
SEMESTER: Jan- June, 2015

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CERTIFICATE

This is to certify that thesis entitled, "CHARACTER ASSOCIATION AND GENETIC DIVERSITY ANALYSIS OF MAIZE (Zea mays L.) VARIETIES IN BANGLADESH" 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 bona fide research work carried out by Md. Nazmul Huda, Registration No: 09-03450 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, 2015
Place: Dhaka, Bangladesh

.....
(Dr. Md. Ashaduzzaman Siddikee)
Supervisor

DEDICATED TO

MY

BELOVED PARENTS

Some commonly used abbreviations

Full word	Abbreviation	Full word	Abbreviation
Percent	%	Etcetera	etc.
Degree Celsius	ºC	Edition	ed.
Abstract	Abst.	Food and Agricultural Organization	FAO
At the rate	@	Gram	g
Agro-Ecological Zone	AEZ	Genotype	G
Agriculture	Agric.	Genetic advance	GA
Agricultural	Agril.	Genetics	Genet.
Agronomy	Agron.	General combining ability	GCA
Analysis of variance	ANOVA	Hectare	ha
Annals	Ann.	International	*Intl.*
Applied	Appl.	Journal	*J.*
Archives	Arch.	Least significant difference	LSD
Bangladesh Agricultural Research Institute	BARI	kilogram	kg
Bangladesh Bureau of Statistics	BBS	Meter	m
Biology	Bio.	Muriate of potash	MP
Biological	Boil.	Ministry of agriculture	MOA
Biological science	Biosci.	Pharmaceutical	Pharm.
Biotechnology	Biot.	Principal component analysis	PCA
Botany	Bot.	Principal coordinate analysis	PCO
Breeding	Breed.	Randomized Complete Block Design	RCBD
Centimeter	cm	Research	Res.
Cytology	Cyt.	Sher-e-Bangla Agricultural University	SAU
Canonical variate analysis	CVA	Science	Sci.
Degrees of freedom	df	Specific combining ability	SCA
Ecology	Ecol.	Squre meter	m^2
And others	*et al.*		

ACKNOWLEDGEMENT

First of all, I would like to bow my heartfelt gratitude and praise to the Almighty ALLAH, the most beneficent and merciful who granted me to complete the dissertation work successfully.

I sincerely express my deepest sense of gratitude, respect, profound appreciation to my research supervisor Dr. Md. Ashaduzzaman Siddikee, Associate Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his kind and scholastic guidance, untiring effort, valuable suggestions, inspiration, co-operation and constructive criticisms through the entire period of the research work and the preparation of the manuscript of this thesis.

I would like to express my deepest respect and boundless gratitude to my co-supervisor Dr. Firoz Mahmud, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for his valuable teaching, direct continuous direction, constructive criticism, encouragement and valuable suggestions in carrying out the research work and preparation of this thesis.

I am also highly grateful to my honorable teacher Prof. Dr. Md. Sarowar Hossain, 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 also highly grateful to my honorable teachers Prof. Dr. Md. Shahidur Rashid Bhuiyan, Prof. Dr. Naheed Zeba, Prof. Dr. Mohmmad Saiful Islam, Prof. Dr. Jamilur Rahman, Associate Prof. Dr. Md. Abdur Rahim and all the teachers of 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 feel proud of expressing my sincere appreciation and gratitude to Minister of Science and Technology of People's Republic of Bangladesh for selecting me National Science and Technology (NST) fellow and funding.

I would like to thank all my friends and well aishers who always inspired me during my research specially Md. Nazmul Huda, Arif Hossain, Md. Mehedi hassan, Md Anisur Rahman, Farhana Parvin, Khondakar Sadia Siddika, Tanjina Arfin and elder brother Md. Delowar Hossain who helped me with their valuable suggestions and directions during the preparation of this thesis paper.

I can never repay the debt of my beloved Father Md. Golam Mostafa, Mother Ferdowshi Begum, uncle, brothers, cousins and well wishers for their inspiration, constant encouragement and sacrifice for my higher education

Finally, I expresses my immense gratefulness to all of them who assisted and inspired me to achieve higher education and regret for my inability for not to mention every one by name.

June, 2015. *The Author*

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ABSTRACT

An experiment was carried out at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207, Banladesh during the period of Kharif-1 season in 2014 with 25 maize genotypes to study on character association, genotypic and phenotypic variance, heritability, genetic advance, genotypic and phenotypic co-efficient of variation, correlation co-efficient effect, path co-efficient effect and the genetic divergence considering different important yield and yield contributing characters. Analysis of variance showed the presence of significant variation among the tested genotypes for all the characters studied. Minimum differences of genotypic and phenotypic variances as well as high heritability coupled with high genetic advance in percent of mean were observed for almost all the traits of genotypes indicated additive gene effects of these traits. Correlation studies revealed highly significant positive association of total yield per plant with ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000 kernel weight. Path analysis showed that day to 50% tasseling, ear length, ear circumference, number of kernel per cob and 1000 kernel weight had positive direct effect on the yield per plant. The genotypes were grouped into five different clusters. Cluster IV consist of highest 10 genotypes and cluster II had only two genotypes. The highest intra- cluster distance was computed for cluster II. The maximum inter cluster divergence was observed between cluster II and III and the lowest was between cluster I and IV. Considering diversity pattern and genetic status Barnali and VB-100 from cluster II; PAC-399 and 4536 from cluster III; BHM-9, Dekalb Super Gold, Dekalb 962 and Dekalb 9120 from cluster IV might be considered better parents for future hybridization programme.

Chapter 1

Introduction

CHAPTER I

INTRODUCTION

Maize belongs to the tribe Maydeae of the grass family *Poaceae*. The genus Zea consists of four species of which *Zea mays* L. is economically important. The term "Zea" (zela) was derived from an old Greek name for a food grass. The number of chromosomes in *Zea mays* is 2n= 20. Maize is a tall, determinate annual C4 plant varying in height from 1 to 4 meters producing large, narrow, opposing leaves (about a tenth as wide as they are long), alternately along the length of a solid stem. The center of origin for *Zea mays* has been established as the Mesoamerican region, i.e. Mexico and Central America (Matsuoka *et al.,* 2002). Maize is a cross pollinated crops particularly geitonogamy. Therefore, pollination mechanism is major constraint for hybrid development.

Maize is a versatile crop grown over a range of agro climatic zones. In fact, the suitability of maize to diverse environments is unmatched by any other crop. It is grown from 58° N to 40° S, from below sea level to altitudes higher than 3000 m, and in areas with 250 mm to more than 5000 mm of rainfall per year (Shaw, 1988; Dowswell *et. al.,* 1996) and with a growing cycle ranging from 3 to 13 months (CIMMYT, 2000). However the major maize production areas are located in temperate regions of the globe. The United States, China, Brazil and Mexico account for 70% of global production. India has 5% of corn acreage and contributes 2% of world production. Like as India, climate condition of Bangladesh favors maize cultivation. Maize acreage and production have an increasing tendency with the introduction of hybrid since 1993 in Bangladesh. Area, production, and yield of maize have increased by 17%, 33% and 16%, respectively, which reflect the effect of adopting improved technology (Saleque, 2005). In Bangladesh it is the third most important crop after rice and wheat and it accounts for 4.8% of the total cropped land area and 3.5% of the value of agricultural output (Ahmad *et al.,* 2011). Since the early 1990s, the

Bangladesh maize area has increased at an average rate of 20% per year to reach 338973 ha with production 812949 million ton in 2009-10 (BBS, 2011 and CIMMYT, 2008). Moreover, population of Bangladesh is growing very fast and this situation necessitated producing more food. In addition, the country is losing about 200 hectares of cropland everyday owing to industrialization, urbanization and river erosion. Therefore to face this challenge, cultivation of high productive crop like maize, breeding is necessary. Besides higher demand of maize grains in poultry industry has opened up an ample opportunity to cultivate hybrid maize throughout the whole country. Maize is an important feed for all classes of livestock and is widely used all over the world.

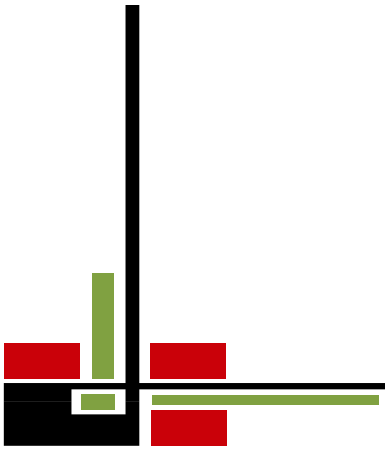
Today, the variability of the agricultural crops has been massively lost as a result of the commercial varieties use. For example, only about 5% of maize germplasm is used for commercial purposes (Hoisington *et al.,* 1999). Preservation of the genetic resources in the country is associated with rigorous characterization and evaluation of the genetic diversity (Salillari *et al.*, 2007). However, due to the continuous regeneration and the limited number of the individuals for accessions as well as genetic erosion, the collection is damaged (Fetahu *et al.,* 2005). The plant genetic resources are considered as the main source for the conservation of the biological diversity and long-term sustainability of human life. Identification of the genetic variability by means of the morphological indicators also helps for the determination of the duplicate accessions.

Characterization of morphological variability allows breeders to identify accessions with desirable characteristics such as earliness, disease resistance, or improved ear morphology. Characterization and grouping of germplasms allow breeders to avoid duplication in sampling populations. Also, in the absence of pedigree records or information on combining ability it would be useful to organize the collection based on morphology. This may allow breeders to identify potential combining ability groups. The variance component is derived

from further partitioning of genotypic differences into phenotypic, genotypic and environmental coefficient of variation and heritability are good index of transmission of characters from parents to their off springs (Falconer, 1960). Genetic diversity values (GDVs) calculated from field data have been suggested as measures of genetic diversity (Williams and Hallauer, 2000). Better knowledge on genetic diversity or genetic similarity could help to sustain long term selection gain (Chowdhury *et al.*, 2002 and Belaj *et al.*, 2002). Because, genetically diverse parents are known to produce high heterotic effects and wide segregates for developing high yielding varieties or vice versa. Moreover, evaluation of genetic divergence is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). In general, genetic diversity among and within cultivars of our major crop species is desirable to reduce potential impact of economic losses due to environmental and biological stresses. Knowledge of genetic diversity among plant population and quantitative assessment usually helps a breeder in choosing desirable parents for breeding programs.

We therefore in the present study used 25 promising maize varieties for characterization to determine genetic diversity and to identify potential genotype from the breeding point of view. To achieve these goals the research work was conducted specifically for the following objectives:

- To estimate the nature and magnitude of genetic variations among the maize genotype in respect of different morphological characters
- To determine the nature of relationship between yield and yield contributing characters
- To estimate diversity among genotypes and to find out diverse germplasm suitable for the utilization in varietal improvement and future hybridization programme



Chapter 2

Review of literature

CHAPTER II

REVIEW OF LITERATURE

Maize is the third important cereal crop which has received much attention of research workers throughout the world. Various investigators at home and abroad worked with different maize lines and studied their performance regarding the characterization and diversity of maize. The information available on this subject from different studies by various workers at home and abroad has been reviewed in this chapter with following heading:

2.1 Taxonomy and Geographic Origin

Maize belongs to the tribe Maydeae of the grass family Poaceae. The genus Zea consists of four species of which *Zea mays* L. is economically important. The other zea sp., referred to as teosintes, is largely wild grasses native to Mexico and Central America (Doeblay, 1990). The number of chromosomes in Zea mays is 2n= 20. Tribe Maydeae comprises seven genera which are recognized, namely old and new world groups. Old world comprises Coix (2n = 10/20), Chionachne (2n = 20), Sclerachne (2n = 20), Trilobachne (2n = 20) and Polytoca (2n = 20), and new world group has Zea and Tripsacum. It is generally agreed that maize phylogeny was largely determined by the American genera Zea and Tripsacum, however it is accepted that the genus Coix contributed to the phylogenetic development of the species Zea mays (Radu *et al.*, 1997).The closest wild relatives of maize are the teosintes which all belong to the genus Zea outside the Zea genus, the closest wild relatives are from the genus Tripsacum. (CFIA, 1994 and OECD, 2006)

The center of origin for Zea mays has been established as the Mesoamerican region, i.e. Mexico and Central America (Watson and Dallwitz, 1992). Archaeological records suggest that domestication of maize began at least 6000 years ago, occurring independently in regions of the southwestern United States, Mexico, and Central America (Mangelsdorf, 1974). In India, Portuguese

introduced maize during the seventeenth century. From India it went to China and later it was introduced in Philippines and the East Indies. Various hypotheses have been proposed on the origin/domestication of maize (OECD, 2006). Teosintes (*Z. diploperennis* and *Z. mays* sp. *mexicana*) and Tripsacum species are often described as having roles in the domestication process of maize (Mangelsdorf, 1974 and Galinat, 1988).

The possibility of inter-generic hybridization of either *Z. diploperennis* or Tripsacum with extinct wild maize has also been proposed as the ancestral origin of *Z. mays* (Radu *et al.*, 1997 and Purseglove, 1972). Eubanks (1993, 1997) suggests that domesticated maize may have arisen via human selection of natural hybrids between Tripsacum and perennial teosinte.

Maize is a cultivated crop throughout the world and accordingly germplasm resources are preserved ex-situ in many parts of the world. The great diversity of environments and conditions have created the basis for the development of maize varieties well adapted to harsh conditions of soil and climate as well as to biotic stresses. There is a close correlation among community culture, production system and the type of consumption of maize, with the diversification and variation of maize (Aguirre *et al*., 1998 and Louette and Smale, 1998).

2.2 Reproductive biology

Maize is a tall, determinate, monoecious, annual plant. It produced large, narrow, opposite leaves, borne alternatively along the length of stem. All maize varieties follow same general pattern of development, although specific time and interval between stages and total number of leaves developed may vary between different hybrids, seasons, time of planting and location.

Silking stage involving the formation of the female flowers or cobs is the first reproductive stage and occurs 2-3 days after tasseling stage. This stage begins when any silks are visible outside the husk. These are auxillary flowers unlike tassels that are terminal ones. Pollination occurs when these new moist silks

catch the falling pollen grains. Maize is a monoecious plant, that is, the sexes are partitioned into separate pistillate (ear), the female flower and staminate (tassel), the male flower. It has determinate growth habit and the shoot terminates into the inflorescences bearing staminate or pistillate flowers (Dhillon and Prasanna, 2001).

Maize is generally protandrous, that is, the male flower matures earlier than the female flower. Within each male flower spikelet, there are usually two functional florets, although development of the lower floret may be delayed slightly in comparison to the upper floret. Each floret contains a pair of thin scales i.e. lemma and palea, three anthers, two lodicules and rudimentary pistil. Pollen grains per anther have been reported to range from 2000 to 7500 (Kiesselbach, 1949). Kiesselbach (1949) estimated that 42,500 pollen grains are produced per square inch of cornfield. The pollen grains are very small, barely visible to the naked eye, light in weight, and easily carried by wind. The wind borne nature of the pollen and protandry lead to cross-pollination, but there may be about 5 per cent self-pollination. In maize, the pollen shed is not a continuous process and usually begins two to three days prior to silk emergence and continues for five to eight days. The silks are covered with fine, sticky hairs which serve to catch and anchor the pollen grains. Pollen shed stops when the tassel is too wet or too dry and begins again when temperature conditions are favourable. Under favourable conditions, pollen grain remains viable for only 18 to 24 hours. Cool temperatures and high humidity favor pollen longevity. Under optimal conditions the interval between anthesis and silking is one to two days. Fertilization occurs after the pollen grain is caught by the silk and germinates by growth of the pollen tube down the silk channel within minutes of coming in contact with a silk and the pollen tube grows the length of the silk and enters the embryo sac in 12 to 28 hours. Pollen is light and is often carried considerable distances by the wind. Under field conditions 97% or more of the kernels produced by each plant are pollinated by other plants in the field. Fertilization of ovules begins about one third of the way up from the base of the ear.

2.3 Studies on morphological characterization

Plant height is the function of cell growth and vertical cell enlargement (Hsiao *et al.*, 1976). Chowdhury and Islam (1993), reported that maize varieties Barnali. Khoibhutta, Mohor and Shuvra were 200, 160, 210 and 175 cm tall respectively.

Akhtar and Mitra (1990), found that plant height was significantly different among the 6 CIMMYT entries and one local cheek. Jotshi *et al*. (1988) working with 25 varieties of maize and observed that leaves per plant differed significantly among the varieties. Lee *et al*. (1986) studying with 28 maize hybrids also observed significant differences in number of leaves per plant among the varieties.

Mei *et al*. (1983); reported that there was no significant difference between the spring crop and the autumn crop in the number of days to silking and the autumn crop showed higher grain yield and potential ear dry weight than the spring crops.

Okigbo (1973), showed that maize planted on ridge produced more than one ear per plant. Grain yield depends on what extent of dry matter accumulated in the ears (Allison and Watson, 1966).

Singh *et al*. (1991); conducted an experiment with varieties Ganga 5 and HLL and found that Ganga 5 was significantly superior to HLL with regard to growth and yield which was due to ear length. In an experiment with 5 maize cultivars (R_2, Ganga 5, Ganga 11, HH 216 and D765), Paradkar and Sharma (1993) found that Ganga 11 gave more ear length followed by Gonga 5 and D 7654.

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.

Paradkar and Sharma (1993) observed that out of 5 maize varieties (R_1, Ganga 5, Ganga ll, HH2l6 and D765), Ganga ll gave increased grain rows per ear.

Kamen (1983), observed that early maturity hybrids had fewer grain rows per ear than late maruriting hybrids. Number of grains per row may differ among the varieties. Grains per ear, one of the important yield contributing characters, varied with variety. Khaibhutta produced significantly higher (432.5) number of grains per ear than Barnali (343.5) as reported by Anonymous (1988). On the other hand, Khoibhutta produced the highest number of grains per ear when compared with variety Pirsabak 8l46, Lamaquina 7827 and Guaira 8045 (Anonymous, l987).

Number of grain-rows per ear 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 in inheritance of all of investigated traits 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.

