GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS FOR YIELD OF COMMERCIAL MAIZE VARIETIES (*Zea mays* L.)

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BY

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CERTIFICATE

This is to certify that the thesis entitled **'GENETIC DIVERSITY, CORRELATION AND PATH CO-EFFICIENT ANALYSIS FOR YIELD OF COMMERCIAL MAIZE VARIETIES (*Zea mays* L.)'** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **Master of Science in Genetics and Plant Breeding**, embodies the result of a piece of bonafide research work carried out by **Md. Asadur Rahaman**, Registration number: **10-03827** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2015
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Prof. Dr. Firoz Mahmud
Supervisor

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ABSTRACT

The experiment was held in the experimental area of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka during January to May 2015 to study the genetic diversity, correlation and path co-efficient analysis for yield and yield contributing characters of maize. For the accomplishment of the experiment 37 maize genotypes were used as experimental materials that was basically laid out in Randomized Complete Block Design (RCBD) with three replications. Mean performance, variability, correlation matrix and path analysis on different yield contributing characters and yield of maize genotypes were calculated. The maximum grain yield/plant (163.84 g) was recorded in the genotype of DEKALB-9120, whereas the minimum grain yield/plant (60.00 g) was from the genotype of BHM-7. In fact, phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation for all the yield contributing traits. In correlation study, significant positive association was recorded for grain yield/plant of maize genotypes with cob length (0.502), cob breadth(0.196),row per cob(0.524), seed per row(0.882), seed per cob(0.986), cob weight(0.642) and 100-seed weight(0.994). Path analysis revealed that leaf per plant (0.74) had positive direct effect, leaf length (0.23) had positive direct effect, cob length (0.39) had positive direct effect, cob breadth (0.13) had positive direct effect and seed per cob (2.26) had positive direct effect on yield/plant. Plant height (-0.12), diameter of leaf (-0.81), row per cob (-0.73), seed per row (-0.06), cob weight (-0.57) and 100-seed weight (-0.77) had negative direct effect on grain yield. Clustering pattern denoted that, cluster V was the largest cluster comprising of 13 genotypes and cluster II and III belonged to three genotypes of maize. The maximum inter-cluster divergence was observed between cluster I and II (14.57) followed by cluster I and IV (13.09).Considering diversity pattern, genetic status and other agronomic performance Khaivutta, PAC-984 and DEKALB super gold from cluster V; BARI Mishty-1 and DEKALB-962 from cluster VI; Pacific-984, BM-5 and HP-222 from cluster II and III might be considered better parents for efficient hybridization program.

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SOME COMMONLY USED ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et al.*
Accessions	ACC
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	Cm
Co-efficient of Variation	CV
Etcetera	etc.
Figure	Fig.
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	$\delta^2{}_g$
Gram	G
Heritability in broad sense	h^2b
Journal	j.
Kilogram	Kg
Meter	M
Mean Sum of Square	MSS
Millimeter	Mm
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	$\delta^2{}_p$
Randomized Complete Block Design	RCBD
Replication	R
Research	Res.
Sher-e-Bangla Agricultural University	SAU

CHAPTER I

INTRODUCTION

Maize (*Zea mays* L.) has been originated from teosinte (*Zea mays* L. spp Mexicana) in the Western Hemisphere about 7,000 to 10,000 years ago. Maize constitutes as one of the most important cereal crop in the world after wheat and rice. Maize is the member of the tribe Maydeae under the *Poaceae* family. The term "*Zea*" (zela) was derived from an old Greek name for a food grass. The genus *Zea* consists of four species of which *Zea mays* L. is economically important one. Chromosomes number 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. It is mostly photo-insensitive, cross pollinated cereal crops. The Mesoamerican region is known to the center of origin for *Zea mays* (Matsuoka *et al.,* 2002). Maize is a versatile crop grown from 58º N to 40º S from below sea level to altitudes higher than 3000 m and in areas with (250 – 5000) mm of rainfall per year (Shaw, 1988; Dowswell *et. al.,*1996) and with a growing cycle ranging from 3 to 13 months. In fact, worldwide the major maize production areas are located in temperate regions.

Though it was originated from subtropical regions, probably from the highlands of Mexico but nowadays it has been a leading crop in many temperate regions. 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.

In Bangladesh Maize production have an increasing tendency with the introduction of hybrid since 1993. Area, production, and yield of maize have increased by 17%, 33% and 16%, respectively, which reflects the effect of adopting improved technology. Comparing to the production level in Bangladesh maize ranks 3rd in acreage. It accounts for 4.8% of the total cropped land area and 3.5% of the value of agricultural output (Ahmad *et al*., 2011). In Bangladesh maize cultivated in about 152 thousand hectares of land and total annual production is 887 thousand Metric tons with an average yield of 5.83 tha^{-1} (BBS, 2014). Introduction of quality protein maize (QPM) in Bangladesh is a long aspiration to feed the million malnourished populations. Thus, maize should get priority considering the protein malnutrition of the people because it contains more digestible protein than the other cereals (Ahamed, 2010).