Viola *et al*. (2004); reported that maize display an orderly sequence of development of yield components namely number of ear per plant, number of kernel per row, number of kernel row per ear and hundred kernel weights. Grzesiak (2001), observed considerable genotypic variability among various maize genotypes for different traits. Ibsan *et al*. (2005) also reported significant genetic differences for morphological parameter for maize genotypes.

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 seeds 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 and hence, it was inferred that there was a better scope for improvement of these traits through direct selection.

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

Farhan *et al*. (2012); revealed that testcrosses differed significantly for all the characters studied except days to 50% anthesis, days to 50% silking, and ASI. The Genotype x Location interaction was also significant for all the traits except for ear length. Mean values for days to 50% tasseling, anthesis and silking, anthesis silking interval (ASI), plant and ear height were 55.3, 58.2, 59.9, 1.69, 157.7 and 72.1, respectively.

Praveen *et al*. (2014**);** revealed that the mean sum of squares due to genotypes showed significant differences for all the 12 characters studied. Traits yield per plant, plant height, ear height, number of kernels per row, 100-kernel weight were showed 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 per cent tasseling, days to 50 per cent silking, shelling percentage, ear length and days to maturity ear girth and number of kernel rows per ear.

Abel and Pollak (1991), evaluated test crosses of exotic maize accessions with several testers and 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.

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 also, dominance variance for leaf area index, plant and ear height, ear length, and number of kernel per row. However the magnitude of VA was consistently larger than that of VD for all characteristics with exception of specific leaf weight, silking date, stay green, 100- kernel 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 silking date, 39% for plant height, 44% for ear height, 27% for ear length, 31% for ear circumference, 29% for number of rows per ear, 23% for number of kernel per row and 36% for grain yield.

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 silking 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 silking to high (72.03) in number of ear per plant. Days to anthesis and silking, 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.

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 ear (13.67) and grain yield (5927 kg ha^{-1}) were recorded for Jalal-2003. Broad sense heritability (h^2_b) 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.

2.4 Studies on correlation co-efficient and path co-efficient

Determination of genotypic and phenotypic correlation is very fundamental step in the formulation and implementation of various breeding programs and activities. The correlations between the traits is also of great importance for success in selections to be conducted in breeding programs, and analysis of correlation coefficient is the most widely used one among numerous methods that can be used (Yagdi and Sozen, 2009).

Two types of correlations, phenotypic and genetic, are commonly discussed in plant breeding. Phenotypic correlation (r_p) involves both genetic and environmental effects. Genetic correlation is the association of breeding values (i.e., additive genetic variance) of the two characters. Both measure the extent to which degree the same genes or closely linked genes cause co-variation in two different characters (Hallauer and Miranda, 1988)

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

When there is positive association of major yield characters component breeding would be very effective but when these characters are negatively associated, it would be difficult to exercise 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 ear, number of kernel per row and 100-kernel 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 kernels per row. It also revealed that the most sources of variation in plant yield were the direct effects of number of kernels per row and both number of kernels per row and ear circumference.

Ahemed *et al*. (1978); reported that both ear length and ear circumference were positively correlated with 1000-kernel weight and grain yield. A positive correlation between number of kernels per row and kernel rows per ear was observed by Zuzulya (1979). Jha *et al*. (1979); described that number of rows per ear had little direct effect on grain yield.

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

Bikal and Deepika (2015), showed that traits plant height, ear height, ear length, ear girth, ear weight, no. of kernel row per ear, no. of kernel per row exhibited positive and highly significant correlation with grain yield per hectare and five hundred kernel weight given significant correlation. The analysis also indicated that days to 50% tasseling and days to 50% silking explained negative and highly significant correlation with grain yield per hectare.

Similarly, days to maturity showed negative and non significant correlation with grain yield per hectare.

Bahoush and Abbasdokht (2008), showed that number of grains per ear and 100 grain weights had high and positive direct effects and ear 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, ear 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 study.

Garcia *et al*. (2003); revealed that correlation coefficient measures the mutual association only between a pair of variables, when more than two variables are involved; the correlations may not provide a clear picture of the importance of each component in determining grain yield. Path coefficient analysis provides more information among variables than do correlation coefficients since this analysis provides the direct effects of specific yield components on yield, and indirect effects via other yield components.

Mohan *et al*. (2002); studied path analysis on corn cultivars (169 cultivars) for grain yield and oil content and resulted that number of seed per row, 100 seed weight, number of seed row and ear, length had direct effect on grain yield and ear 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 seed rows per ear, number of seeds per row and 100-seed weight positively influenced the yield directly and also indirectly through several components.

Mohammadi *et al*. (2003); reported that 100-grain weight and total number of kernels per ear revealed highest direct effects on total grain weight, while ear length, ear circumference, number of kernel rows, and number of kernels 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 effect 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 kernel had the highest direct effecton grain yield. However, the study carried out by Selvaraj and Nagarajan (2011) revealed that direct selection for ear length and numbers of rows per ear 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.

Mustafa et al. (2014); revealed 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 characters which contribute largely to the fresh shoot length of maize seedlings. These traits had reasonable heritability estimates, 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% silking, ear weight and number of grains per ear had the highest direct effect on grain yield, while number of grains per ear 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 in improving open pollinated maize varieties and hybrids for high grain yield.

Days to 50% tassel and number of kernel rows per ear 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)

2.5 Studies on genetic divergence

The importance of genetic diversity in selecting genetically diverse parents either to exploit heterosis or to get 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). In most of the cases genetic divergence analysis is attempted to identify specific parents for realizing heterosis and recombination in breeding program.

Singh and Chaudhari (2001), evaluated fifty-five inbred lines for genetic divergence. The 55 inbreds were grouped into 5 clusters. Among these, cluster II had the maximum number of 16 inbreds followed by clusters IV and V with ll and 10 inbreds, respectively. Clusters I and II consisted of 9 inbreds each. The highest inter-cluster distance was observed between clusters I and IV, indicating wide genetic diversity between them. The least inter-cluster distance was between clusters III and V, indicating the genetic closeness between the inbreds 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 inbreds. Based on the result of cluster analysis, 5 dent and 4 flint inbreds 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-kernel weight, ear circumference and number of kernels 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 crosses. Genetic distance 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 inbreds into three clusters. Cluster I consisted of inbred lines derived from BSSS germplasm or germplasm related to it. Cluster II contained the Lancaster lines, while cluster III included two independent lines. Data showed that inbreds most closely related by their pedigree 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 the maximum number of genotypes (18) whereas, cluster XIII to XVI comprised a single genotype in each, 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.l8% across all samples), however, B73 from the Agrogene 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 seed sources of the same inbred line did not vary considerably. Different sources of the same lines were tightly clustered in the UPGMA dendogram.

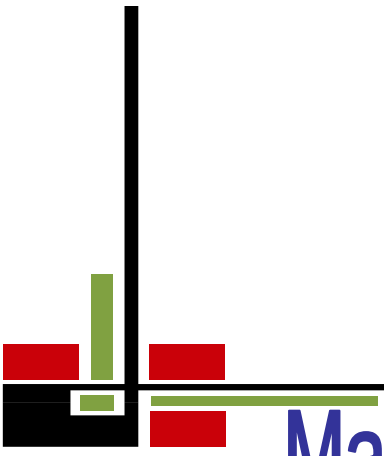
Li *et al.* (2004); showed that the accessions assessed could be clustered into a few groups. This was mostly in accordance with the heterotic groupings previously assigned based on conventional methods, although some notable differences were detected. The results indicated that most of the Italian maize inbreds used in the study were mainly related to the RYD background and most of the Chinese inbreds 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 programmes. 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). Inbreds 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 wide genetic maximum distance between clusters III and VI and the lowest distance between clusters I and IV. The cluster means were higher for 50% tasselling, 50% silking, plant height, cob height, ear length, number of grains per row and I00- 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 ll genotypes and cluster I with 5 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 3

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

A field experiment was conducted at the experimental field of Genetics and Plant Breeding department of Sher-e- Bangla Agricultural University, Dhaka-1207, Bangladesh during March 2014 to July 2014 to study the genetic variation, genetic divergence and correlation and path coefficient in yield contributing characters of maize (*Zea mays* L.). The materials and methods of this experiment are presented in this chapter under these following headings:

3.1 Site of experiment

The research work was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka- 1207. The experimental site was at 90°22′ E longitude and 23°41′ N latitude at an altitude of 8.6 meters above the sea level (Appendix I).

3.2 Soil and climate of the experimental site

The experimental area was under the sub-tropical monsoon climate zone, which is characterized by heavy rainfall, high humidity, high temperature and relatively long day during the *Kharif* season. The land belongs to agro-ecological region of 'Madhupur Tract' (AEZ 28) of Nodda soil series. The soil was sandy loam in texture having pH 5.47-5.63. The mean temperature of the growing period was 26.43°C with average maximum and minimum being 36ºC and 20.54ºC, respectively. Details of the meteorological data in respect of temperature, rainfall, relative humidity, total sunshine and soil temperature during the period of experiment were collected from the weather station, Dhaka, Bangladesh (Appendix II & III)

3.3 Genetic materials used for the experiment

Twenty five (25) genotypes were used in the study. The seeds of 25 accession lines were collected from Bangladesh Agricultural Research Institute (BARI) and other different sources. Descriptions of the genotypes are given in Table 1.

Table 1. The code, accession name and source of collection of the 25 maize genotypes used in the experiment

Sl No.	Code	Accession name	Source of collection
1	G1	BHM-3	BARI
2	G2	BHM-5	BARI
3	G3	BHM-6	BARI
4	G4	BHM-7	BARI
5	G5	BHM-9	BARI
6	G6	Shuvra	BARI
7	G7	BM-5	BARI
8	G8	BM-6	BARI
9	G9	Khai bhutta	BARI
10	G10	BHM-8	BARI
11	G11	Nk-40	Lalteer
12	G12	Pacific-11	ACI Agri. limited
13	G13	PAC-999	ACI Agri. limited
14	G14	Bari misti bhutta-1	BARI
15	G15	PAC-984	ACI Agri. limited
16	G16	Dekalb super gold	Agrovet limited
17	G17	Dekalb 962	Agrovet limited
18	G18	Khai bhutta	BARI
19	G19	Barnali	BARI
20	G20	VB-100	Lalteer
21	G21	Pacific 98	ACI Agri. limited
22	G22	4536	Lalteer
23	G23	Dekalb 9120	Agrovet limited
24	G24	VA-786	Lalteer
25	G25	Profit	ACI Agri. limited

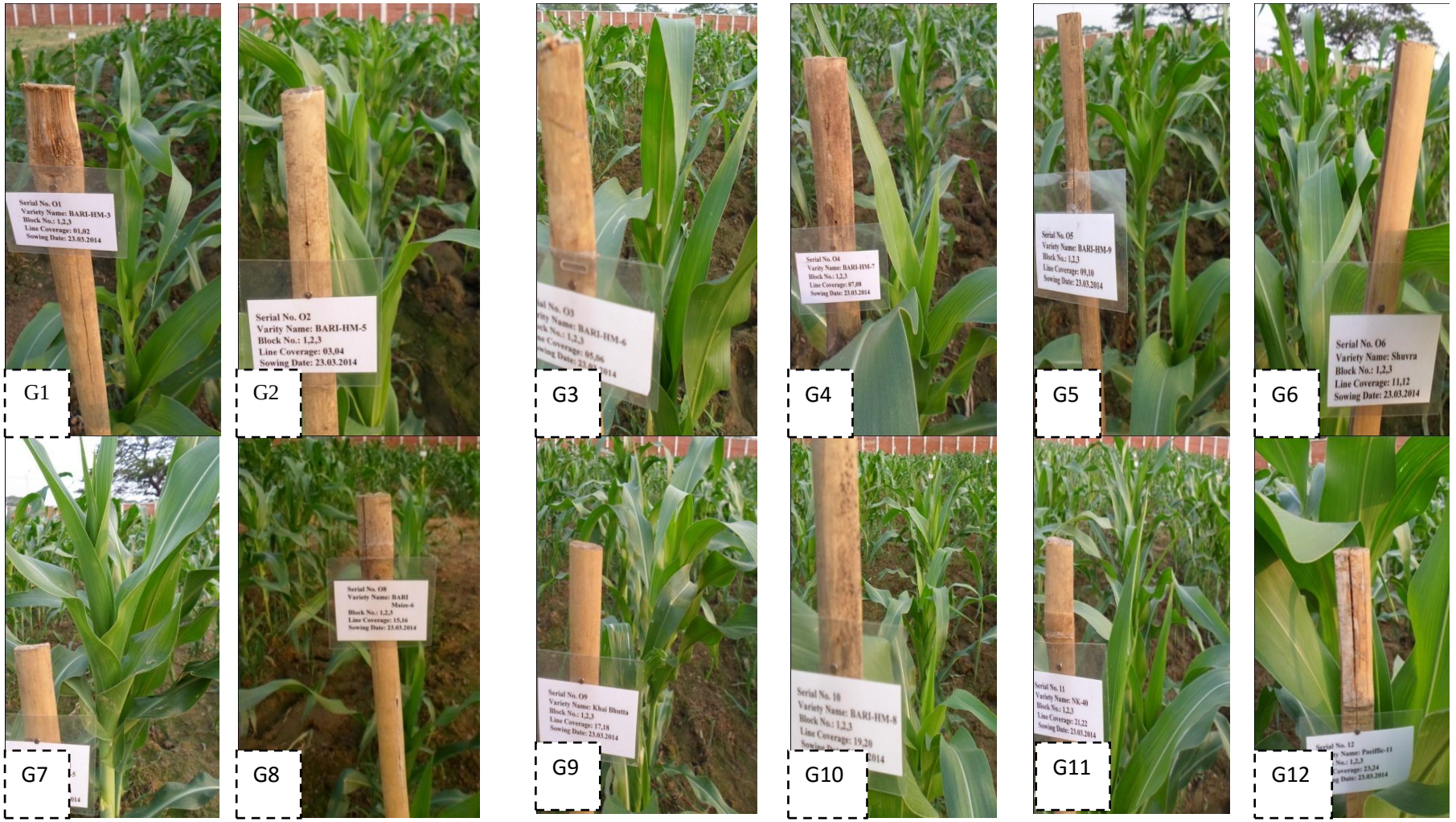


Plate 1. Photograph showing differences of line of 25 maize genotypes in the experimental plot

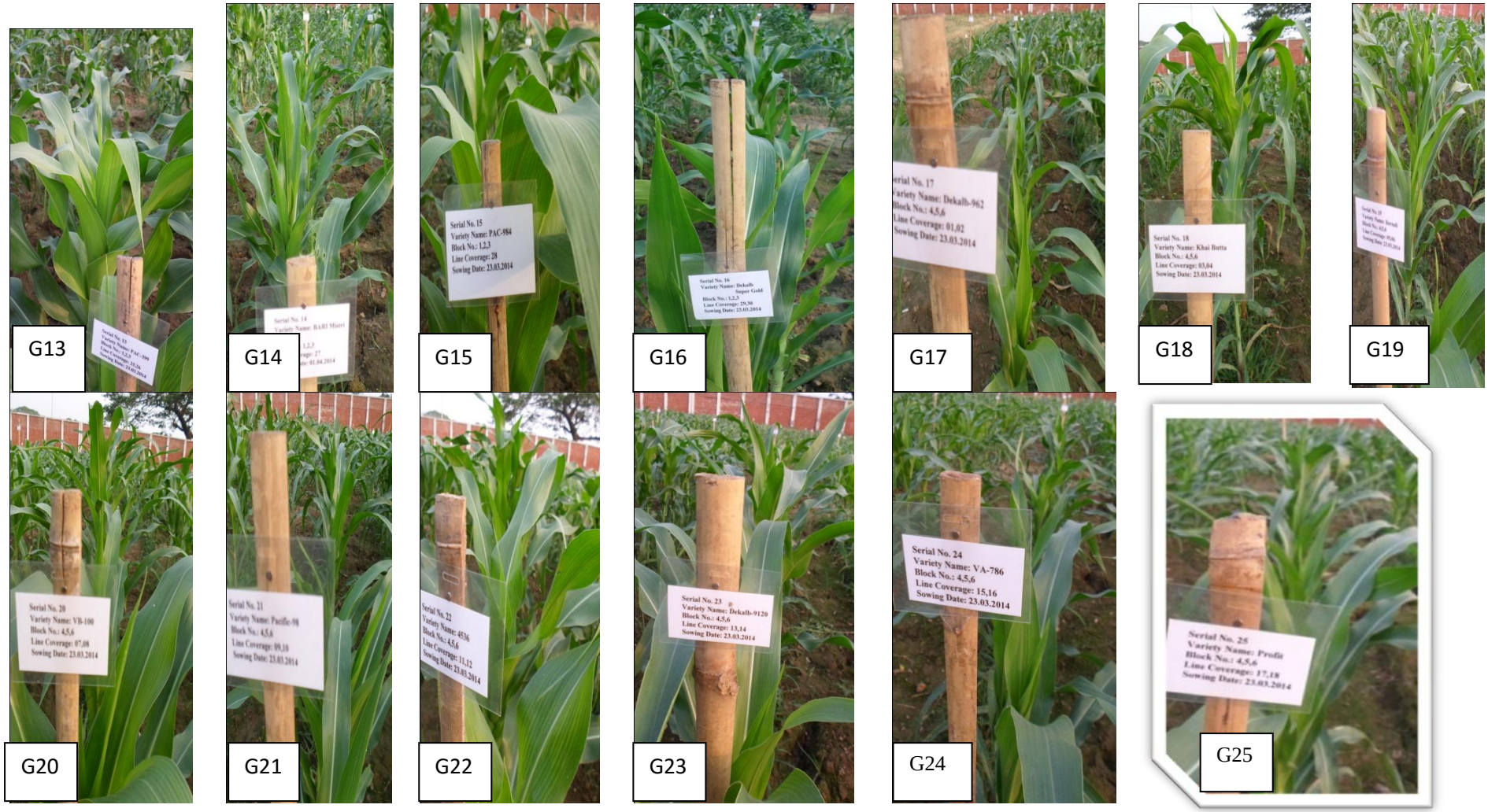


Plate 1(Cont'd).

3.4 Design and layout of the experiment

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 3.5 cm × 20 cm. Block to block distance was 1 m, plant to plant distance was 20 cm and row to row distance was 75 cm. The genotypes were distributed to each row in each block randomly.

3.5 Preparation of the experimental 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 good tilth 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. Each unit blocks was prepared keeping 5 cm height from the drains. The bed soil was made friable and the surface of the bed was leveled.

3.6 Manures and fertilizer application

Manures and fertilizers such as cow dung, urea, triple super phosphate (TSP), muriate of potash (MP), gypsum and borax were applied at the rate shown in Table 2. Urea was applied by three installments. The entire cow dung, TSP, MP, gypsum, borax and half of the urea was applied at the time of final land preparation. The remaining half of urea was applied as top dressing in two installments. First top dressing was done at 20 days after and second at 35 days after sowing. In this study fertilizer was applied as per the recommendation of Bangladesh Agricultural Research Institute (BARI).

Table 2. Doses of different fertilizers and manure applied in the experimental field

Sl. No.	Manure and fertilizer	Doses
1	Cowdung	5 tons/ha
2	Urea	250 kg/ha
3	TSP	180 kg/ha
4	MP	120 kg/ha
5	Gypsum	110 kg/ha
6	Borax	6 Kg/ha

3.7 Seed sowing

Seeds of 25 accessions were sown on 23 March, 2014. Planting distance was maintained as 20 cm from hill to hill and two or three seeds were sown per hill. The seedlings were emerged after 5-7 days of sowing.

3.8 Intercultural operations

The growing seedlings were always kept under care observation. After 15 days of seed sowing, thinning operation was done. One healthy seedling was kept in each hill and other seedlings were pulled out from each hill. Weeding and mulching were necessary to keep the plots free from weeds, easy aeration and for conserving soil moisture. When the plants were well established, the soil around the base of plants was pulverized. A shallow irrigation was applied in the experimental field just after sowing the seeds. The crop was irrigated three or more times when needed depending on the moisture status of the soil and requirement of the plants. The remaining two doses of urea were applied as top dressing in two equal installments. First top dressing was done at 20 DAS and second at 35 DAS. Malathion 57 EC insecticide was applied after one month of seeds sowing at 12 days interval for 3 times with 1 ml in 2.5 liters water as a

preventative measure against different insects. Birds are severe pest for maize during fruiting time. So, the field was covered with net over the plant to protect from the birds.

3.9 Harvesting

Different genotypes matured at different times. Ten plants from each genotype from every plot were randomly selected to collect data and these were harvested by uprooting. Border plants were discarded to avoid border effect.

3.10 Data collection

In order to study the genetic divergence among the genotypes, the data were collected in respects of three qualitative and seventeen quantitative traits and recorded. Data of tasseling and data of silking were recorded on whole plant basis. The other parameters were noted on individual plant basis from ten randomly selected competitive plants.

3.11 Method of data collection

To study the stable diagnostic characteristics, data on the morphological characters were collected from ten randomly selected plants from each replicated plot. The plants were selected from middle of the plot to avoid border effect and portion of the plot. In addition to prepare the descriptors, the test genotypes were classified according to ***Suresh*** *et al.* (2013). The descriptors are appended in the Appendix III. The observations for characterization were recorded under field condition as follows:

3.11.1 Number of leaves per plant

The total number of leaves was counted from each of the sample plants and the average was taken.

3.11.2 Leaf length

It was measured in centimeter scale from the jointing point of leaf and to the tip point of leaf.

3.11.3 Leaf breadth

Leaf breadth was measured in cm scale at the middle of leaf and categorized by following groups as per descriptors.

1- Very small
2- Small
3- Medium
4- Large
5- Very large

3.11.4 Days to 50% tasseling

Data regarding days to 50% tasseling were recorded by regular visits to the field and days were counted from sowing to the day when 50% of the plants produced tassels in a block.

3.11.5 Days to anthesis

The number of days required from planting till 50% of plants was shedding pollen in a plot. The days were counted from date of sowing. According to days required, the test genotypes were classified into three different categories as per descriptors.

1- Medium
2- Late
3- Very late

3.11.6 Days to silk emergence

The number of days required from planting till first of the plants showed silks. The days were counted from date of sowing. According to their days required, the test genotypes were classified into five different categories as per descriptors.

1- Very early
2- Early
3- Medium
4- Late
5- Very late

3.11.7 Days to 50% silking

Silking data were recorded as the number of days from sowing until 50% of the plants in each plot showed silks.

3.11.8 Plant height (cm)

The average height of the 10 plants from the plant base to the tip of the tassel was measured in centimeters. According to their length, the test genotypes were classified into five different categories as per descriptors.

1- Short
2- Medium
3- Medium long
4- Long
5- Very long

3.11.9 Ear height (cm)

Ear height was measured in cm from ground level to node bearing the upper most ears. Ten randomly selected plants were averaged for each genotype from each block. According to ratio height of insertion of upper ear to plant length (ear placement), the test genotypes were classified into five different categories as per descriptors.

1- Short
2- Medium
3- Medium long
4- Long
5- Very long

3.11.10 Cobs per plant

Number of cobs per plant was counted during the harvesting time.

3.11.11Ear shape

Shape of the ear was observed and the genotypes were categorized as following.

1- Conical

2- Conical-cylindrical
3- Cylindrical

3.11.12 Color of top kernel

It was observed after harvest in presence of sufficient sun light and categorized by following groups.

1- pure white
2- brown
3- yellow

3.11.13 Ear length (cm)

Ear length was measured in cm from the tip point of peduncle to the tip of the selected ear. According to their length, the test genotypes were classified into five different categories as per descriptors.

1- Very small
2- Small
3- Medium
4- Large
5- Very large

3.11.14 Ear circumference (cm)

Ear circumference was measured in cm at the central part of the uppermost ear. According to their diameter, the test genotypes were classified into five different categories as per descriptors.

1- Very small
2- Small
3- Medium
4- Large
5- Very large

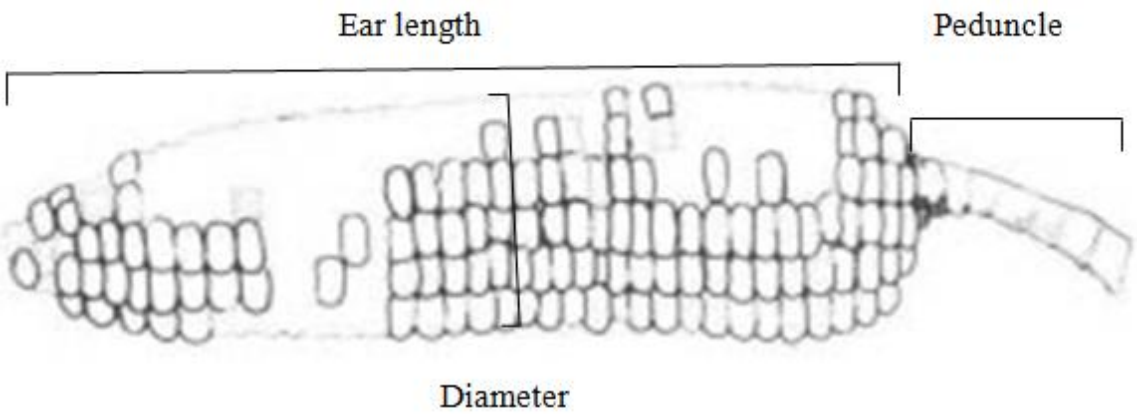


Figure 1. Descriptors of the ear

1. Regular 2. Irregular 3. Straight 4. Spiral

Figure 2. Kernel row arrangement

3.11.15 Number of kernel row per cob

Number of kernel rows per cob was counted in the central part of the uppermost ear and recorded for ten randomly selected ears and average value was taken and the test genotypes were classified into five different categories as per descriptors.

1- Very few
2- Few
3- Medium
4- Many
5- Very many

3.11.16 Kernel row arrangement

The uppermost ear was used to show kernel row arrangement. The test genotypes were classified into three different categories as per descriptors (Figure 2)

1- Straight
2- Spiral
3- Irregular
4- Regular

3.11.17 Number of kernels per row

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

3.11.18 Number of kernel per cob

Number of kernels per ear was counted and recorded for ten randomly selected ears and average value was taken.

3.11.19 1000-kernel weights (g)

1000 kernel weights of samples was recorded along with their moisture content by using moisture meter and then it was converted to fourteen percent (14%) moisture content.

3.11.20 Total yield per plant

Randomly selected plants per replication were harvested, seeds were sun dried for few days and weighed and then averaged. Seed yield was adjusted at 14% moisture content.

3.12 Statistical analysis

The genetic variability was computed based on the grand mean, mean squares and error variances of the traits evaluated. An analysis of variance according to randomized complete block design model was computed to derive mean squares and their interaction with location using computer package 'MSTATC'. LSD was applied at both 1% and 5% level of significance. Heritability (h^2) was calculated from the mean squares obtained from ANOVA.

3.12.1 Estimation of phenotypic and genotypic variance

Formula given by Chaudhary and Prasad (1968) was used to calculate phenotypic and genotypic variance.

Genotypic variance (σ^2_g) = (TMSS – EMSS) / R

Error variance = σ^2_e

Phenotypic variance = $\sigma^2_p = \sigma^2_g + \sigma^2_e$

Where, TMSS is treatment mean sum of square

EMSS is error mean sum of square

R is number of replication

3.12.2 Estimation of genotypic and phenotypic coefficient of variation (GCV and PCV)

They are expressed as percentage according to Burton & Devane (2008).

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

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

Where, σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{X}$= General mean of the trait

As indicated by Sivasubramanjan & Menon (1973), GCV and PCV are categorized as follows:

0 – 10 %: Low

10 – 20 %: Moderate

>20 %: High

3.12.3 Estimation of broad sense heritability (h^2_b)

Hanson *et al.* (1956) estimated broad sense heritability as the ratio of genotypic variance (Vg) to the phenotypic variance (Vp) and expressed in percentage.

Broad sense heritability (h^2_b) = (V g /V p)

Robinson *et al.* (1949) categorized broad sense heritability as follows:

0 – 0.30: Low

0.30 – 0.60: Moderate

> 0.60: High

3.12.4 Estimation of genetic advance (GA)

It was calculated by using the following formula given by Robinson *et al*. (1949).

GA = i. σ_p. h^2b

Where, i = Efficacy of selection (2.06 at 5% selection intensity)

σ_p = Phenotypic standard deviation

h^2_b = Broad Sense Heritability

3.12.5 Estimation of genetic advance as percent of means (GAM)

GA as per cent of mean (GAM) = (GA/$\overline{X}$) × 100

GA = Genetic advance; $\overline{X}$ =General mean of the trait

Johnson *et al*. (1955) categorized GAM as follows:

0 - 10 %: Low

10 -20 %: Moderate

> 20 %: High

3.12.6 Estimation of genotypic and phenotypic correlation co-efficient

For calculating the genotypic and phenotypic correlation coefficient in all possible combination the formula suggested by Johnson *et al*. (1955) and Hanson *et al.* (1956) were adopted. The genotypic covariance components between two traits and of the phenotypic covariance component were derived in the same way as for the corresponding variance components. The covariance components were used to compute genotypic and phenotypie correlation between the pairs of the characters as follows:

Genotypic correlation $=\sigma^2_{gxy}/\sqrt{\sigma^2_{gx}+\sigma^2_{gy}}$

Where, σ^2_{gxy}= Genotypic covariance between the traits x and y.

σ^2_{gx}= Genotypic variance of the trait x

σ^2_{gy}= Genotypic variance of the trait y

Thus, Phenotypic correlation (r_{phxy}) $=\sigma^2_{phxy}/\sqrt{\sigma^2_{phx}+\sigma^2_{phy}}$

Where, σ^2_{phxy}= Phenotypic covariance between the traits x and y.

σ^2_{phx}= Phenotypic variance of the trait x

σ^2_{phy}= Phenotypic variance of the trait y

3.12.7 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure employed by Dewey and Lu (1959) and Dabholkar (1992), using simple correlation values. In path analysis, correlation co-efficient was partitioned into direct and indirect effects of independent variables on the dependent variable.

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

$r_{yx1} = P_{yx1} + P_{yx2rx1x2} + P_{yx3rx1x3}$

$r_{yx2} = P_{yx1rx1x3} + P_{yx2} + P_{yx3rx2x3}$

$r_{yx3} = P_{yx1rx1x3} + P_{yx2rx2x3} + P_{yx3}$

P_{yx1}= the direct effect of x_1 on y

$P_{yx2rx1x2}$=the indirect effect of x_1 via x_2 on y

$P_{yx3rx1x3}$= the indirect effect of x_1 via x_3 on y

After calculating the direct effect and indirect effect of the characters, residual effect (R) was calculated by using the formula given below:

$P^2_{RY} = 1 - \sum P_{iy}.riy$

Where, $P^2_{RY} = (R^2)$ and hence residual effect, $R = (P^2_{RY})\ 1/2$

P_{iy}= direct effect of the character on yield

riy= correlation of the character with yield

3.13. 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.

3.13.1 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).

3.13.2 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.

3.13.3 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.

3.13.4 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.

3.13.5 Computation of average intra-cluster distance

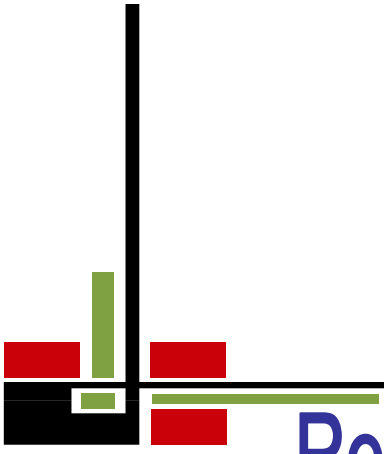
Computation of average intra-cluster distance for each cluster was calculated by taking possible D^2 values within the members of a cluster obtained from the PCO after the clusters are formed. The formula utilized was $\sum D^2/n$, where $\sum D^2$ is the sum of distances between all possible combinations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

3.13.6 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.

3.13.7 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.



Chapter 4

Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The data pertaining to different qualitative and quantative traits were recorded, computed and statistically analyzed and thus results are described below under the following heads:

4.1 Characterizations of yield and yield contributing traits of maize genotypes
4.2 Correlation co-efficient analysis
4.3 Path co-efficient analysis
4.4 Genetic diversity of maize genotypes

4.1 Characterizations of yield and yield contributing traits of maize genotypes

4.1.1 Variability in maize genotypes in respect of leaf number, length and breadth

In case of leaves per plant, leaf length and leaf breadth; ANOVA were not performed. For these three characters; mean value and pearson correlation were performed and are described based on mean and correlation coefficients. Differences of leaves of 25 maize genotypes are showed in Plate 2.

4.1.1.1 Leaves per plant

Maximum leaves per plant (24) were observed in G9 followed by G1, G7, G8, G16 and G21, while minimum in G2 and G23 (20.67) (Appendix V). These results are in line with those of Dijk *et al*. (1999) who observed significant differences while evaluating maize genotypes for different morphological and yield traits. Pearson correlation coefficient analysis showed that leaf per plant

was highly significantly and positively correlated with leaf length, leaf breadth, ear length, ear circumference and 1000-kernel weight (Table 3). Triveni *et al*. (2014) found number of leaf per plant of maize highly significantly and positively correlated with its grain yield. Results of this study imply that maize grain yield can be improved, by considering number of leaf per plant.

4.1.1.2 Leaf length

Maximum leaf length was noted in G7 (102.22 cm) followed by G15, G1, G4, and G3, while minimum in G16 (77.08 cm) (Figure 3 and Appendix V). Pearson correlation coefficient analysis showed that leaf length was highly significantly and positively correlated with leaves per plant; leaf breadth and 1000-kernel weight (Table 3). It's positively correlated with yield per plant. But it showed negative correlation with ear length and ear circumference (Table 3). 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, ear length and low seed yield.

4.1.1.3 Leaf breadth

Maximum leaf breadth was noted in G12 (10.74 cm) followed by G8, G13, G5, and G15, while minimum in G19 (8.68 cm) (Figure 3 and Appendix V). Pearson correlation coefficient analysis showed that leaf breadth was highly significantly and positively correlated with leaves per plant, leaf length, ear length, ear circumference, 1000-kernel weight and yield per plant (Table 3).

Plate 2. Photograph showing differences of leaves of 25 maize genotypes

Table 3. Pearson correlation coefficient among different pairs of yield and yield contributing characters for different genotypes of maize

	Leaf length	Leaf breadth	L/P	EL	EC	TKW	TYP
Leaf length	1						
Leaf breadth	0.152**	1					
L/P	0.236**	0.185**	1				
EL	-0.013	0.112**	-0.119**	1			
EC	-0.012	0.192**	-0.174**	0.666**	1		
TKW	0.148**	0.355**	0.154**	0.440**	0.776**	1	
TYP	0.079	0.338**	0.047	0.685**	0.850**	0.824**	1

** Significant at the 1% level of probability, * Significant at the 5% level of probability

L/P=Leaves per plant, EL=Ear length, EC=Ear circumference, TKW=1000-kernel weight and TYP=Total yield per plant

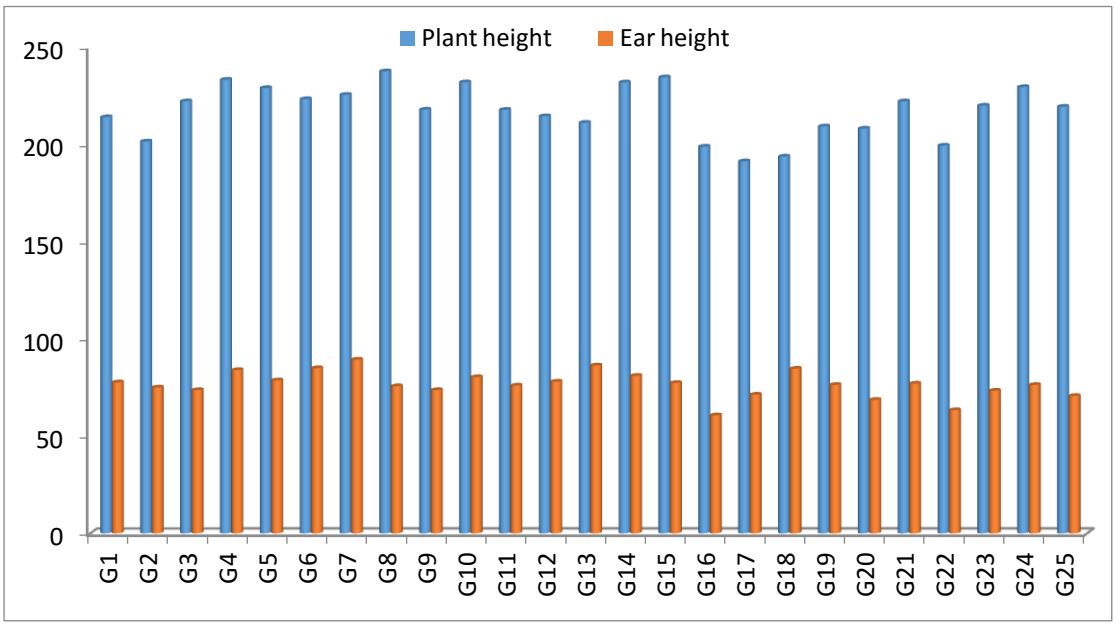


Figure 3. Diagram shows the performance of different maize genotype in respect of leaf length and leaf breadth

4.1.2 Genetic variability, heritability and genetic advance in maize genotypes

The genotypes differed significantly for all the characters (Table 4). The extent of variation among the genotypes in respect of other 12 characters were studied and mean value, range, genotypic variance (σ^2g), phenotypic variance (σ^2p), genotypic coefficient variation (GCV), phenotypic coefficient variation (PCV), genetic advance (GA) and genetic advance in percent of mean have been presented in Table 5 and Figure 4 & 5. The mean values of all genotypes for each character are also shown in Appendix VI. Performances of the genotypes are described below for each character.