Maize is grown as grains as well as fodder crop, although it has been cultivated in limited area ranking 3rd most important cereal crops in Bangladesh. Recently its cultivation gaining popularity and it occupied 2nd position next to rice in the preceding year (DAE, 2012). As food, it can be consumed directly as green cob, roasted cob or popped grain. Maize grain can be used for human consumption in various ways such as corn meal, fried grain and flour. Its grain has high nutritive value containing 66.2%, starch 11.1% protein, 7.12% oil and 1.5% minerals. Moreover, 100 g maize grains contain 90 mg carotene, 1.8 mg niacin, 0.8 mg thiamin and 0.1 mg riboflavin (Chowdhury and Islam, 1993). Maize oil is used as the best quality edible oil. Green parts of the plant and grain are used as the feed of livestock and poultry. Stover and dry leaves are used as good fuel (Ahmed, 1994). The important industrial use of maize includes in the manufacture of starch and other products such as glucose, high fructose sugar, maize oil, alcohols, baby foods and breakfast cereals (Kaul, 1985).

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

To ensure higher maize production, farmer's intention to grow advanced varieties individually or along with other local varieties, that results in diversity among cultivars grown within. Genetic variability, is marked as a heritable difference among cultivars, is required in an optimal level within a population for the sake of sustainable and effective long-term plant breeding program. Progress from selection has been reported to be directly related to the magnitude of genetic variance in the population (Helm *et al.*, 1989; Hallauer and Miranda, 1995; Tabanao and Bernardo, 2005). Larger genetic variability has been found in the original accessions and races among sampled population that represents different climatic, geographical regions (Ilarslan *et al.,* 2002). Abayi *et al.* (2004) observed significant genetic variation in important agronomic traits, especially earliness to sufficiently justify the initiation of selection program.

Information of genetics on yield and other associated characters is prerequisite for breeding purposes in respect to develop high yielding varieties (Agrawal, 2002). Grain yield is the most important and complex quantitative traits in maize controlled by numerous genes (Zdunic *et al*., 2008). Different contributing yield components like ear height, plant height and 1000-grain weight influences yield trait (Rahman *et al*., 1995). In order to achieve highest yield hybrid maize parent lines were selected using discriminate analysis techniques (Oz, 2012). Grain yield is proportionately associated with ear weight. Yield achievement can be improved by selection for grain yield, plant height and ear height (Prodhan, 1997).

We therefore having the above scheme and discussion in mind, the study was conducted to determine the genetic diversity among the different maize genotypes in Bangladesh to fulfill the following objectives:

- To study the genetic variability among maize varieties;
- To carry out genetic study of the yield and yield contributing characters of maize;
- To select suitable variety to meet the demand of maize in Bangladesh.

CHAPTER II

REVIEW OF LITERATURE

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

2.1 Genetic Variability, Heritability and Genetic Advance

2.2 Correlation co-efficient and path analysis

2.3 Genetic diversity

2.1 Genetic Variability, Heritability and Genetic Advance

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

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

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

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

Shanthi *et al*. (2011); found that grain yield and its component characters viz., total anthers dehiscence period, total period of silk appearance, active pollination period, number of 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. Hence, it was inferred that direct selection was a better scope for improvement of these traits.

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

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

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

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

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

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

Breeders are interested in screening and development of open pollinated population in maize. Ishaq *et al.* (2015); showed highly significant differences ($P \leq 0.01$) for all the traits. The highest values for plant height (169.1 cm), ear height (75.13 cm), leaves per plant (11.33), flag leaf area (106.5 cm), grain rows per cob (13.67) and grain yield (5927 kg/ha) were recorded for Jalal-

2003. Broad sense heritability (h^2b) ranged from 0.29 to 0.95 for various traits. Among the tested populations Jalal-2003 proved to be superior for most of the traits studied. The study revealed a considerable amount of genetic variation and heritability estimates that could be manipulated for further improvement in maize breeding.

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

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

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

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

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

(72.03) in number of ear per plant. Days to anthesis and silk emergence, plant height and number of leaf per plant were positively correlated. Grain yield was positively correlated with ASI, plant and ear heights, number of leaf per plant and leaf area.

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

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

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

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

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

2.2 Correlation co-efficient and path analysis

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

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

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

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

AL-Ahmad (2004); Aydin *et al*. (2007) and Najeeb *et al*. (2009) found positive and significant correlation between grain yield and each of plant height, number of rows per cob, number of seed per row and 100-seed 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 seeds per row. It also revealed that sources of variation in plant yield were the direct effects on both number of seeds per row and ear circumference.

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

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

It was found by Singh and Nigam (1977) that 1000-seed weight and seed rows per cob had positively 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.

Field trials were initiated in 16 localities of Italy (of which three were conducted in Friuli-Venezia Giulia) to compare performance of 56 hybrids of FAO maturity groups 500, 600 and 700 by Barbiani *et al.* (2008). The final stage of the trials was conducted in 11 localities with medium late hybrids compared with 30 early hybrids of which 17 belonging to the maturity group 400. Information is gathered on soil characteristics, irrigation, cropping systems, use of fertilizers, herbicides and control of Pyralidae with Contest [alpha-cypermethrin]. Data are presented on plant height, grain humidity level at harvest, hectolitric weight and yield of hybrids belonging to maturity groups 300, 400, 500, 600 and 700 which ultimately showed significant differences.

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

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

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

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

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

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

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

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

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

2.3 Genetic diversity

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

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

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

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

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

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

Brkic *et al.* (2003); used one hundred Simple Sequence Repeats (SSR) as molecular markers to analyze the genetic relationship among 9 maize inbred lines. Genetic variation was also examined between the inbred lines B73 and M017 obtained from two different sources. Genetic dissimilarity ranged from 8 (between the M017 lines obtained from different sources) to 92 (between M017 and Os438-95). Mean heterozygosity values within samples were relatively low (with an average of 2.18% across all samples). However, B73 from the Agro gene source showed a much higher level of within sample heterozygosity at 14%. The relationship among samples determined by the SSR markers and UPGMA clustering agreed with the pedigree of these lines. The results showed that different 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 inbred used in the study were mainly related to the RYD background and most of the Chinese inbred were associated more with the Huangzaosi (HZS) background. In addition, the results supported the establishment of a new heterotic group. That is, the PN group derived from Pioneer hybrids in Chinese maize breeding programs. The study indicated that AFLP markers were suitable for the assessment of genetic diversity in maize germplasm because of its high polymorphism and for the identification of pedigrees of those germplasm with unknown or uncertain genetic background.

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

An experiment was conducted by Singh *et al.* (2005) to study genetic divergence of 23 genotypes of maize using D2 analysis. The genotypes fell into 6 clusters. The inter-cluster distances were higher than intra-cluster distances suggesting maximum genetic distance between clusters III and VI and the lowest distance between clusters I and IV. The cluster means were higher for 50% tasselling, 50% silk emergence, plant height, cob height, ear length, number of grains per row and 100- grain weight in cluster IV; for cob girth, days to maturity and number of rows per cob in cluster II; and for grain yield per plant in cluster III followed by cluster II. The genotypes of these clusters would offer a good scope for the improvement of this crop through selection and hybridization.

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

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

CHAPTER III

MATERIALS AND METHODS

The experiment was conducted to study the genetic variability, correlation and path co-efficient analysis for yield of some commercial major maize varieties in Bangladesh. The details of the materials and methods i.e. description of the experimental site, soil and climatic condition of the experimental plot, materials used, experimental design, data collection and procedure of data analysis that used or followed in this experiment has been presented below under the following points:

3.1 Description of the experimental site

3.1.1 Experimental period

The field experiment was conducted during the period of January to May, 2015.

3.1.2 Location of the experiment

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

3.1.3 Climatic condition

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

3.1.4 Soil characteristics of the experimental plot

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

3.2 Experimental details

3.2.1 Planting materials

In this experiment 37 maize genotypes (Table 1) were used as experimental materials which were produced in the 2013-2014 cropping season, purity and germination percentage were leveled as 94% and 91% respectively.

3.2.2 Experimental design and layout

The experiment was laid out in randomized complete block design (RCBD) with 3 replications. The field was divided into 3 blocks. The individual block size was 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. Experimental field is presented in Plate 1.

3.3. Growing of crops

3.3.1 Preparation of the Main Field

The selected field for growing maize was first opened with power tiller and was exposed to the sun for a week. Then the land was prepared to obtain 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.

3.3.2 Application of Manure and Fertilizers

Green manure and decomposed organic matter are used @ of 6.0 ton /hectare before final land preparation. The chemical fertilizers such as Urea, TSP, MOP, Gypsum, Boric acid and Zinc sulphate were applied in the rows at the rate of 50-195-35-100-10-10 and 10 kg/ha respectively as basal doze. The rest 120 kg Urea was applied in three equal splits (i.e. 40 kg/splits) at 25, 45 and 65 days after planting as side dressing, 3-5 cm away from the plant and the furrows of the fertilizer are hilled up immediately. At the time of third dressing of Urea 35 kg of MOP (rest) was also used. The dose and method of application of fertilizer are shown in Table 2.

3.3.3 Planting of Seeds in the Field

The maize seeds were planted in lines each having a line to line distance of 75 cm under direct planting in the well prepared plot on 17 January 2015.

3.3.4 Post Care

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

Table 1. Name and origin of the maize (*Zea mays*) genotypes used in the present study

Sl.	Code	Genotypes	Source of collection
1.	G1	Bio seed	BARI
2.	G2	Bornali	BARI
3.	G3	Shuvra	BARI
4.	G4	BHM-6	BARI
5.	G5	BHM-3	BARI
6.	G6	BHM-7	BARI
7.	G7	BARI Mishty-1	BARI
8.	G8	KhaiVutta	BARI
9.	G9	BHM-9	BARI
10.	G10	BM-6	BARI
11.	G11	BM-5	BARI
12.	G12	BHM-5	BARI
13.	G13	BHM-8	BARI
14.	G14	Krishibid-102	Krishibid group
15.	G15	HP-222	Petrocem Co.
16.	G16	PAC-984	LalTeer
17.	G17	Kaberi Profit	ACI
18.	G18	PAC-60	LalTeer
19.	G19	AS-999	ACI
20.	G20	Uttoron-2	LalTeer

Table 1. Continued

Sl.	Code	Genotypes	Source of collection
21.	G21	PAC-984	LalTeer
22.	G22	Pioneer-07	Petrocem Co.
23.	G23	PAC-399	LalTeer
24.	G24	GP-901	Getco
25.	G25	Mirakkel Super	Agora
26.	G26	PAC-740	ACI
27.	G27	NK-40	LalTeer
28.	G28	DEKALB-962	Agrovet limited
29.	G29	VA-786	Getco
30.	G30	DEKALB-9120	Agrovet limited
31.	G31	Pacific-98	ACI
32.	G32	Profit	ACI
33.	G33	Pacific-11	ACI
34.	G34	PAC-536	LalTeer
35.	G35	Badsha	BARI
36.	G36	DEKALB Super Gold	Agrovet limited
37.	G37	4536	LalTeer

3.3.4.1 Irrigation

Irrigation was provided at knee stage, pre-flowering stage and milking stage at 45, 65 and 78 days after planting (DAP) for three times for proper growth and development of the plants.