4.1.2.1 Days to 50% tasseling

The analysis of variance showed that the genotypes varied significantly for days to 50% tasseling (Table 4). The minimum and maximum duration for 50% tasseling was observed in the genotype G5 (55.33 days) and G14 (63.33 days), respectively (Appendix VI). The estimates of GCV (3.78) and PCV (4.18) were low with very little difference which suggesting that the genotypes were less variable for this trait (Table 5 and Figure 5). Heritability (59.46%) of this trait was moderate; genetic advance (3.51) and GA% of mean was also low (6.00) (Table 5 and Figure 4). It revealed non-additive gene action involved in the maintenance of this trait and almost high heritability was exhibited due to influence of favorable environment rather than genotypes, so selection may not be rewarded. Grzesiak (2001) reported high heritability for days to 50% tasseling and days to 50% silking. But Mohar *et al.* (1999) reported that days to 50% flowering showed higher estimates of heritability along with genetic advance in lentil.

Table 4. Mean sum of square from the ANOVA of 25 maize genotypes in respect of 12 characters

Characters	Mean sum of square			Degrees of freedom	Co-variance (%)
	Genotype	Replication	Error		
Plant height (cm)	523.450**	107.062	79.546	48	4.10
Days to 50% tasseling	13.114**	0.973	3.334	48	3.12
Days to 50% silking	10.303**	5.293	2.543	48	2.63
Ear height (cm)	134.520**	11.640	10.223	48	4.18
Cobs per plant	0.015**	0.003	0.009	48	8.88
Ear length (cm)	9.851**	0.399	0.521	48	4.15
Ear circumference (cm)	5.827**	0.027	0.415	48	4.57
Number of kernel row per cob	4.025**	0.053	0.564	48	5.42
Number of kernel per row	76.086**	0.190	4.385	48	7.45
Number of kernel per cob	23476.690**	254.209	352.199	48	4.78
1000-kernel weight (g)	6839.250**	44.333	76.625	48	3.08
Total yield per plant (g)	2297.910**	104.460	36.889	48	5.24

** Significant at the 1% level of probability * Significant at the 5% level of probability

4.1.2.2 Days to 50% silking

Days required to 50% silking along with other maturity traits are commonly used by plant breeders as basis of determining maturity of maize. The mean square due to genotypes differed significantly for days to 50% silking (Table 4). The mean for this character was 60.69 days, which ranged from 57 - 65.33 days. The minimum days required for 50% silking was in G5 (57 days) and maximum days were for G14 (65.33 days) (Appendix VI). The phenotypic variance (6.42) was higher than genotypic variance (3.88). So, environment plays an important role for the expression of this trait. The genotypic (3.25) and phenotypic (4.18) coefficient of variation were low with a little difference indicates that environment had a little effect on the expression of this character and genotypes were less variable (Table 5 and Figure 5). The heritability (60.41%) of this trait was high and GA% was low (5.25) but genetic advance (3.15) was also low (Table 5 and Figure 4). It revealed non-additive gene action involved in the maintenance of this trait and high heritability was exhibited due to influence of favorable environment, so selection may not be rewarded. Neguly *et al.* (1983) observed that yield was indirectly affected by days to 50% silking via ear height. High heritability (0.85) for the same was recorded by Mulamba *et al.* (1983).

4.1.2.3 Plant height

Plant height is an important agronomic character for selecting desirable genotype for breeding program (Ali *et al.*, 2012). Significant mean sum of square for plant height indicated considerable difference among the genotypes studied (Table 4). Plant height ranged from 191.3 cm (G17) to 237.7 cm (G8) with mean value 217.56 (Table 5 and Appendix VI). The phenotypic and genotypic variances for this trait were comparatively high (301.50 and 221.95) (Table 5). 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 (7.98) was higher than the genotypic coefficient of variation (6.85) (Table 5 and Figure 5),

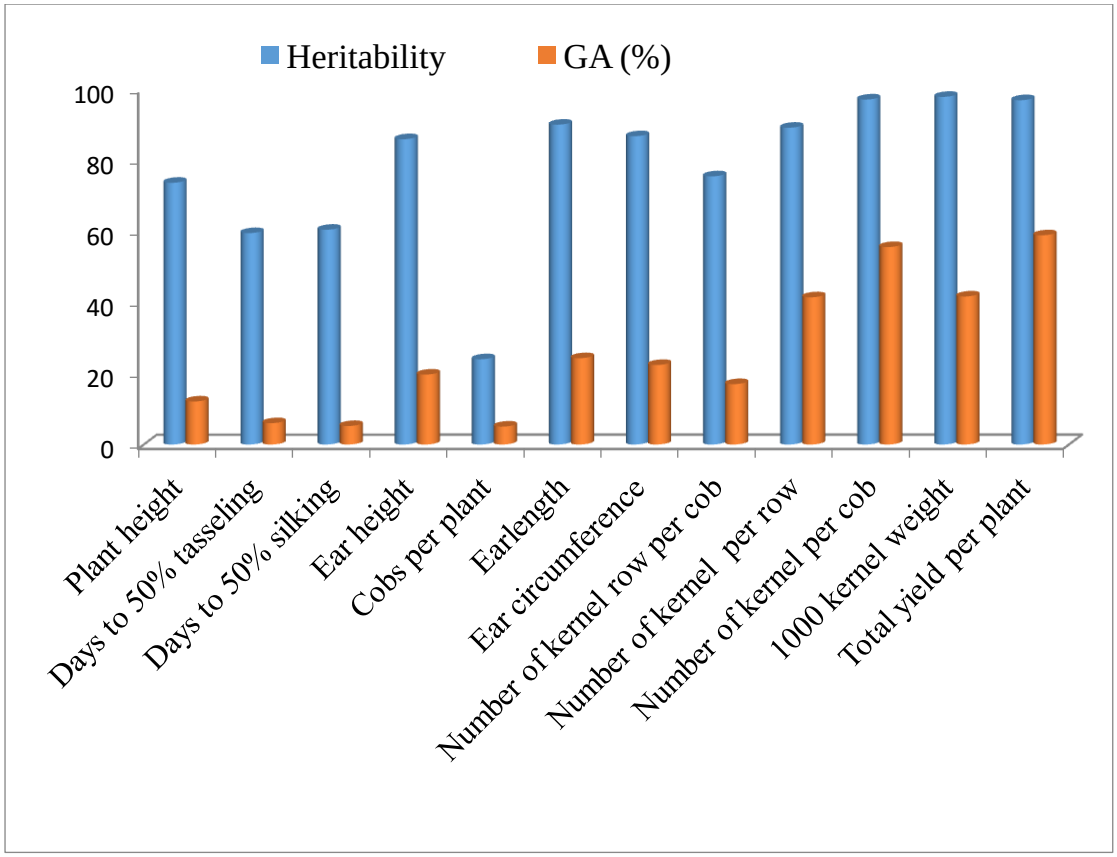


Figure 4. Heritability (%) and genetic advance in percent of mean performance of twelve characters of maize genotypes

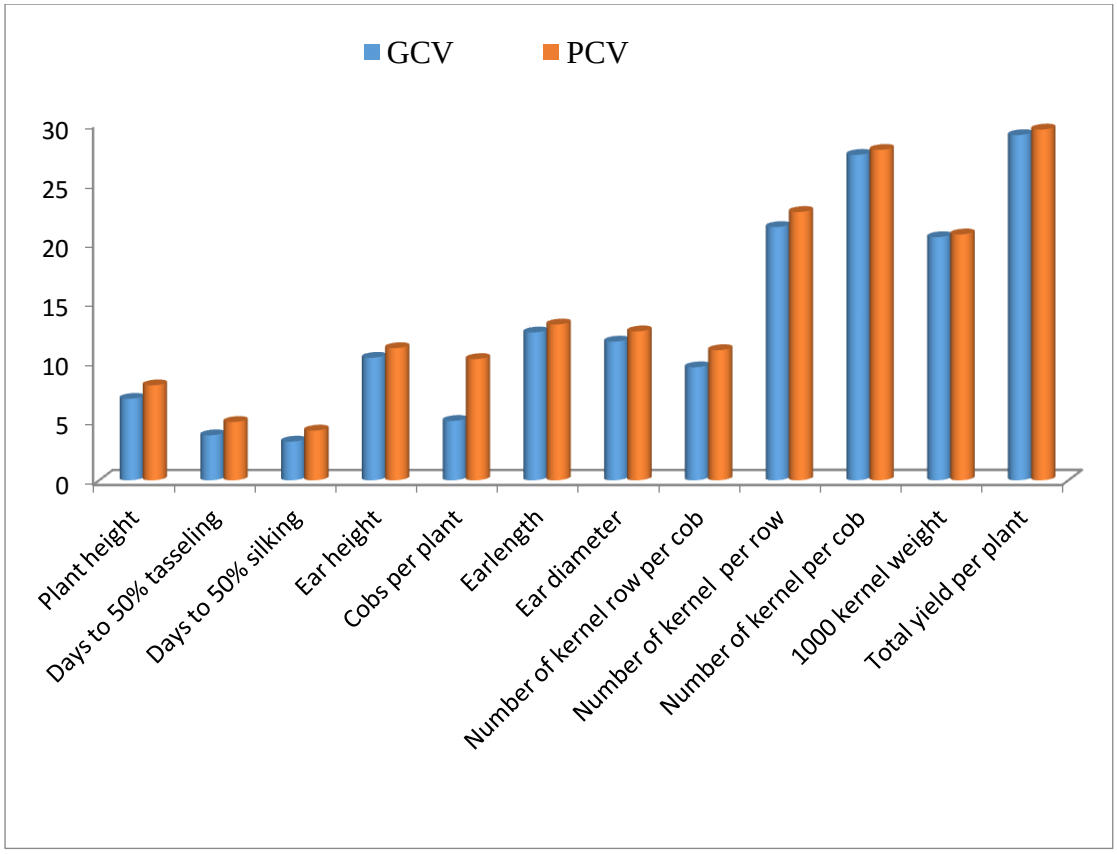


Figure 5. Genotypic coefficient variation (GCV) and phenotypic coefficient variation (PCV) performance of twelve characters of maize genotypes

which indicated the environment has a significant role on the expression of this trait. Heritability estimates was high (73.62%) with high genetic advance (26.33) and moderate genetic advance in percent of mean (12.10) (Table 5 and Figure 4) was considerable for this trait indicating apparent variation was due to genotypes. So, selection based on this trait would 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 greater the heritability of a particular trait, the lesser will be the environmental effect on its expression.

4.1.2.4 Ear height

Highly significant variations were observed among genotypes for ear height (Table 4). Our results were in agreement with those of Abel and Pollak (1991). While Genter and Alexander (1965) results after testcross evaluation are in disagreement with our results. Ear height ranges from 60.67 cm (G16) to 89.33 cm (G7) with mean value 76.56 cm (Table 5 and Appendix VI). The phenotypic and genotypic variance for this trait was comparatively high (72.37 and 62.15) (Table 5). The difference between variance suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (11.11) was higher than the genotypic coefficient of variation (10.30) (Table 5 and Figure 5), which indicated the environment has a significant role on the expression of this trait. Heritability value for ear height in our experiment was moderately high (85.87%) with high genetic advance (19.66) and moderate genetic advance in percent of mean (15.06) (Table 5 and Figure 5) was considerable for this trait indicating apparent variation was due to genotypes. Due to its high heritability it can easily be improved by selection (Ali *et al*., 2011 and Alam, 1999). Similarly, Ajmal *et al*. (2000) reported moderate heritability for ear height which is in line with our finding.

Table 5. Variability, heritability (h^2_b), genetic advance (GA) and GA in percent of mean for 12 yield and its related characters of maize

Traits	Minimum	Maximum	Mean	Genotypic variance (o^2_g)	Phenotypic variance (o^2_P)	GCV (%)	PCV (%)	Heritability (h^2_b)	GA	GA (%)
PH	191.3	237.7	217.56	221.95	301.50	6.85	7.98	73.62	26.33	12.10
D50T	55	63.33	58.51	4.89	8.22	3.78	4.90	59.46	3.51	6.00
D50S	57	65.33	60.69	3.88	6.42	3.25	4.18	60.41	3.15	5.20
EH	60.67	89.33	76.56	62.15	72.37	10.30	11.11	85.87	15.05	19.66
CPP	1	1.21	1.08	0.00	0.01	4.99	10.19	23.97	0.05	5.03
EL	15.07	21.67	17.38	4.67	5.19	12.43	13.10	89.95	4.22	24.28
EC	9.99	15.7	14.11	2.71	3.12	11.66	12.52	86.71	3.16	22.36
NKRC	11.04	15.6	13.85	1.73	2.29	9.50	10.94	75.43	2.35	16.99
KKR	16.27	40.4	28.12	35.85	40.24	21.29	22.56	89.10	11.64	41.40
NKC	216.7	591.4	392.94	11562.25	11914.44	27.36	27.78	97.04	218.21	55.53
TKW	143.3	340	284.53	3381.31	3457.94	20.44	20.67	97.78	118.45	41.63
TYP	47.1	153.4	115.85	1130.51	1167.40	29.02	29.49	96.84	68.16	58.84

PH= Plant height (cm), D50T= Days to 50% tasseling, D50S= Days to 50% silking, EH= Ear height (cm), CPP= Cobs per plant, EL= Ear length (cm), EC= Ear circumference (cm), NKRC= Number of kernel row per cob, NKR= Number of kernel per row, NKC= Number of kernel per cob, TKW=1000 kernel weight (g), TYP=Total yield per plant (g).

4.1.2.5 Cobs per plant

Statistically cobs per plant showed significant variation in case of genotype mean square (Table 4) but mean performance of genotypes showed almost similar results (Appendix V). The phenotypic and genotypic variance for this trait was minimum (0.00 and 0.01) (Table 5). The phenotypic coefficient of variation (10.19) was higher than the genotypic coefficient of variation (4.99) (Table 5 and Figure 5) which indicated that the environment has a significant role on the expression of this trait. Heritability value for this trait in our experiment was low (23.97%) with minimum genetic advance (0.05) and low genetic advance in percent of mean (5.03) (Table 5 and Figure 4) which indicating non additive gene action controlling this trait. So, selection based on this trait would not be effective. Similar results were reported by Amer and Mosa (2004) and Yassien (1993).

4.1.2.6 Ear length

There were significant variations among the genotypes based on the ear length (Table 4). Ear length ranged from 15.07 cm to 21.67 cm which was observed in G13 and G18, respectively. Average value for ear length was 17.38 cm (Appendix V). Phenotypic variance (5.19) was higher than the genotypic variance (4.67) as well as the phenotypic and genotypic coefficient of variations was 13.10 and 12.43 (Table 5 and Figure 5) respectively, which differed very little with each other indicating less influence of environment on this trait. Heritability of this trait was high (89.95%) but genetic advance was low (4.22) along with high genetic advance as a percentage of mean (24.28) (Table 5 and Figure 4). The high heritability was exhibited due to additive gene action involved in controlling for this trait and less influence of environment that means selection may be effective. Naushad *et al.* (2007) was observed significant variation in maize genotypes for ear length.

4.1.2.7 Ear circumference

Ear circumference showed significant differences among the genotypes (Table 4). The highest ear circumference was found in G23 (15.70 cm) and lowest ear circumference was found in G18 (9.99 cm) with mean value of 14.11 (Table 5 and Appendix VI). The phenotypic variance (3.12) was little different with genotypic variance (2.71) (Table 5). The phenotypic coefficient of variance (12.52) and the genotypic coefficient of variance (11.66) (Table 5 and Figure 5) were moderate. Heritability estimates was high (86.71%), genetic advance was very low (3.16) but genetic advance in percent of mean (22.36) was high (Table 5 and Figure 4) which indicated a character was less influenced by environmental effects and additive gene controlling the expression of this traits and selection may be effective in early generations for these traits. Similar results were reported by Ojo *et al.* (2006).

4.1.2.8 Number of kernel row per cob

Significant differences among the genotypes were observed due to number of kernel row per cob (Table 4). The highest number of kernel row per cob was 15.6, produced by the G22 and the lowest number of number of kernel row per cob was 11.04, produced by G18 and mean of this character was 13.85 (Appendix VI and Table 5). The phenotypic variance (2.29) was slightly higher than genotypic variance (1.73) (Table 5 and Figure 5). Moderate genotypic coefficient of variation (9.50) and phenotypic coefficient of variation (10.94) (Table 5 and Figure 4) were found for this trait with a non-significant difference which indicated that there was little environmental effect on the expression of character.