3.3.4.2 Thinning and Gap Filling

The seedling were first thinned from all of the plots at 10 Days after planting (DAP) 2nd thinning was carried out after seven days for maintaining proper spacing the experimental plots.

3.3.4.3 Weeding

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

3.3.4.4 Plant Protection

After 50 days of planting, first spray of chloropyriphose was done against sucking pest such as jassid and aphids.

3.4 Harvesting, threshing and cleaning

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

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

Manures and Fertilizers	Dose/ha	Application (kg)			
		Basal	25 DAP	45 DAP	**65 DAP**
Cowdung	06 tons	06 tons	--	--	--
Urea	170 kg	50 kg	40 kg	40 kg	**40 kg**
TSP	195 kg	195 kg	--	--	--
MP	70 kg	35 kg	--	--	**35 kg**
Gypsum	100 kg	100 kg	--	--	--
Zinc Sulphate	10 kg	10 kg	--	--	--
Magnesium	10 kg	10 kg	--	--	--
Boric acid	**10 kg**	**10 kg**	--	--	--

3.5 Data recording

3.5.1 Plant height (cm)

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

3.5.2 Number of leaves per plant

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

3.5.3 Leaf length (cm)

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

3.5.4 Diameter of leaf (cm)

Diameter of leaf 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

3.5.5 Cob length (cm)

It was measured in millimeter from the base to the tip of the cob with the help of a meter scale.

3.5.6 Cob breadth (cm)

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

3.5.7 Number of rows per cob

Number of 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

3.5.8 Number of seeds per row

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

3.5.9 Number of seeds per cob

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

3.5.10 Cob weight (g)

Cob weight was taken of randomly selected plants in each plot and data was recorded.

3.5.11 Weight of 100-grains (g)

From the composite sample of ears of five randomly selected plants in each plot, weight of 100-grain was taken.

3.5.12 Total yield/plant (Kg)

Weight of cleaned and well dried grains of five randomly selected plants in each plot was weighted in grams.

3.6 Statistical analysis

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

3.7 Estimation of variability

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

3.7.1 Estimation of components of variance from individual environment

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

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

Where,

MS_V = genotype mean square

MS_E = error mean square

r = number of replication

The phenotypic variance (σ^2_p) was derived by adding genotypic variances with the error variance, as given by the following formula –

Phenotypic variance (σ^2_{ph}) = $\sigma^2_g + \sigma^2_e$

Where,

σ^2_{ph} = phenotypic variance

σ^2_g = genotypic variance

σ^2_e = error variance

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

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

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

Where,

σ_g= genotypic standard deviation;

$\bar{x}$ = population mean

% Phenotypic coefficient of variance = $\frac{\sigma_{ph}}{\bar{x}} \times 100$

Where,

σ_{ph} = phenotypic standard deviation;

$\bar{x}$ = population mean

3.7.3 Estimation of heritability

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

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

Where,

$\sigma^2{}_g$ = genotypic variance and

$\sigma^2{}_{ph}$ = phenotypic variance

3.7.4 Estimation of genetic Advance

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

$$GA = \frac{\sigma^2{}_g}{\sigma^2{}_p} \times K.\ \sigma_p$$

Where,

GA = Genetic advance

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

$\sigma^2{}_{ph}$ = phenotypic variance

σ_{ph}= phenotypic standard deviation

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

3.7.5 Estimation of Genetic Advance in percentage of mean

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

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

3.8 Estimation of correlation

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

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

Where,

$\sum$ = Summation

x and y are the two variables

N = Number of observations

3.9 Path co-efficient analysis

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

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

$$ryx_1 = Pyx_1 + Pyx_2rx_1x_2 + Pyx_3rx_1x_3$$

$$ryx_2 = Pyx_1rx_1x_2 + Pyx_2 + Pyx_3rx_2x_3$$

$$ryx_3 = Pyx_1rx_1x_3 + Pyx_2\,rx_2x_3 + Pyx_3$$

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

Pyx_1 = The direct effect of x_1 on y

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

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

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

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

Where,

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

Piy = Direct effect of the character on yield

riy = Correlation of the character with yield

3.10 Multivariate analysis

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

3.10.1 Principal component analysis (PCA)

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

3.10.2 Principal coordinates analysis (PCO)

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

3.10.3 Canonical variate analysis (CVA)

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

3.10.4 Cluster analysis (CLSA)

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

3.10.5 Computation of average intra-cluster distance

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

3.10.6 Computation of average inter-cluster distances

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

3.10.7 Cluster diagram

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

3.11 Analysis of genetic divergence

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

Mahalanobis' D^2 statistics

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

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

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

Where,

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

p = number of variables or characters

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

n = df for error + varieties

e = 2.7183

Data were then analysed for D^2 statistics according to Rao (1952). Error variance and covariance matrix obtained from analysis of variance and covariance were inverted by pivotal condensation method. Using the pivotal elements the original means of the characters (X_1, X_2---------X_8) were transformed into a set of uncorrelated variables (Y_1, Y_2---------Y_8).

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

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

Where,

D^2ij = Genetic divergence between 'i' th and 'j' th genotypes

Vik = Transformed mean of the 'i' th genotype for 'k' th character

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

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

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

Where,

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

N = All possible combinations.

Plate 1: Photograph showing experimental field

CHAPTER IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The data pertaining to 37 maize genotypes as well as yield and its contributing characters were computed, statistically analyzed and the results thus obtained are discussed below under the following headings:

4.1 Analysis of variance

4.2 Genetic variability, heritability and genetic advance

4.3 Correlation analysis.

4.4 Path coefficient analysis

4.5 Genetic diversity analysis

4.1 Analysis of variance

The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied *viz*., Plant height, Leaf per plant, Leaf length, Diameter of leaf, Cob length, Cob Breadth, Row per cob, Seed per row, Seed per cob, Cob weight ,100 seeds weight and Yield per plant (Table 3). The variation due to replication was non-significant for all the characters studied.