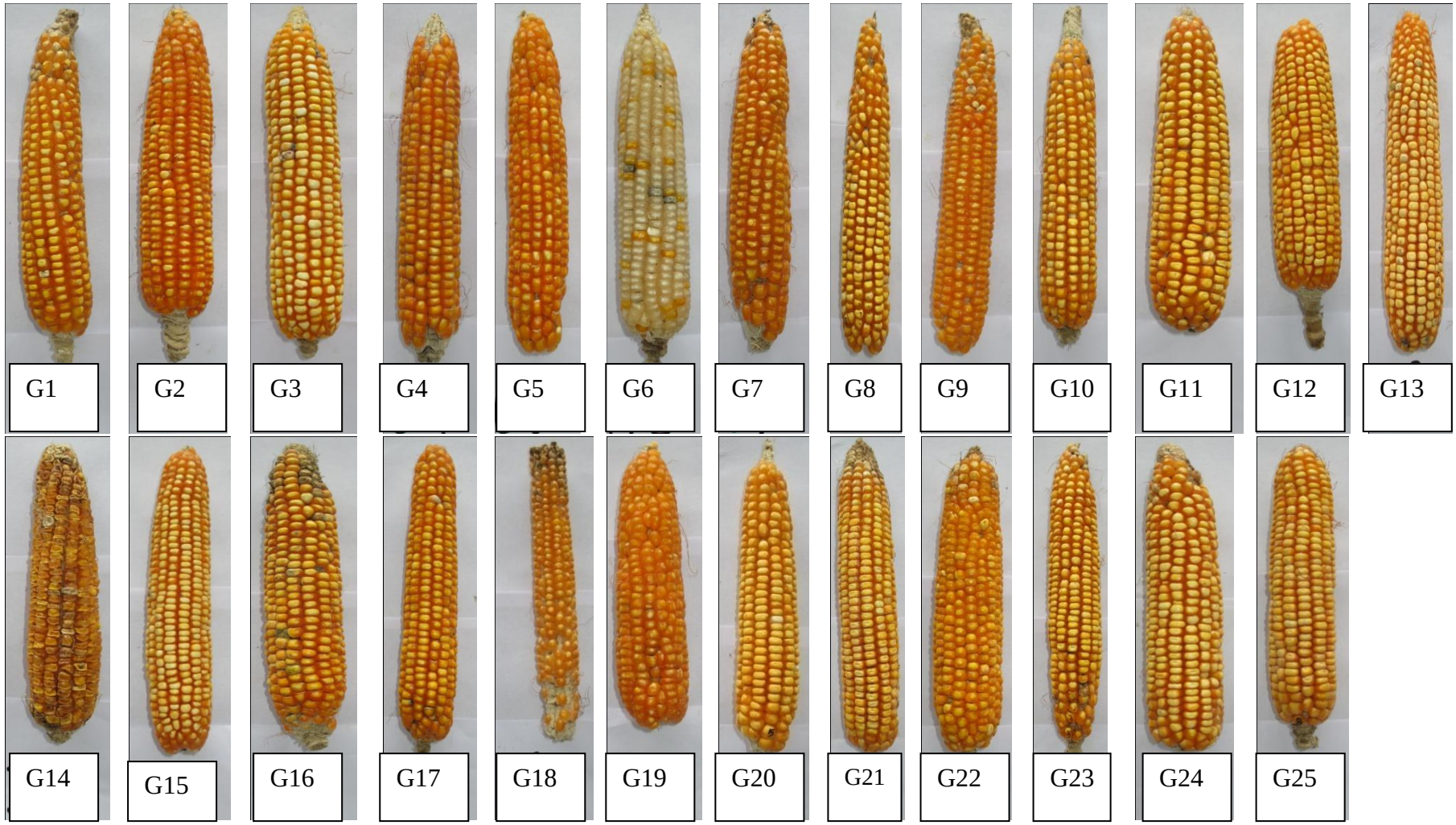


Plate 3: Photograph showing differences of cobs of 25 maize genotypes (numbers represent each genotype)

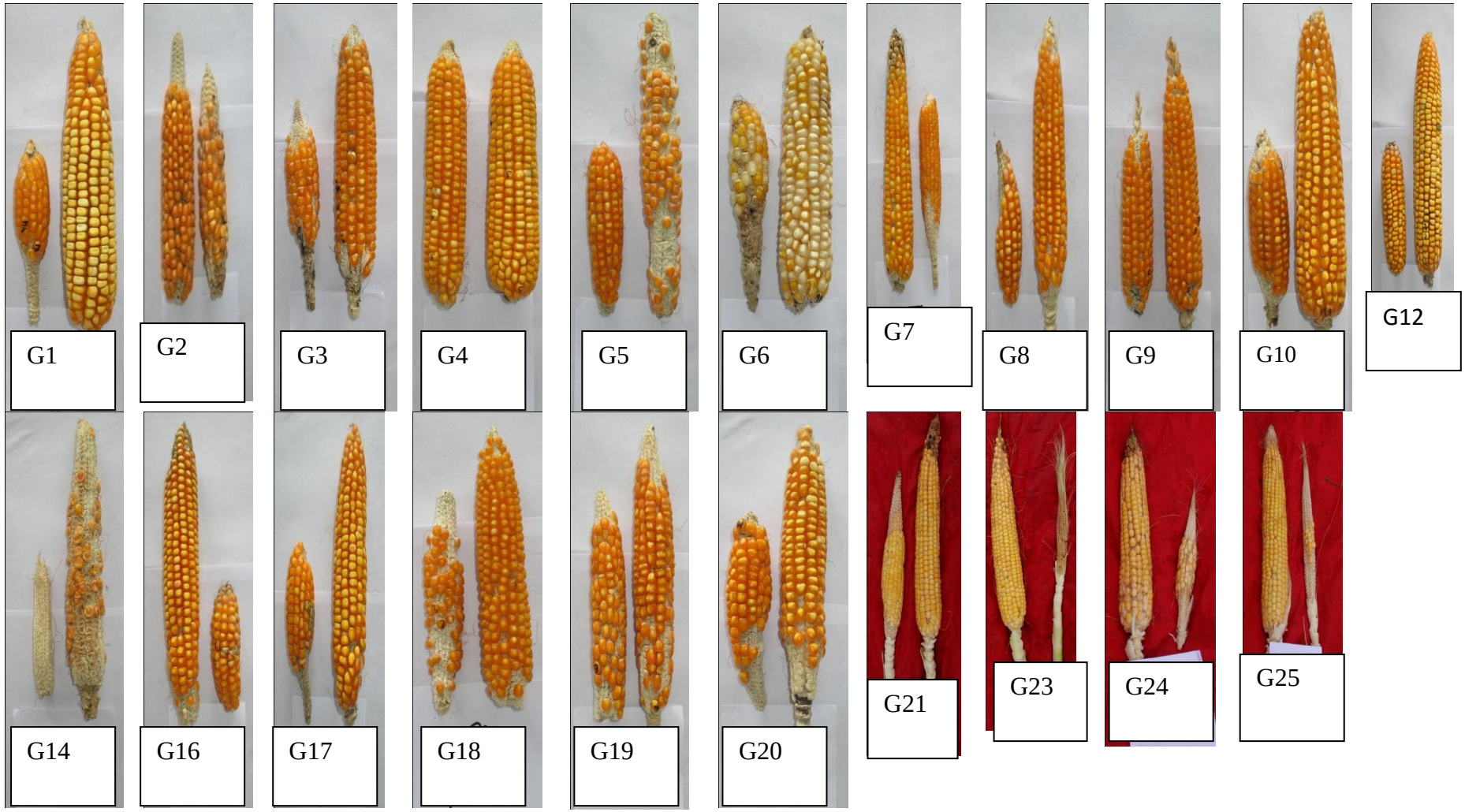


Plate 4. Photograph of different genotypes of maize which shows more than one cob per plant

The heritability was very higher (75.43%) together with low genetic advance (2.35) and moderate genetic advance in percent of mean (16.99) indicating the selection for this character would be effective (Table 5 and Figure 4). Similar results were reported by Chen *et al*. (1996), Satyanarayan and Kumar (1995) and Ojo *et al*. (2006). High heritability accompanied with moderate GA, GCV and genetic advance in percent of mean indicates that most likely the heritability is due to additive gene effects.

4.1.2.9 Number of kernel per row

Significant differences among the genotypes were observed due to number of kernel per row (Table 4). The maximum number of kernel per row were found (40.4) in the genotype G13 and minimum number of kernel per row were found (16.27) in the genotype G18, (Appendix VI). The phenotypic variance (40.24) was higher than genotypic variance (35.85) and the PCV (22.56) was also a little greater than GCV (21.29) (Table 5 and Figure 5) indicating the role of environment on the expression of this trait. The genetic advance was moderate (11.64) with high genetic advance in percent of mean (41.40) for this trait (Table 5 and Figure 4). Similar results were reported by Rather *et al.* (2003) and Rajesh *et al.* (2013). Heritablity was found to be highest for this trait (89.10%) (Table 5 and Figure 4), 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 kernel per row were also reported by Abd El-Sattar (2003).

4.1.2.10 Number of kernel per cob

Significant differences among the genotypes were observed for number of kernel per cob (Table 4). The highest and the lowest number of kernel per cob were produced by the G13 (591.3) and G18 (216.67) respectively and mean of this character was 392.94 (Appendix VI). The phenotypic and genotypic variance were high and the difference between the phenotypic variance

(11914.44) and the genotypic variance (11562.25) were significant (Table 5). High genotypic coefficient of variation (27.78) and phenotypic coefficient of variation (27.36) (Table 5 and Figure 5) were found for this trait with a non-significant difference which indicated that there was little environmental effect on the expression of the character. This character showed high heritability (97.04%) along with high genetic advance (218.21) and high genetic advance in percent of mean (55.53) (Table 5 and Figure 4) indicated that the heritability was due to additive gene effect and phenotypic selection might be effective. Similar results were reported by Mahmud *et al.* (2004), Hemavathy *et al*. (2008), and Anshuman *et al.* (2013).

4.1.2.11 1000-kernel weight

Significant differences among the genotypes were observed due to 1000-kernel weight (Table 4). Maximum number of 1000-kernel weight was found in G11 (340.00 g) and minimum in G18 (143.33 g) with a mean value of 284.53 (Appendix VI). The phenotypic and genotypic variance was high and the difference between the phenotypic variance (3457.94) and the genotypic variance (3381.31) was not significant. Little influence of environment upon this trait was reported due to difference between the estimation of GCV (20.44) and PCV (20.67) which suggesting existing of sufficient variability and offers scope for selection (Table 5 and Figure 5). High heritability (97.78%), high genetic advance (118.45) and high genetic advance in percent of mean (41.63) were found for this trait (Table 5 and Figure 4) 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 1000-kernel 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).

4.1.2.12 Total yield per plant

The genotypes varied significantly for total yield per plant (Table 4). The highest total yield per plant was observed in the genotype G13 (153.38 g) and the lowest total yield per plant was observed in the genotype G14 (47.07 g) (Appendix VI). The phenotypic variance (1167.40) differed slightly from genotypic variance (1130.51) for this trait. Moderate genotypic (29.02) and phenotypic (29.49) coefficient of variation and high heritability (96.84%) along with high genetic advance (68.16) and high genetic advance in percent mean (58.84) were estimated for this character (Table 5 and Figure 4 &5). 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).

4.1.3 Categorization of genotypes based on morphological traits

In the present investigation different phenotypic traits were studied for 25 genotypes of maize according to the guidelines for the conduct of DUS test (distinctiveness, uniformity, stability) and characterized (Table 6). All the genotypes showed diversity among them indicating number of phenotypic descriptors was able to discriminate between them. However, as reported by Kumar *et al*. (2003) and Rana *et al*. (2005) in cotton and Kwon *et al.* (2005) in pepper, the genetic diversity estimates were found to be of high magnitude for maize.

Table 6. Frequency distribution of genotypes belonging to different phenotypic classes

Traits	Category	Total genotypes	Genotype
Width of the leaf blade (cm)	Very small	0	Nil
	Small	0	Nil
	Medium	4	G3, G18, G19, G23
	large	21	G1, G2, G4, G5, G6, G7, G8, G9, G10, G11, G12, G14, G15, G16, G17, G20, G21, G22, G24, G25
Plant height(cm)	Short	0	Nil
	Medium	0	Nil
	Medium long	4	G16, G17, G18, G22
	Long	13	G1, G2, G3. G6, G9,G11 G12, G13, G19, G20,G21,G23, G25
	Very long	8	G4,G5, G7,G8, G10, G14, G15, G24
Ear placement (cm)	Short	23	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G14, G15, G16, G17, G19, G20, G21, G22, G23, G24, G25
	Medium	2	G13 and G18
	Medium long	0	Nil
	Long	0	Nil
	Very long	0	Nil
Time of anthesis	Very early	0	Nil
	Early	3	G18, G5, G7
	Medium	22	G1, G2, G3, G4, G6, , G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, , G19, G20, G21, G22, G23, G24, G25
	Late	0	Nil
	Very late	0	Nil

Table 6 (cont'd).

Time of silk emergence	Very early	14	G2, G3, G4, G5, G6, G7, G9, G11, G12, G18, G20, G21, G22, G25
	Early	10	G1, G8, G10, G13, G15, G16, G17, G19, G23, G24
	Medium	1	G14
	Late	0	Nil
	Very late	0	Nil
Color of top grain	Pure white	1	G6
	Brown	11	G1, G2, G4, G5. G7, G14, G17, G18, G19, G22, G9
	Yellow	14	G3, G8, G10, G11, G12, G13, G15, G16, G20, G21, G23, G24, G25
Ear shape	Conical	10	G3, G4, G12, G15, G17, G18, G19,G21, G22, G25
	Conical-cylindrical	10	G1, G2, G5, G6, G10, G11, G13, G16, G20, G24
	Cylindrical	5	G7, G8, G9, G14, G23
Ear circumference without husk (cm)	Very small	0	Nil
	Small	0	Nil
	Medium	0	Nil
	Large	0	Nil
	Very large	25	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G24, G25
Ear length (cm)	Very small	1	G7
	Small	16	G1, G2, G3, G4, G5, G6, G8, G9, G10, G12, G14, G15, G17, G18, G19, G20
	Medium	6	G11, G16, G21, G22, G24, G25
	Large	2	G13,G23
	Very large	0	Nil

Table 6 (cont'd).

Number of rows of kernel per cob	Very few	0	Nil
	Few	0	Nil
	Medium	10	G1,G2, G3,G7, G8, G9, G14, G18, G19, G20
	Many	15	G4, G5, G6, G10,G11, G12, G13, G15, G16, G17, G21, G22, G23, G24, G25
	Very many	0	Nil
Kernel row arrangement	Straight	18	G2, G3, G4, G5, G6, G9, G10, G11, G12, G13, G15, G16, G17, G20, G21, G22, G24, G25
	Spiral	3	G1, G7, G14
	Irregular	4	G8, G18, G19, G23
1000-kernel weight (g)	10-15g	1	G18
	15.1-20g	2	G9. G14
	20.1-25g	0	Nil
	25.1-30g	10	G2, G3, G4, G5, G7, G8, G15, G16, G23, G24
	30.1-35g	12	G1, G6, G10, G11, G12, G13, G17,G19, G20, G21, G22, G25
	35.1-40g	0	Nil

4.2 Correlation coefficients analysis

Yield is a complex character and associated with several yield contributing characters. Selection for yield may not be effective unless other yield components influencing it directly or indirectly are taken into consideration. When selection pressure is exercise for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Hence knowledge regarding association of characters with yield and among themselves provides guideline to the plant breeder for making improvement through selection. Genotypic and phenotypic correlations between pairs of characters are presented in Table 7. 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:

4.2.1 Days to 50% tasseling

Days to 50% tasseling showed highly significant positive correlation with days to 50% silking at both the genotypic and phenotypic level. It showed non-significant positive correlation with cobs per plant, ear length, ear circumference, number of kernel per row and number of kernel per cob for both genotypic and phenotypic levels (Table 7). Non-significant negative phenotypic and genotypic correlation was also observed with ear height, number of kernel row per cob, 1000-kernel weight and total yield per plant (Table 7). Similar findings were reported by Kumar *et al*. (2014). This means with more days to 50% tasseling and silking there will be more vegetative growth and less time for reproductive growth which consequently results in fewer yields. Similar observation was noted by Kwaga (1994). This is somewhat in disagreement with the findings of Sumathi *et al.* (2005) who reported highest significant positive correlation between grain yield and days to anthesis in maize.

Table 7. Genotypic (r_g) and phenotypic (r_p) correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of maize

Ch		D50T	D50S	EH	CPP	EL	EC	NKRC	NKR	NKC	TkW	TYP
PH	r_g	0.469	0.378	0.430*	-0.514	-0.059	0.162	0.093	0.119	0.053	0.065	-0.029
	r_p	0.379	0.304	0.416*	-0.283	-0.021	0.152	0.076	0.116	0.054	0.058	-0.015
D50T	r_g		0.924**	-0.003	-0.068	0.065	0.107	-0.063	0.013	-0.002	-0.087	-0.018
	r_p		0.863**	-0.004	0.035	0.048	0.086	-0.043	0.030	0.015	-0.073	-0.026
D50S	r_g			0.047	-0.205	0.078	-0.005	-0.171	-0.127	-0.124	-0.319	-0.230
	r_p			0.018	-0.036	0.056	-0.004	-0.103	-0.086	-0.095	-0.281	-0.209
EH	r_g				0.086	-0.157	-0.362	-0.302	-0.145	-0.218	-0.213	-0.358
	r_p				0.041	-0.143	-0.336	-0.275	-0.127	-0.200	-0.200	-0.342
CPP	r_g					-0.832**	-0.859**	-0.643*	-0.581	-0.688*	-0.327	-0.539
	r_p					-0.532**	-0.613**	-0.494*	-0.388	-0.444*	-0.211	-0.352
EL	r_g						0.695**	0.681**	0.581**	0.671**	0.450*	0.706**
	r_p						0.666**	0.634**	0.559**	0.652**	0.440*	0.686**
EC	r_g							0.801**	0.726**	0.702**	0.810**	0.879**
	r_p							0.757**	0.677**	0.680**	0.776**	0.851**
NKRC	r_g								0.908**	0.975**	0.606**	0.853**
	r_p								0.839**	0.909**	0.557**	0.800**
NKR	r_g									0.966**	0.647**	0.853**
	r_p									0 .944**	0.625**	0.829**
NKC	r_g										0.526**	0.827**
	r_p										0.523**	0.819**
TKW	r_g											0.834**
	r_p											0.824**

**Significant at the 1% level of probability.*Significant at the 5% level of probability. r_g= genotypic correlation, r_p= phenotypic correlation

PH= Plant height (cm), D50T= Days to 50% tasseling, D50S= Days to 50% silking, EH= Ear height (cm), CPP= Cobs per plant, EL= Ear length (cm), EC= Ear circumference (cm), NKRC= Number of kernel row per cob, NKR=Number of kernel per row, NKC=Number of kernel per cob, TKW=1000-kernel weight (g), TYP=Total yield per plant (g).