4.2 Genetic variability, heritability and genetic advance

The estimation of mean, range, genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent mean for all the characters were studied and the results are presented in Table 4 and depicted in Fig. 1 and 2. The mean performance of Maize genotypes for various growth characters and yield components are presented in Appendix 4.

4.2.1 Plant height

Plant height is an important agronomic character for selecting desirable genotype for breeding program (Ali *et al*., 2012). Significant mean sum of

Table 3. Analysis of variance (ANOVA) of different characters in maize(*Zea mays*)

Source	**df**	**Mean sum of square**											
		PH	**LOP**	**LL**	**LD**	**CL**	**CB**	**RPC**	**SPR**	**SPC**	**CW**	**HSW**	**YPP**
Replication	2	1,349.72	19.00	0.94	0.60	0.22	0.03	7.38	1.47	15,955.32	1,438.08	144.11	6,217.09
Treatment	36	386.73**	2.70**	81.50**	0.95**	12.80**	6.78**	1.40*	22.88**	5,642.64**	1,804.53**	45.75**	2,333.80**
Error	72	32.39	1.08	8.12	0.17	0.27	0.05	0.88	1.69	1,014.63	124.80	7.82	308.87

*= Significant at the 0.05 level ** = Significant at the 0.01 level.

PH = Plant height (cm), LPP = Leaf per plant, LL = Leaf length (cm), LD = Diameter of leaf (cm), CL = Cob length (cm), CB = Cob Breadth (cm), RPC = Row per cob, SPR = Seed per row, SPC = Seed per cob, CW = Cob weight (g), HSW = 100 seeds weight (g) and YPP = Yield per plant (g).

square for plant height indicated considerable difference among the genotypes studied (Table 3 and plate 2). Plant height ranged from 99.33 cm (G1) to 154.77 cm (G25) (Table 4 and Appendix 4).The phenotypic and genotypic variances for this trait was comparatively high (150.50 and 118.12) (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (8.61) was higher than the genotypic coefficient of variation (7.63) (Table 4 and Figure 1) which indicated the environment has a significant role on the expression of this trait. Heritability estimates was high (78.48%) with high genetic advance (19.83) and moderate genetic advance in percent of mean (13.91) (Table 4 and Figure 2) 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 (Plate 3 & 4).

4.2.2 Leaves per plant

Maximum leaves per plant (12) were observed in G18 followed by G11, G13, G23, G29 and G35, while minimum in G30 (8.00) (Appendix 4). These results are in line with those of Dijak *et al.* (1999) who observed significant differences while evaluating maize genotypes for different morphological and yield traits. This analysis showed that leaf per plant was highly significantly and positively correlated with leaf length, leaf breadth and 100-seed weight. 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.

4.2.3 Leaf length

Maximum leaf length was noted in G8 (57.87 cm) followed by G3, G16, G18 and G23 while minimum in G7 (37.10 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 32.58 and 24.46 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (12.15) was higher than the genotypic coefficient of variation (10.53) (Table 4 and Figure 1).This analysis showed that leaf length was highly significant and positively correlated with leaves per plant; leaf breadth and 100-seed weight. It's positively correlated with yield per plant. If length was increased then leaf area also was increased and consequently more photosynthesis will take place which lead to vigorous vegetative growth which resulted increased plant length and low seed yield.

4.2.4 Leaf diameter

Maximum leaf diameter was noted in G18 (6.53 cm) followed by G19, G35, G36 and G12 while minimum in G30 (3.87 cm) (Appendix 4). The phenotypic and genotypic variances for this trait were 0.43 and 0.26 (Table 4).

The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (12.03) was higher than the genotypic coefficient of variation (9.34) (Table 4 and Figure 1).

Leaf diameter was highly significant and positively correlated with leaves per plant, leaf length, 100-seed weight and yield per plant.

4.2.5 Cob length

Maximum cob length was recorded in G20 (19.27 cm) followed by G30, G16, G1, G13 and G12 while minimum in G6 (8.03 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 4.45 and 4.18 (Table 4).

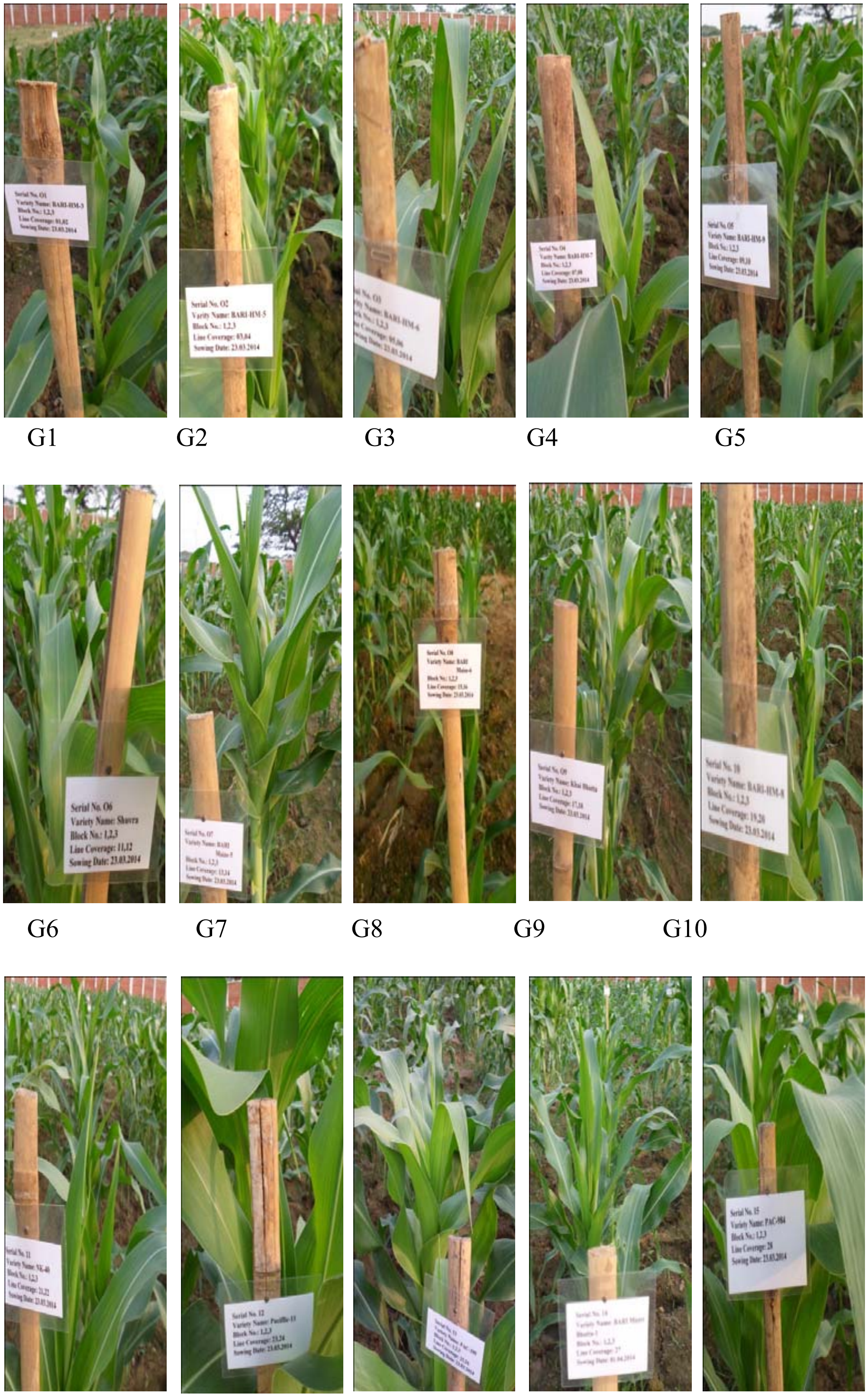
The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (12.69) was higher than the genotypic coefficient of variation (12.30) (Table 4 and Figure 1).Cob length was highly significant and positively correlated with plant height, leaf length, 100-seed weight and yield per plant (Plate 5).

4.2.6 Cob breadth

Maximum cob breadth was recorded in G23 (15.17 cm) followed by G22, G27, G28, G13 and G18 while minimum in G7 (7.37 cm) (Appendix 4).The phenotypic and genotypic variances for this trait were 2.29 and 2.24 (Table 4). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling traits. The phenotypic coefficient of variation (11.83) was higher than the genotypic coefficient of variation (11.71) (Table 4 and Figure 1).Cob length was highly significant and positively correlated with plant height, leaf length, 100-seed weight and yield per plant.

4.2.7 Number of row per cob

Significant differences among the genotypes were observed due to number of seed row per cob (Table 3). The highest number of seed row per cob was 14.67, produced by the G18 and the lowest number of seed row per cob was 11.16, produced by G7 (Appendix 4 and Table 4). The phenotypic variance (1.05) was slightly higher than genotypic variance (0.17) (Table 4 and Figure 1). Moderate genotypic coefficient of variation (3.12) and phenotypic coefficient of variation (7.70) (Table 4 and Figure 2) were found for this trait with a non-significant difference which indicated that there was little environmental effect on the expression of character.



G1 G2 G3 G4 G5

G6 G7 G8 G9 G10

G11 G12 G13 G14 G15

Plate:2 Photograph showing different plant height among various genotypes

Table 4. Estimation of genetic parameters in twelve characters of 37 genotypes in maize (*Zea mays*)

Parameters	**MS**	**σ^2 p**	**σ^2g**	**σ^2 e**	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
PH	386.73**	150.50	118.12	32.39	8.61	7.63	3.99	78.48	19.83	13.91
LPP	2.69**	1.62	0.54	1.08	12.49	7.19	10.22	33.15	0.87	8.53
LL	81.50**	32.58	24.46	8.12	12.15	10.53	6.07	75.08	8.83	18.79
LD	0.95**	0.43	0.26	0.17	12.03	9.34	7.57	60.36	0.82	14.95
CL	12.79**	4.45	4.18	0.27	12.69	12.30	3.14	93.89	4.08	24.54
CB	6.77**	2.29	2.24	0.05	11.83	11.71	1.68	97.97	3.05	23.86
RPC	1.39*	1.05	0.17	0.88	7.70	3.12	7.03	16.47	0.35	2.61
SPR	22.88	8.75	7.06	1.69	9.49	8.52	4.17	80.69	4.92	15.77
SPC	5,642.64**	2557.30	1542.67	1014.63	12.04	9.35	7.58	60.32	62.84	14.95
CW	1,804.53**	684.71	559.91	124.80	16.93	15.31	7.23	81.77	44.08	28.51
HSW	45.75**	20.46	12.64	7.82	17.62	13.85	10.89	61.78	5.76	22.42
YPP	2,333.80**	983.85	674.98	308.87	28.21	23.37	15.81	68.61	44.33	39.87