4.2.2 Days to 50% silking

Days to 50% silking did not showed any significant positive correlation for all characters at both the genotypic and phenotypic level (Table 7). But it showed non-significant positive correlation with ear height, ear length for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with cobs per plant, ear circumference, number of kernel row per cob, number of kernel per cob, number of kernel per row, 1000-kernel weight and total yield per plant (Table 7). Similar findings were reported by Kumar *et al.* (2014). This means with least days to 50% tasseling and silking there will be less vegetative growth and more time for reproductive growth which consequently results in higher yields. But Afzal *et al.* (2005) reported that days to silking showed positive correlation with grain yield per plant.

4.2.3 Plant height

Plant height showed highly significant positive correlation with ear height at both the genotypic and phenotypic level (Table 7). It showed non-significant positive correlation with days to 50% tasseling, days to 50% silking, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000-kernel weight for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with cobs per plant, ear length and total yield per plant (Table 7). Mohammadi *et al.* (2003); Ojo *et al.* (2006); Sadek *et al.* (2006) and Abou-Deif (2007) reported that plant height was significantly and positively correlated with each of number of rows per ear and ear height. However, Srekove *et al.* (2011) reported negative correlation between grain yield and plant height.

4.2.4 Ear height

Ear height showed highly significant positive correlation with plant height at both the genotypic and phenotypic level (Table 7). But it showed non-significant positive correlation with days to 50% silking, cobs per plant for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was observed with days to 50% tasseling, ear length, ear circumference, number of kernel row per cob, number of kernel per cob, number of kernel per row, 1000-kernel weight and total yield per plant (Table 7). Lackney and Russell (1971) observed that ear height was significantly correlated with yield at low, intermediate and high plant densities. Burgess and West (1993) reported that for low ear height, grain yield had declined 29% in Tennesse Late Low-Ear synthetic. Ear height showed significant and positive phenotypic correlations with each of number of rows per ear and ear circumference; on the other hand, it was significantly and negatively correlated with number of kernel per row (Amin *et al*. 2003; Sadek *et al.* 2006 and Abou-Deif 2007).

4.2.5 Cobs per plant

Cobs per plant showed highly significant negative correlation with ear length, ear circumference, number of kernel row per cob and number of kernel per cob at both the genotypic and phenotypic level (Table 7). It did not showed any significant positive correlation for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with plant height, days to 50% tasseling, days to 50% silking, number of kernel per row, 1000 kernel weight and total yield per plant (Table 7).

4.2.6 Ear length

Ear length showed highly significant positive correlation with cobs per plant, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob, 1000-kernel weight and total yield per plant at both the genotypic and phenotypic level (Table 7). It showed non-significant

positive correlation with days to 50% tasseling and days to 50% silking for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with ear height and plant height (Table 7). Rafique *et al.* (2004) reported positive correlations of ear length with grain yield per ha. EL-Beially, (2003); Mohammadi *et al*. (2003) and Sadek *et al*. (2006) found significant and positive correlations with 100-kernel weight and number of kernel per row while negative correlations with number of rows per ear and ear circumference with ear length.

4.2.7 Ear circumference

Ear circumference showed highly significant positive correlation with cobs per plant, ear length, number of kernel row per cob, number of kernel per row, and number of kernel per cob, 1000-kernel weight and total yield per plant at both the genotypic and phenotypic level (Table 7). It showed non-significant positive correlation with plant height and days to 50% tasseling for both genotypic and phenotypic levels (Table 7). Non-significant negative phenotypic and genotypic correlation was also observed with days to 50% silking and ear height (Table 7). Such results were in harmony with those obtained by Salama *et al.*, (1994) and Yasien (2000).

4.2.8 Number of kernel row per cob

Number of kernel row per cob showed highly significant positive correlation with ear length, ear circumference, number of kernel per row, number of kernel per cob, 1000-kernel weight and total yield per plant at both the genotypic and phenotypic level (Table 7). It showed highly significant negative correlation with cobs per plant at both the genotypic and phenotypic level (Table 7). 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% tasseling, days to 50% silking and ear height (Table 7). 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 ear showed significant and negative correlations with 1000-kernel weights and number of kernel per row.

4.2.9 Number of kernel per row

Number of kernel per row showed highly significant positive correlation with ear length, ear circumference, number of kernel row per cob, number of kernel per cob, 1000-kernel weight and total yield per plant at both the genotypic and phenotypic level (Table 7). It showed non-significant positive correlation with plant height and days to 50% tasseling for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with days to 50% silking, ear height and cobs per plant (Table 7). Amin *et al.* (2003) indicated that number of kernels per row and 100- kernel weight were the highest contributors to variation in grain yield directly or indirectly.

4.2.10 Number of kernel per cob

Number of kernel per cob showed highly significant positive correlation with ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob, 1000-kernel weight and total yield per plant at both the genotypic and phenotypic level (Table 7). It showed highly significant negative correlation with cobs per plant at both the genotypic and phenotypic level (Table 7). It showed non-significant positive correlation with plant height and days to 50% tasseling for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with days to 50% silking and ear height (Table 7). Alvi *et al.* (2003) and Sofi and Rather (2007) also found strong association between grain yield and kernel row number.

4.2.11 1000-kernel weight

Highly significant positive correlation were observed between 1000-kernel weight with ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and total yield per plant at both the genotypic and phenotypic level (Table 7). 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% tasseling, days to 50% silking, ear height and cobs per plant (Table 7). Grain yield is considered to have positive correlation with plant height and hundred kernel 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-kernel weight.

4.3 Path co-efficient analysis

Association of character determined by correlation co-efficient might not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on total yield per plant. As a matter of fact, in order to find out a clear picture of the inter-relationship between total yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at genotypic level which also measured the relative importance of each component. Total yield per plant was considered as reluctant (dependent) variable and plant height, days to 50% tasseling, days to 50% silking, ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob, 1000-kernel weight were casual (independent) variables. Estimation of direct and indirect effect of path co-efficient analysis for maize was presented in Table 8.

Days to 50% tasseling, ear length, ear circumference, number of kernel per cob, 1000-kernel weight showed positive direct effect and plant height, days to 50%

silking, number of kernel row per cob, number of kernel per row showed negative direct effect on total yield per plant (Table 8). Zarei *et al.* (2012) reported similar result.

Plant height showed positive indirect effects on ear length but it showed negative indirect effect on days to 50% tasseling, days to 50% silking, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000-kernel weight (Table 8). Plant height is an important trait that effect grain yield. Taller plants need more plant nutrients to complete more vegetative growth than reproductive phase that results in late maturation of cob. The results indicated that plant height had negative direct effect (-1.7514) on yield because of its negative indirect effect through ear length and grain weight (Emer, 2011 and Mohan *et al.* 2002)

Path analysis showed that days to 50% tasseling had positive indirect effects on plant height, days to 50% silking, ear length, ear circumference and number of kernel per row (Table 8). It showed negative indirect effect on number of kernel per cob and 1000-kernel weight. Days to 50% silking showed positive indirect effects on ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000-kernel weight (Table 8).

It was found that ear length had positive indirect effect on days to 50% tasseling, days to 50% silking, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000-kernel weight (Table 8). Its indirect effects via plant height and grain weight were also negative (Parh *et al.*, 1986). Ear circumference had positive indirect effects on plant height, days to 50% tasseling, ear length, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000-kernel weight and it showed negative indirect effect on days to 50% silking (Table 8). Wannows *et al.* (2010) reported similar findings. These results coincide with those obtained by Amin *et al.* (2003); AL-Ahmad, (2004) and Sadek *et al.* (2006).

Table 8. Path coefficient analysis showing direct and indirect effects of different characters on yield of maize

Characters	Indirect effect									Genotypic correlation with yield
	PH	D50T	D50S	EL	EC	NKRC	NKR	NKC	TKW	
PH	**-0.099**	-0.047	-0.038	0.006	-0.016	-0.009	-0.011	-0.005	-0.006	-0.015
FDT	0.379	**0.808**	0.747	0.052	0.087	-0.051	0.011	-0.002	-0.070	-0.026
FDS	-0.389	-0.952	**-0.103**	-0.080	0.005	0.176	0.131	0.128	0.329	-0.209
EL	-0.010	0.011	0.013	**0.171**	0.118	0.116	0.099	0.115	0.077	0.685**
EC	0.140	0.092	-0.004	0.602	**0.866**	0.693	0.628	0.608	0.701	0.851**
NKRC	0.089	0.061	0.165	-0.656	-0.772	**-0.963**	-0.875	-0.939	-0.584	0.800**
NKR	-0.007	-0.001	0.008	-0.036	-0.045	-0.056	**-0.062**	-0.060	-0.040	0.829**
NKC	0.056	-0.002	-0.130	0.703	0.736	0.102	0.101	**0.104**	**0.550**	0.819**
TKW	-0.008	0.011	0.039	-0.055	-0.099	-0.075	-0.079	-0.065	**0.532**	0.824**

Residual effect = 0.063 ** Significant at the 1% level of probability.

PH=Plant height (cm) , D50T= Days to 50% tasseling, D50S= Days to 50% silking, EL=Ear length (cm), EC= Ear circumference (cm), NKRC= Number of kernel row per cob, NKR=Number of kernel per row, NKC=Number of kernel per cob, TKW=1000-kernel weight (g), TYP=Total yield per plant (g).

Path analysis revealed that kernel row per cob had positive indirect effect on days to 50% tasseling, days to 50% silking and it showed negative indirect effect on plant height, ear length, ear circumference, number of kernel per row, number of kernel per cob and 1000-kernel weight (Table 8). These results were in agreement with results which Ahmad and Saleem (2003) and Najeeb *et al.* (2009) found in their research. Rafiq *et al.* (2010) also found positive direct effect of kernel row number on grain yield, but it wasn't significant.

Number of kernel per row showed positive indirect effects on days to 50% silking but it showed negative indirect effect on plant height, days to 50% tasseling, ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000-kernel weight (Table 8).

Number of kernel per cob showed positive indirect effects on plant height, ear length, ear circumference, number of kernel row per cob, number of kernel per row and 1000-kernel weight (Table 8). But it showed negative indirect effect on days to 50% tasseling, days to 50% silking (Table 8). Nemati *et al.* (2009) reported that ear weight has direct effect on grain yield.

Path analysis showed that 1000-kernel weight had positive indirect effects on days to 50% tasseling and days to 50% silking (Table 8). It showed negative indirect effect on plant height, ear height, ear length, ear circumference, number of kernel row per cob, number of kernel per row and number of kernel per cob (Table 8).

4.4 Genetic diversity of maize genotypes

Diversity is the function of parent selection and also heterosis. The availability of transgressive segregants in a breeding programme depends upon the divergence of parents. Thus, the accurate information on the nature and degree of diversity of the parents is the pre-requisite of an effective breeding programme. The knowledge of genotypic variation within genotypes in relation to morphology, phenology and yield would help to screen better genotypes for hybridization programme.

4.4.1 Multivariate analysis

Genetic diversity of 25 maize varieties was determined by using the multivariate analysis and the result are presented in Table 9 to Table 15 and Figure 6 & 7 and discussed under the following headings:

4.4.1.1 Principal Component Analysis

Eigen values and latent vectors of corresponding twelve principal component axes and percentage of total variation accounting for them obtained from the principal component analysis are presented in Table 9. Eigen values represents that the cumulative eigen values of first six principal components accounted for 96.93 per cent of the total variation among the varieties. The first principal component accounted for 47.63% of the total variation, the second, third, fourth, fifth and sixth components accounted for 18.12%, 10.97%, 7.48%, 6.07% and 4.56% of the total variation respectively. The rest of the components accounted for only 3.07% of the total variation.

Table 9. Eigen values and yield percent contribution of 12 characters of 25 genotypes of maize

Principal component axes	Eigen values	Percent variation	Cumulative % of percent variation
I	5.716	47.63	47.63
II	2.174	18.12	65.75
III	1.316	10.97	76.72
IV	0.898	7.48	84.2
V	0.728	6.07	90.27
VI	0.547	4.56	94.83
VII	0.252	2.1	96.93
VIII	0.15	1.25	98.18
IX	0.101	0.84	99.02
X	0.066	0.55	99.57
XI	0.034	0.28	99.85
XII	0.017	0.15	100.00

4.4.1.2 Construction of scatter diagram

Based on the values of principal component scores l and 2 (Table 10) obtained from the principal component analysis, a two- dimensional scatter diagram, using component score 1 as X-axis and component score 2 as Y- axis was constructed, which has been presented in Figure 6. The position of the varieties in the scatter diagram was apparently distributed. The distribution of 25 varieties based on their principle component score and superimposed with clusters indicated that the varieties were apparerently distributed into five groups (Figure 6). The scattered diagram for the maize genotype of five clusters revealed that the varieties Khaibhutta, PAC-399, BARI Misti Bhutta 1,PAC-984, Barnali, VB-100 and 4536 were distantly located which suggesting more diverged from rest of the varieties.

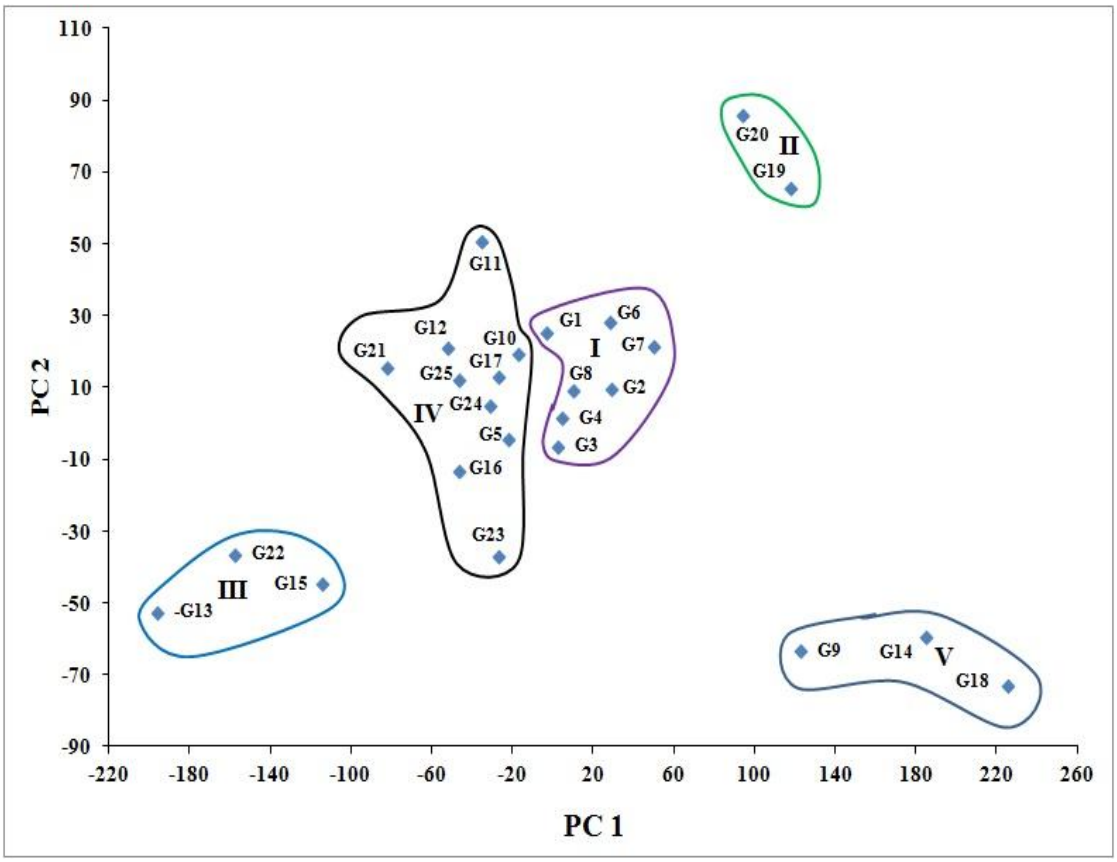


Figure 6. Scatter distribution of 25 maize varieties based on their principal component scores superimposed with clusters

Table 10. Pricipal component scores of 25 genotype

Genotype number	Genotype name	PC1	PC2
G1	BHM-3	-3.83	25.37
G2	BHM-5	28.44	10.05
G3	BHM-6	2.25	-6.15
G4	BHM-7	4.05	1.76
G5	BHM-9	-22.18	-4.09
G6	SHUVRA	27.79	28.67
G7	BM-1	49.65	21.79
G8	BM-6	9.38	9.48
G9	KHAIBHUTTA	122.38	-63.08
G10	BHM-8	-17.87	19.65
G11	NK-40	-35.97	50.82
G12	PACIFIC11	-52.79	21.54
G13	PAC-399	-196.21	-52.28
G14	BARI MISTI BHUTTA-1	184.5	-59.2
G15	PAC-984	-114.76	-44.53
G16	DEKALB SUPER GOLD	-47.04	-12.97
G17	DEKALB 962	-27.38	13.39
G18	KHAI BHUTTA	224.71	-72.76
G19	BARNALI	117.68	65.88
G20	VB-100	93.69	85.93
G21	PACIFIC 98	-82.72	15.77
G22	4536	-157.79	-36.21
G23	DEKALB 9120	-27.29	-36.7
G24	VA-786	-31.72	5.25
G25	PROFIT	-46.97	12.63

4.4.1.3 Principal coordinate analysis

Principal coordinate analysis (PCO) was performed on auxiliary principal component analysis. This analysis helps in estimating distances (D^2) for all combinations between pairs of varieties. The highest inter genotype distance (2.001) was observed between the genotype G13 and G18 followed by the genotype G18 and G22 (1.841). The tenth highest pair distance was (1.629) observed between genotype G14 and G22. The lowest distance (0.135) was observed between the genotypes G24 and G25 followed by the varieties genotype G21 and G25 (0.153). The tenth lowest distance (0.187) was observed between the genotype G4 and G10. The difference between the highest and the lowest inter-genotypes distance indicated the prevalence of variability among the 25 varieties of maize (Table 11).