**, * Correlation is significant at the 0.01 and 0.05 level, respectively.

PH = Plant height(cm), LPP = Leaf per plant, LL = Leaf length (cm), LD = Diameter of leaf (cm), CL = Cob length (cm), CB = Cob Breadth (cm), RPC = Row per cob, SPR = Seed per row, SPC = Seed per cob, CW = Cob weight (g), HSW = 100 seeds weight (g) and YPP = Yield per plant (g), MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2 e = Environmental variance, PCV = Phenotypic Coefficient of Variation, GCV= Genotypic Coefficient of Variation and ECV= Environmental Coefficient of Variation.

The heritability was very higher (65.47%) together with low genetic advance (0.35) and moderate genetic advance in percent of mean (2.61) indicating the selection for this character would be effective (Table 4 and Figure 2). Similar results were reported by Chen *et al*. (1996), Satyanarayan and Kumar (1995) and Ojo *et al*. (2006). High heritability accompanied with moderate GA, GCV and genetic advance in percent of mean indicates that most likely the heritability is due to additive gene effects.

4.2.8 Number of Seed per row

Significant differences among the genotypes were observed due to number of seed per row (Table 3). The maximum number of seed per row were found (37.33) in the genotype G20 and minimum number of seed per row were found (24.33) in the genotype G37, (Appendix 4). The phenotypic variance (8.75) was higher than genotypic variance (7.06) and the PCV (9.49) was also a little greater than GCV (8.52) (Table 4 and Figure 1) indicating the role of environment on the expression of this trait. The genetic advance was moderate (4.92) with high genetic advance in percent of mean (15.77) for this trait (Table 4 and Figure 2). Similar results were reported by Rather *et al.* (2003) and Rajesh *et al.* (2013). Heritablity was found to be highest for this trait (80.69%) (Table 4 and Figure 2), which indicated this character was less influenced by environmental effects. High heritability accompanied with high to moderate GCV and high genetic advance in percent of mean indicated that most likely the heritability was due to additive gene effects and selection may be effective in early generations for these traits. High heritability estimates for number of seed per row were also reported by Abd El-Sattar (2003).

4.2.9 Number of seed per cob

Significant differences among the genotypes were observed for number of seed per cob (Table 3). The highest and the lowest number of seed per cob were produced by the G30 (496.33) and G6 (316.00) respectively (Appendix 4). The phenotypic and genotypic variance was high and the difference between the phenotypic variance (2557.30) and the genotypic variance (1542.67) were