Table 11. Ten of each lower and higher inter genotypic distances (D^2) between pairs of maize varieties

10 highest inter genotypic distances				**10 lowest inter genotypic distances**			
Sl	Genotypes	Genotypes	Values	Sl	Genotypes	Genotypes	Values
1	G13	G18	2.001	1	G24	G25	0.135
2	G18	G22	1.841	2	G21	G25	0.153
3	G13	G14	1.785	3	G11	G25	0.154
4	G15	G18	1.755	4	G4	G5	0.162
5	G18	G21	1.744	5	G6	G7	0.168
6	G11	G18	1.684	6	G11	G24	0.169
7	G18	G25	1.679	7	G5	G10	0.174
8	G12	G18	1.647	8	G11	G21	0.179
9	G18	G24	1.632	9	G11	G12	0.185
10	G14	G22	1.629	10	G4	G10	0.187

4.4.1.4 Non-hierarchical clustering

With the application of co-variance matrix for non-hierarchical clustering, 25 maize genotypes were grouped into 5 different clusters (Table 12), Cluster IV had maximum 10 genotypes (G5, G10, G11, G12, G16, G17, G21, G23, G24 and G25) followed by cluster I which had 7 genotypes (G1, G2, G3, G4, G6, G7 and G8). Cluster III and Cluster V which had 3 genotypes of each (G13, G15, and G22) and (G9, G14 and G18) respectively, Cluster II comprises with two genotypes (G 19 and G 20). These results confirmed the clustering pattern of the genotypes according to the principal component analysis. Composition of different clusters with their corresponding genotypes and collection site included in each cluster are presented in Table 12. Results of different multivariate techniques were superimposed in Figure 6. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. It is clear from the above that the results obtained through PCA were supported by non-hierarchical clustering.

4.4.1.5 The intra-cluster distances

The intra-cluster distances were computed by the values of intra-genotypic distance matrix of PCO according to Singh and Chowdhury (2001). There were marked variations in intra-cluster distances, which ranged from 0.760 to 2.184 (Table 13). The magnitudes of the intra-cluster distances were not always proportional to the number of genotypes in the clusters. In the present study it was found cluster IV composed of the largest number of genotypes (10) and their intra-cluster distances were 1.471 among the five clusters (Table 13 and Figure 7). The intra-cluster distances in all the 5 clusters were more or less low which indicated the genotypes within the same cluster were closely related. The highest intra-cluster distances was computed for cluster II (2.184) composed of 2 genotypes followed by the cluster I (2.031) composed of 7 genotypes. However the lowest value (0.760) of intra-cluster distance in cluster V indicated three genotypes constituted this cluster might have diverged characters. This contributed to the formation of this cluster (Table 13 and Figure 7).

Table 12. Distribution of 25 maize genotypes into five different clusters

Cluster	Population size	Genotype number	Genotype name
I	7	G1, G2, G3, G4, G6, G7 and G8	BHM-3, BHM-5, BHM-6, BHM-7, SHUVRA, BM-1 and BM-6
II	2	G19 and G20	BARNALI and VB-100
III	3	G13, G15 and G22	PAC-399, PAC-984 and 4536
IV	10	G5, G10, G11, G12, G16, G17, G21, G23, G24 and G25	BHM-9, BHM-8, NK-40, PACIFIC11, DEKALB SUPER GOLD, DEKALB 962, PACIFIC 98, DEKALB 9120, VA-786 and PROFIT
V	3	G9, G14 and G18	KHAIBHUTTA, BRRI MISTI BHUTTA-1 and KHAI BHUTTA

Table 13. Average inter cluster distance (D^2) and intra-cluster distance (bold) for 25 varieties of maize

Cluster	I	II	III	IV	V
I	**2.031**	6.478	9.463	2.870	8.498
II		**2.184**	15.662	8.685	11.458
III			**1.726**	6.981	14.060
IV				**1.471**	10.522
V					**0.760**

4.4.1.6 Canonical variate analysis

Canonical variate analysis was performed to obtain the inter-cluster distances. These values of inter-cluster distance (D^2) are presented in Table 13. Statistical distances represent the index of genetic diversity among the clusters. The inter-cluster distances were bigger than the intra-cluster distances suggesting wider genetic diversity among the varieties of different groups. The inter-cluster distance was maximum between cluster II and III (15.665) followed by the distance between cluster III and V (14.060), II and V (11.458), IV and V (10.522), I and III (9.463), I and V (8.498). The distance was minimum between cluster I and IV (2.870) followed by cluster I and II (6.478), whereas a similar distance was found between II and IV (8.685) and III and IV (8.685), suggesting a close relationship among those clusters (Figure 7). The maximum values of inter-cluster distance indicated that the varieties belonging to cluster II were far diverged from those of cluster III. Similarly, the higher inter-cluster values between clusters III and V, II and V, IV and V, I and III, I and V, indicated the varieties belonging to each pair of clusters was far diverse. These relations were also reflected in the scatter diagram (Figure 6). The varieties belonging to the distant clusters could be used for further base population improvement. Similar reports were also made by Mokate *et al*. (1998). The varieties belonging to cluster II and III having greater inter-cluster distance are recommended for inclusion in a hybridization program as they are expected to produce good segregant. Thus it could be suggested that crosses should be made between varieties belonging to the distant clusters for higher heterotic response.

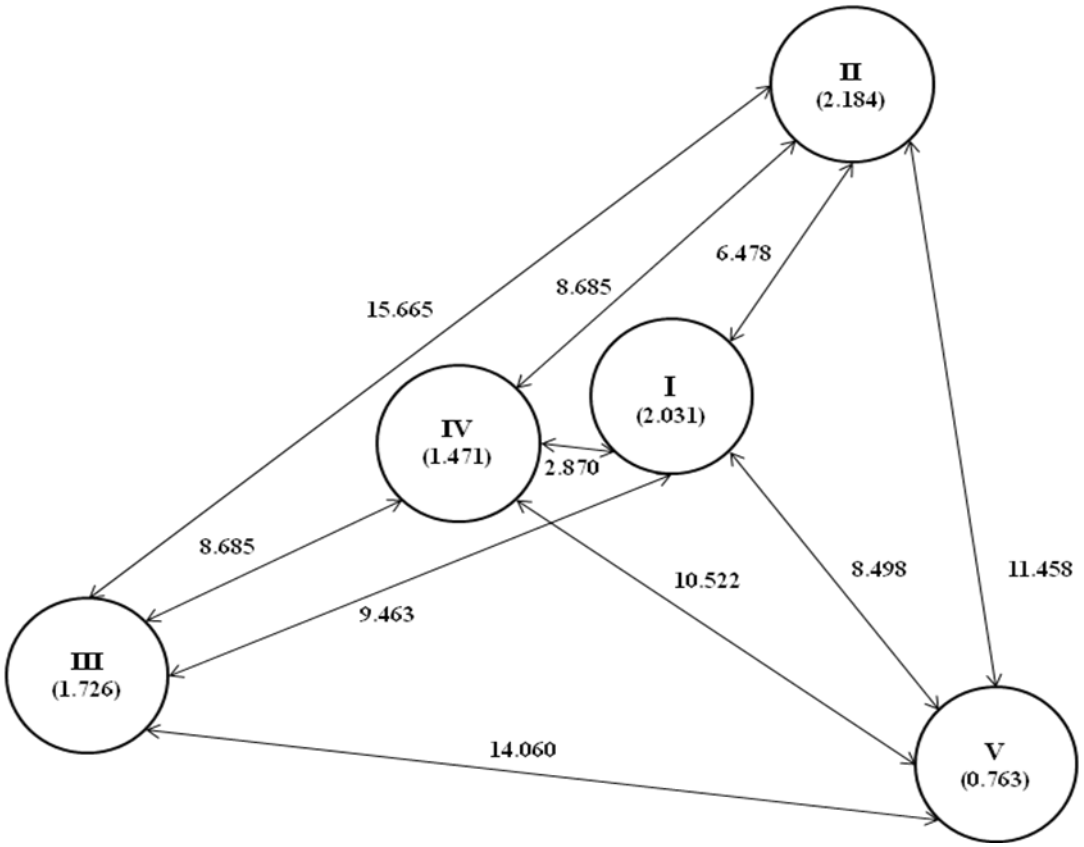


Figure 7. Diagram showing intra and inter cluster distances of twenty five maize varieties

4.4.1.7 Intra-cluster mean

An attempt was made to characterize the individual genotype in respect of their mean values for different characters with a view to get idea that weather genotypes having similar characteristics could be disseminated. The mean values for all the characters along with the marking of the highest (H) and the lowest (L) for each of the cluster are presented in Table 14. The data revealed that different clusters exhibited different mean values for almost all the characters.

Cluster I (constituted 7 genotypes) produced the highest mean for plant height (222.5 cm) and ear height (80 cm) (Table 14).

Cluster II produced the highest mean for 1000-kernel weight (316.7 g). But the lowest mean for days to 50% tasseling (57.5 days) and days to 50% silking (59.8 days), plant height (208.7 cm) and ear height (72.5 cm). That means the genotypes of this cluster were early maturing genotype with short plant (Table 14).

It was observed that cluster III produced the highest mean for ear length (19 cm), ear circumference (15 cm), number of kernel row per cob (15.3), number of kernel per row (36.7), number of kernel per cob (552.4) and total yield per plant (142.4 g). But the lowest mean for cobs per plant (1). Cluster IV comprising 10 genotypes scored the second highest mean for plant height (217.5 cm), days to 50% tasseling (59 days), ear length (18.3 cm), ear circumference (14.9 cm), number of kernel row per cob (14.5), number of kernel per row (29.4), number of kernel per cob (424.6), 1000 kernel weight (304 g) and total yield per plant (131.1 g) (Table 14).

Cluster V produced the highest mean for days to 50% tasseling (59.3 days) and days to 50% silking (62 days) and the lowest mean ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob, 1000 kernel weight and total yield per plant. That means the genotypes of this cluster were late maturing genotypes with lower yield (Table 14).

Table 14. Cluster mean values of 12 different characters of 25 genotypes

Parameters	I	II	III	IV	V
Plant height (cm)	222.5	208.7	215.1	217.5	214.5
Days to 50% tasseling	57.8	57.5	58.3	59	59.3
Days to 50% silking	60.6	59.8	60.4	60.6	62
Ear height (cm)	80	72.5	75.7	74.2	79.8
Cobs per plant	1.1	1.1	1	1.1	1.1
Ear length (cm)	16.5	16.7	19	18.3	15.2
Ear circumference (cm)	13.9	14.2	15	14.9	11.1
Number of kernel row per cob	13.6	12.3	15.3	14.5	11.9
Number of kernel per row	27.8	23.3	36.7	29.4	19.2
Number of kernel per cob	373.3	267.2	552.4	424.6	257.6
1000-kernel weight (g)	291.9	316.7	297.8	304	167.8
Total yield per plant (g)	110.5	107.8	142.4	131.1	56.3

4.4.1.8 Contribution of characters towards divergence

Contribution of characters towards divergence obtained from CVA is presented in Table 15. The values of vector-1 and vector-2 revealed that both the vectors had positive values for plant height, cobs per plant, ear length, number of kernel per row and 1000-kernel weight. These results indicated that these characters had the highest contribution towards the divergence among the 25 maize varieties. In vector-1 the other important characters responsible for the genetic divergence are days to 50% silking and total yield per plant having positive vector values. While in vector-2 (the second axis of differentiation) ear circumference and kernel row per plant were important. Negative values in both vectors for days to 50% tasseling, ear height and number of kernel per cob had the lowest contribution to the divergence. From the above results it was revealed that the characters plant height, cob per plant, ear length, number of kernel per row and 1000-kernel weight contributed maximum total divergence in maize.

4.4.2 Comparison of result based on different multivariate techniques

Results obtained from different multivariate techniques were super imposed in Figure 6 from which it was concluded that all techniques gave more or less similar results and one technique supplemented and confirmed the results of the other. The cluster pattern of D^2 analysis through non-hierarchical clustering has been taken care of simultaneous variation in all the characters under study. However the distribution of varieties in different clusters of the D^2 analysis has followed more or less similar trend of the principal component score 1 and component score 2 of the principal component analysis. The D^2 and principal component analysis were found to be alternative methods in giving the information regarding the clustering pattern of varieties. Nevertheless, the canonical variate analysis (CVA) provides the information regarding the contribution of characters towards divergence of maize varieties.

Table 15. Relative contributions of the tweelve characters of 25 varieties to the total divergence

Parameters	Vector-1	Vector-2
Plant height (cm)	0.0345	0.0124
Days to 50% tasseling	-0.5397	-0.244
Days to 50% silking	0.5368	-0.0844
Ear height (cm)	-0.0538	-0.0417
Cobs per plant	5.2016	9.2827
Ear length (cm)	0.0636	0.3053
Ear circumference (cm)	-0.1529	1.4005
Number of kernel row per cob	-0.3342	0.2967
Number of kernel per row	0.0166	0.3372
Number of kernel per cob	-0.0451	-0.0445
1000-kernel weight (g)	0.0012	0.0407
Total yield per plant (g)	0.0175	-0.0158

4.4.3 Selection of genotypes for future base population development

Selection of genetically diverse parents is an important step for hybridization program. Multivariate analysis is a useful tool to quantify the degree of divergence among biological population at genotypic level and in assessing relative contribution of different components to the total divergence both at intra and inters cluster levels (Sudre *et al*. 2005; Majnu *et al*. 2004 and Senapoti *et al*. 2003). Based on the study of genetic diversity of maize, the genotypes having the different performance and located in the distant clusters could be utilized for hybridization program to develop desired high yielding varieties. Clusters by D^2 statistics are useful in this matter. The genotypes grouped together are less divergent than the ones which into different clusters. Three important points are considered while selecting the genotypes- 1) choice of the particular cluster from which genotypes are to be used as parents; 2) selection of particular genotype from the selected cluster and 3) relative contribution of characters to total divergence (Singh and Chaudhury, 1985). Contribution of individual characters towards divergence was also observed in this study. In respect of cluster mean performance of different cluster revealed that cluster III can be selected for high performance for ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and total yield per plant; cluster II are important for low plant height, low ear height, minimum days for 50% tasseling and silking and high 1000-kernel weight. Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G13 for higher ear length, highest number of kernel per row, number of kernel per cob, highest value for total yield per plant and G22 for highest number of kernel row per cob from cluster III; G2 for lowest days to 50% tasseling from cluster I; G5 for lowest days to 50% silking, G11 for highest 1000-kernel weight, G16 for shortest ear height, G17 for shortest plant height and G23 for high ear circumference from cluster IV were found promising.

Chapter 5

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

In order to observed character association and genetic diversity among maize entries, the present experiment was carried out during March to July, 2014 at the experimental farm of Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka. The experiment was conducted with 25 varieties of maize of different source for characterization in aspect of variability, heritability, genetic advance, genotypic and phenotypic co-efficient of variation, genotype and phenotypic variation, correlation co-efficient effect, path co-efficient effect and the genetic divergence considering different important yield and yield contributing characters. The experiment was laid out in randomized complete block design (RCBD) with 3 replication and seeds of the different genotypes were sown in separate lines. The result of this study is summarized as follows:

Analysis of variance revealed highly significant difference among the accessions for all the characters. The maximum number of leaves per plant was 24 recorded in the genotype khaibhutta and minimum was 20.67 recorded in the genotype BHM-1 and Dekalb 9120. The maximum leaf length was recorded in BM-1 (102.22 cm) and minimum in Dekalb super gold (77.08 cm). Maximum leaf breadth was noted in Pacific 11 (10.74 cm) while minimum in Barnali (8.68 cm). The minimum and maximum duration for 50% tasseling was observed in the genotype BHM-9 (55.33 days) and BARI Misti bhutta (63.33 days), respectively. The minimum days required for 50% silking was in BHM-9 (57 days) and maximum days were for BARI Misti bhutta (65.33 days). The shortest plant was observed in genotype Dekalb 962 (191.3 cm) while longest was BM-8 (237.7 cm). The shortest ear height was observed in genotype Dekalb Super Gold (60.67 cm) while longest was BM-1 (89.33 cm). Ear length ranged from 15.07 cm to 21.67 cm which was observed in PAC-399 and Khaibhutta, respectively. The highest ear circumference was found in

Dekalb 9120(15.70 cm) and lowest ear circumference was found in Khaibhutta (9.99 cm). The highest number of kernel row per cob was 15.6, produced by the 4536 and the lowest number of number of kernel row per cob was 11.04, produced by Khaibhutta. The maximum number of kernel per row were found (40.4) in the genotypes PAC-399 and minimum number of kernel per row were found (16.27) in the genotype Khaibhutta. The highest and the lowest number of kernel per cob were produced by the PAC-399 (591.3) and Khaibhutta (216.67) respectively. Maximum number of 1000-kernel weight was found in NK-40 (340.00 g) and minimum in Khaibhutta (143.33 g). The highest total yield per plant was observed in the genotype PPAC-399 (153.38 g). The lowest total yield per plant was observed in the genotype BARI Misti bhutta 1 (47.07 g).

Characters like ear height, ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob, 1000-kernel weight and total yield per plant exhibited high 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 10.19 and 4.99 respectively, which indicated that cob 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 (29.02 g) followed by number of kernel per cob (27.36), number of kernel per row (21.29) and 1000-kernel weight (20.44 g). The maximum genotypic and phenotypic variations were 11562.25 and 11914.44 respectively in number of kernel per cob.

The highest estimated heritability amongst twelve characters of maize was 97.78% for 1000-kernel weight and the lowest was 23.97% for cobs per plant. The highest genetic advance amongst twelve characters was found in number of kernel per cob is 218.21 and the lowest genetic advance was carried out in

cob per plant (0.05). The maximum genetic advance in percent of mean was observed for total yield per plant (58.84 g), followed by number of kernel per cob (55.53), 1000 kernel weight (41.63 g) and number of kernel per row (41.40). 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 twelve yields contributing characters of 25 maize genotypes, total yield per plant was positively and significantly correlated with ear length, ear circumference, number of kernel row per cob, number of kernel per row, number of kernel per cob and 1000-kernel weight. Path analysis revealed that days to 50% tasseling, ear length, ear circumference, number of kernel per cob and 1000-kernel weight showed positive direct effects on yield per plant. On the other hand plant height, days to 50% silking, number of kernel per row and number of kernel per row showed negative direct effects on yield per plant.

To estimate genetic diversity, multivariate analysis was performed through principal component analysis, principal coordinate analysis, cluster analysis and canonical variate analysis. As per principal component analysis, D^2 statistics and cluster analysis, the genotypes were grouped into five different clusters. Cluster IV consist of highest 10 genotypes viz BHM-9, BHM-8, NK-40, Pacific 11, Dekalb Super Gold, Dekalb 962, Pacific 98, Dekalb 9120, VA-786 and Profit. Followed by cluster I which had 7 genotypes viz BHM-3, BHM-5, BHM-6, BHM-7, Shuvra, BM-1 and BM-6. Cluster III and Cluster V which had 3 genotype of each viz PAC-399, PAC-984 and 4536 and Khaibhutta, Brri Misti Bhutta-1 and Khai Bhutta respectively, Cluster II comprises with two genotypes viz Barnali and VB-100.

The maximum inter-cluster divergence was observed between cluster II and III (15.665) followed by cluster III and V (14.060), II and V (11.458), IV and V (10.522), I and III (9.463), I and V (8.498).) The maximum values of inter-

cluster distance indicated that the varieties belonging to cluster II were far diverged from those of cluster III. The distance was minimum between cluster I and IV (2.870) followed by cluster I and II (6.478), whereas a similar distance was found between II and IV (8.685) and III and IV (8.685), suggesting a close relationship among those clusters. The highest intra-cluster distances was computed for cluster II (2.184) composed of 2 genotypes followed by the cluster I (2.031) composed of 7 genotypes. However the lowest value (0.760) of intra-cluster distance in cluster V indicated three genotypes constituted this cluster might have diverged characters.

In respect of cluster mean performances of different cluster revealed that cluster III can be selected for yield per plant, ear length, ear circumference, number of kernel row per cob, number of kernel per row, and number of kernel per cob. Cluster II were remarkable due to lowest plant height, ear height, days to 50% tasseling and silking and highest value for 1000-kernel weight. Considering diversity pattern, genetic status and other agronomic performance, Barnali and VB-100, from cluster II; PAC-399 and 4536, from cluster III; Dekalb Super Gold, Dekalb 962 and Dekalb 9120, from cluster IV might be considered better parents for efficient hybridization programme. Result of present study revealed that the characters; plant height, cobs per plant, ear length, number of kernel per row and 1000-kernel weight contributed maximum divergence among the maize genotypes. Involvement of such diverse genotypes in crossing programme may produce desirable sergeants. So, divergent genotypes are recommended to use as parent in hybridization programme.

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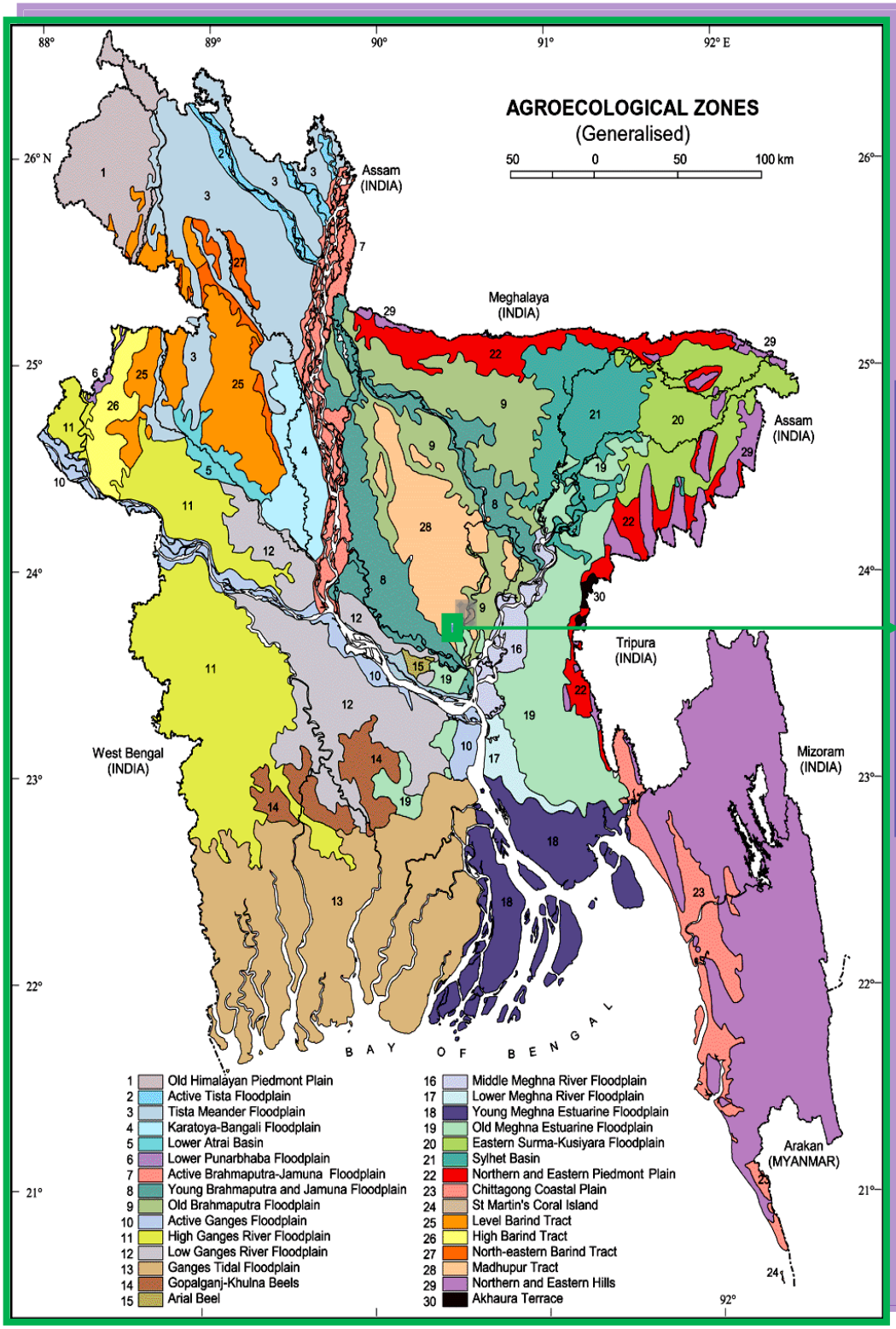
Appendices

Appendix I. Map showing the experimental site



The experimental site

Appendix II. Monthly record of air temperature, relative humidity and rainfall of the experimental site during the period of March, 2014 to July 2014

Month	Air temperature (^{0}C)		Relative humidity (%)		Rainfall (mm) (total)
	Maximum	Minimum	Maximum	Minimum	
March, 2014	37.4	20.2	80.2	32.4	3.80
April, 2014	39.4	19.4	80.2	39.2	65.60
May, 2014	38.2	19.3	89.2	40	202
June, 2014	37.2	17.4	88.4	46.3	282.7
July, 2014	35.6	18.2	88.2	55.4	107.8

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka -1207

Appendix III. Soil test result of the experimental filed reported by Soil Resources Development Institute (SRDI), Khamarbari, Farmgate, Dhaka

Element	Levels in the soil plot
pH	5.9
N	0.071%
K	0.31 meq/100g soil
Ca	6.36 meq/100g soil
P	14.04 µg/g soil
S	15.16 µg/g soil
B	0.30 µg/g soil

Appendix IV. Descriptors with codes for qualitative characteristics

Characteristics	Category	State of expression
Leaf width of the blade	Very small	<5 cm
	Small	5-7 cm
	Medium	7.1-9 cm
	large	9.1-11 cm
Plant height	Short	125-150 cm
	Medium	150-175 cm
	Medium long	175-200 cm
	Long	200-225 cm
	Very long	>225 cm
Plant: Ratio height of insertion of upper ear to plant length (ear placement)	Short	<40%
	Medium	40-50%
	Medium long	51-60%
	Long	61-70%
	Very long	>70%
Time of anthesis	Very early	<40 days
	Early	40-45 days
	Medium	45-55 days
	Late	55-65 days
	Very late	>65 days
Time of silk emergence	Very early	<52 days
	Early	52-57 days
	Medium	58-62 days
	Late	63-67 days
	Very late	>67 days
Color of top grain	Pure white	Pure white
	Brown	Brown
	Yellow	Yellow
Ear shape	Conical	Conical
	Conical-cylindrical	Conical-cylindrical
	Cylindrical	Cylindrical

Appendix IV (Contn'd).

Characteristics	Category	State of expression
Ear circumference without husk	Very small	<2.5 cm
	Small	2.6-3.5 cm
	Medium	3.6-5.0 cm
	Large	5.1-7 cm
	Very large	>7 cm
Ear length	Very small	12.6-15 cm
	Small	15.1-17.5 cm
	Medium	17.6-20 cm
	Large	20.1-22.5 cm
	Very large	>22.5 cm
Number of rows of kernel per cob	Very few	8 rows
	Few	8.1-10 rows
	Medium	10.1-14 rows
	Many	14.1-16 rows
	Very many	>16 rows
Kernel row arrangement	Straight	Straight
	Spiral	Spiral
	Irregular	Irregular
1000-kernel weight	10-15g	10-15g
	15.1-20g	15.1-20g
	20.1-25g	20.1-25g
	25.1-30g	25.1-30g
	30.1-35g	30.1-35g
	35.1-40g	35.1-40g
	40.1-45g	40.1-45g
	>45.1g	>45.1g

Appendix V. Mean performance of 12 characters of 25 genotypes of maize

Genotype	Leaf length (cm)	Leaf breadth (cm)	Leaves per plant	Days to anthesis	Days to silk emergence
G1	94.34	10.11	23.33	48.67	52.33
G2	81.11	9.83	20.67	45.67	48.67
G3	91.44	8.85	21.67	47.67	50.67
G4	92.22	9.06	23	46.67	50.00
G5	91.44	10.19	21.33	45	48
G6	88	9.91	22	45.33	49
G7	102.22	9.66	23.67	43	49.67
G8	88.81	10.33	23.33	52	55
G9	88.44	9.46	24	46.33	49.67
G10	89.44	9.66	21.67	51	52.33
G11	92.4	10.05	22	49.67	50.67
G12	82.22	10.74	21.67	47.67	50.33
G13	92.89	10.33	21.33	51	52.67
G14	82.44	9.94	21	53.33	58
G15	100.33	10.16	21.33	52.33	53.67
G16	100.33	10.16	21.33	52.33	55.67
G17	77.08	9.79	23.33	52	54.33
G18	82.33	9.13	21.67	43.67	50.33
G19	83.88	8.93	21	48	50.67
G20	84.11	8.68	21.33	49	50.67
G21	90.89	10.13	22.67	46	51
G22	82	9.94	23.33	49.33	51
G23	84.11	9.79	22.33	50.33	52.67
G24	85.55	8.72	20.67	54	55.67
G25	88	9.72	22.33	48.33	51

Appendix VI. Mean performance of 12 characters of 25 genotypes of maize

Genotype	PH (cm)	D50T	D50S	EH (cm)	CPP	EL (cm)
G1	214.07a-f	58.33a-c	60.00b-d	77.67b-f	1.20	16.47f-h
G2	201.55c-f	55.00c	58.67cd	75.00c-f	1.08	16.10f-h
G3	222.22a-d	58.33a-c	60.67a-d	73.67def	1.07	16.77e-h
G4	233.33ab	56.67bc	60.00bcd	84.00abc	1.03	15.37gh
G5	229.05a-c	55.33c	57.00d	78.67b-f	1.03	16.98d-h
G6	223.35a-d	56.67bc	59.33bcd	85.00abc	1.07	16.85e-h
G7	225.56a-d	58.33abc	61.33abd	89.33a	1.10	17.63c-h
G8	237.66a	61.33ab	64.00ab	75.67cdef	1.17	15.96fgh
G9	217.91a-f	58.33abc	61.33a-d	73.67def	1.20	15.10h
G10	232.00ab	62.00ab	61.67a-d	80.33a-e	1.10	17.00d-h
G11	217.86a-f	59.67abc	61.00a-d	76.00c-f	1.10	19.15bcd
G12	214.54a-f	59.33abc	59.67bcd	78.00b-f	1.20	16.58fgh
G13	211.19a-f	59.33abc	62.00a-d	86.33ab	1.00	21.67a
G14	231.95ab	63.33a	65.33a	81.00a-d	1.00	15.33h
G15	234.56ab	59.33abc	60.67a-d	77.33b-f	1.00	16.44fgh
G16	198.92def	60.33abc	62.00abcd	60.67h	1.13	18.05cdef
G17	191.33f	59.00abc	61.33a-d	71.33d-g	1.10	16.04fgh
G18	193.78ef	56.33bc	59.33bcd	84.67abc	1.21	15.07h
G19	209.31b-f	57.00bc	59.00bcd	76.33b-f	1.10	16.55fgh
G20	208.17b-f	58.00abc	60.67a-d	68.67fgh	1.07	16.93d-h
G21	222.22a-d	57.00bc	58.33cd	77.00b-f	1.03	19.32bc
G22	199.44def	56.33bc	58.67cd	63.33gh	1.00	18.99bcde
G23	220.00a-e	58.00abc	62.67abc	73.33d-g	1.00	20.80ab
G24	229.55abc	61.67ab	62.67abc	76.33b-f	1.03	19.70abc
G25	219.44a-f	57.67abc	60.00bcd	70.67e-h	1.00	19.59abc
MEAN	**217.56**	**58.51**	**60.69**	**76.56**	**1.08**	**17.38**
LSD5	**28.24**	**5.78**	**5.05**	**10.12**	**0.16**	**2.28**
SE	**5.15**	**1.05**	**0.92**	**1.85**	**0.06**	**0.42**

PH=Plant height (cm), D50T=Days to 50% tasseling, D50S=Days to 50% silking, EH= Ear height (cm), CPP=Cob per plant, EL=Ear length (cm),

Appendix VI (cont'd).

Genotype	EC (cm)	NKRC	NKR	NKC	TKW (g)	TYP (g)
G1	13.05cde	12.60c-f	30.33cd	387.25e-g	310.00b-d	117.98d-h
G2	14.08a-e	13.97a-e	26.53c-f	362.93f-h	283.33d-f	113.29e-i
G3	14.92abc	13.61a-e	27.54c-f	390.83efg	273.33ef	128.68b-f
G4	14.53a-e	14.42abc	28.50cde	389.49efg	286.67def	109.49f-j
G5	14.29a-e	14.24a-d	30.12cd	415.52def	290.00de	114.8d-i
G6	13.84a-e	14.06a-d	27.67c-f	359.39fgh	306.67bcd	98.11ij
G7	12.86de	13.36a-f	25.24d-g	340.61gh	290.00de	101.40hij
G8	14.04a-e	13.43a-e	28.70cd	382.36efg	293.33cde	104.77g-j
G9	10.74fg	13.03b-f	22.67e-h	306.00hi	186.67g	73.21k
G10	14.71a-d	14.18a-d	28.59cde	402.46def	310.00bcd	118.82d-h
G11	15.31ab	14.14a-d	28.67cde	404.87def	340.00a	142.11ab
G12	14.54a-e	14.27a-d	29.59cd	431.86de	320.00abc	138.27abc
G13	15.27ab	15.33ab	40.40a	591.37a	303.33bcd	153.38a
G14	12.55ef	11.67ef	18.67gh	250.00ij	173.33g	47.07l
G15	14.32a-e	14.87abc	37.33ab	514.49bc	283.33def	133.00bcd
G16	14.32a-e	14.86abc	30.46cd	439.76de	286.67def	130.00bcde
G17	14.49a-e	14.48abc	30.09cd	413.15def	306.67bcd	122.74c-g
G18	9.99g	11.04f	16.27h	216.67j	143.33h	48.53l
G19	13.41b-e	11.98def	21.40fgh	261.76ij	306.67bcd	93.85j
G20	14.93abc	12.53c-f	25.11d-g	272.68ij	326.67ab	121.67c-g
G21	14.79a-d	14.72abc	30.74bcd	461.37cd	325.00ab	143.54ab
G22	15.40ab	15.60a	32.43bc	551.47ab	306.67b-d	140.89abc
G23	15.70a	15.07ab	28.70cde	431.57de	260.00f	116.66d-i
G24	15.39ab	14.59abc	28.54cde	417.26def	295.00cde	139.33abc
G25	15.22ab	14.33a-d	28.70cde	428.33de	306.67bcd	144.55ab
MEAN	**14.11**	**13.85**	**28.12**	**392.94**	**284.53**	**115.85**
LSD5	**2.04**	**2.38**	**6.63**	**59.43**	**27.72**	**19.23**
SE	**0.37**	**0.43**	**1.21**	**10.84**	**5.05**	**3.51**

EC=Ear circumference (cm), NKRC=Number of kernel row per cob, NKR=Number of kernel per row, NKC=Number of kernel per cob, TKW=1000-kernel weight (g), TYP=Total yield per plant (g).

Appendix VII. Photograph showing different field view of experimental plot




Appendix VII (Cont'd).