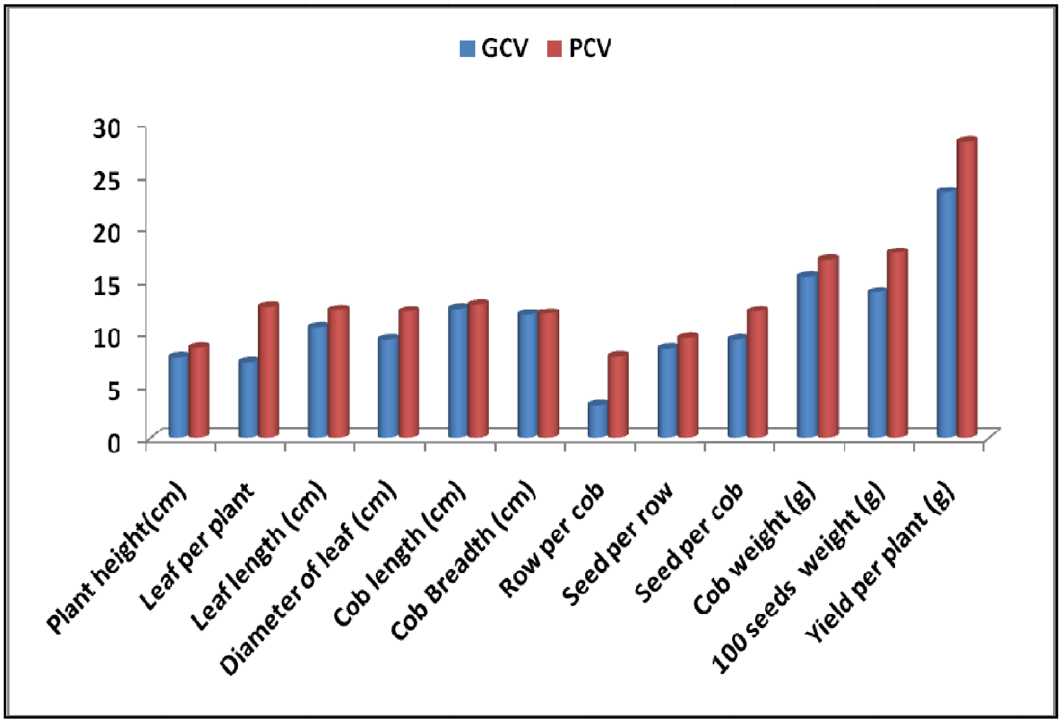


Fig 1 Genotypic and phenotypic variability in maize

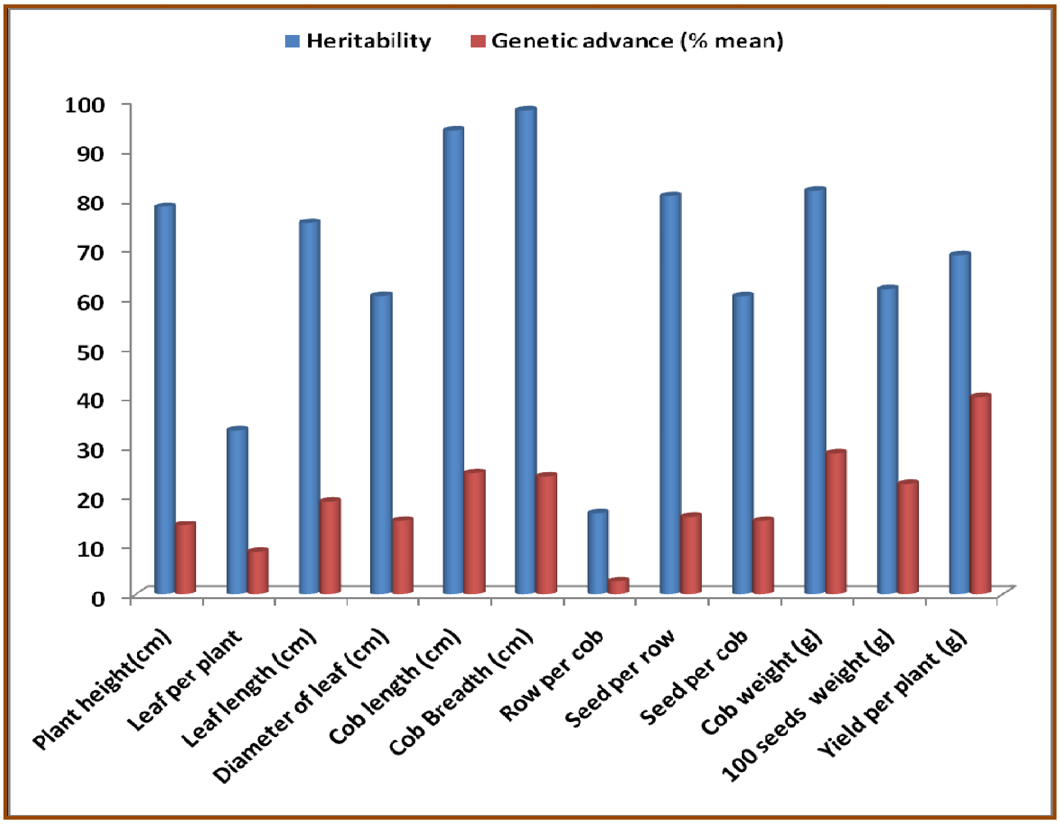


Fig 2 Heritability and genetic advance over mean in maize

significant (Table 4). Genotypic coefficient of variation (9.35) and phenotypic coefficient of variation (12.04) (Table 4 and Figure 1) 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 (60.32%) along with high genetic advance (62.84) and high genetic advance in percent of mean (14.95) (Table 4 and Figure 2) 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).

4.2.10 100-seed weight

Significant differences among the genotypes were observed due to 100-seed weight (Table 3). Maximum number of 100-seed weight was found in G30 (34.00 g) and minimum in G27 (19.12 g) (Appendix 4). The phenotypic and genotypic variance was high and the difference between the phenotypic variance (20.46) and the genotypic variance (12.64) was not significant. Little influence of environment upon this trait was reported due to difference between the estimation of GCV (13.85) and PCV (17.62) which suggesting existing of sufficient variability and offers scope for selection (Table 4 and Figure 1). High heritability (61.78%), high genetic advance (5.76) and high genetic advance in percent of mean 22.42) were found for this trait (Table 4 and Figure 2) which indicating very low or no influence of environment and apparent variability due to additive gene and selection may be effective in early generations for this trait 100-seed weight. Similar results were reported by Anshuman *et al.* (2013). Similar results of PCV and GCV values for this trait were reported by Abirami *et al*. (2005)

4.2.11 Total yield per plant

The genotypes varied significantly for total yield per plant (Table 3). The highest total yield per plant was observed in the genotype G30 (163.84g) and the lowest total yield per plant was observed in the genotype G6 (60.00g)

Plate 3: Photograph showing female flower

Plate 4: Photograph showing male flower

Plate 5: Photograph showing cob structure

(Appendix 4). The phenotypic variance (983.85) differed slightly from genotypic variance (674.98) for this trait. Moderate genotypic (23.37) and phenotypic (28.21) coefficient of variation and high heritability (68.61%) along with high genetic advance (44.33) and high genetic advance in percent mean (39.87) were estimated for this character (Table 4 and Figure 1&2). All these value of statistical analysis indicated that the characters were less influenced by environment and additive gene involved in the expression and selection may be effective in early generations for these traits. Similar results were reported by Chen *et al.* (1996), Ojo *et al*. (2006), Mahmood *et al*. (2004), Hemavathy *et al.* (2008) and Anshuman *et al.* (2013).

4.3 Correlation analysis

The study of yield components and their inter relationship along with yield and their direct and indirect contribution to yield is of immense importance.

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

4.3.1 Plant height

Plant height showed highly significant positive correlation with leaf per plant, row per cob, cob breadth and cob weight at both the genotypic and phenotypic level (Table 5a & 5b).It showed non-significant positive correlation with leaf length, diameter of leaf, Seed per row for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with cob length and 100-seed weight (Table 5a &5b). 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 cob and cob breadth. However, Srekove*et al.* (2011) reported negative correlation between grain yield and plant height.

4.3.2 Leaves per plant

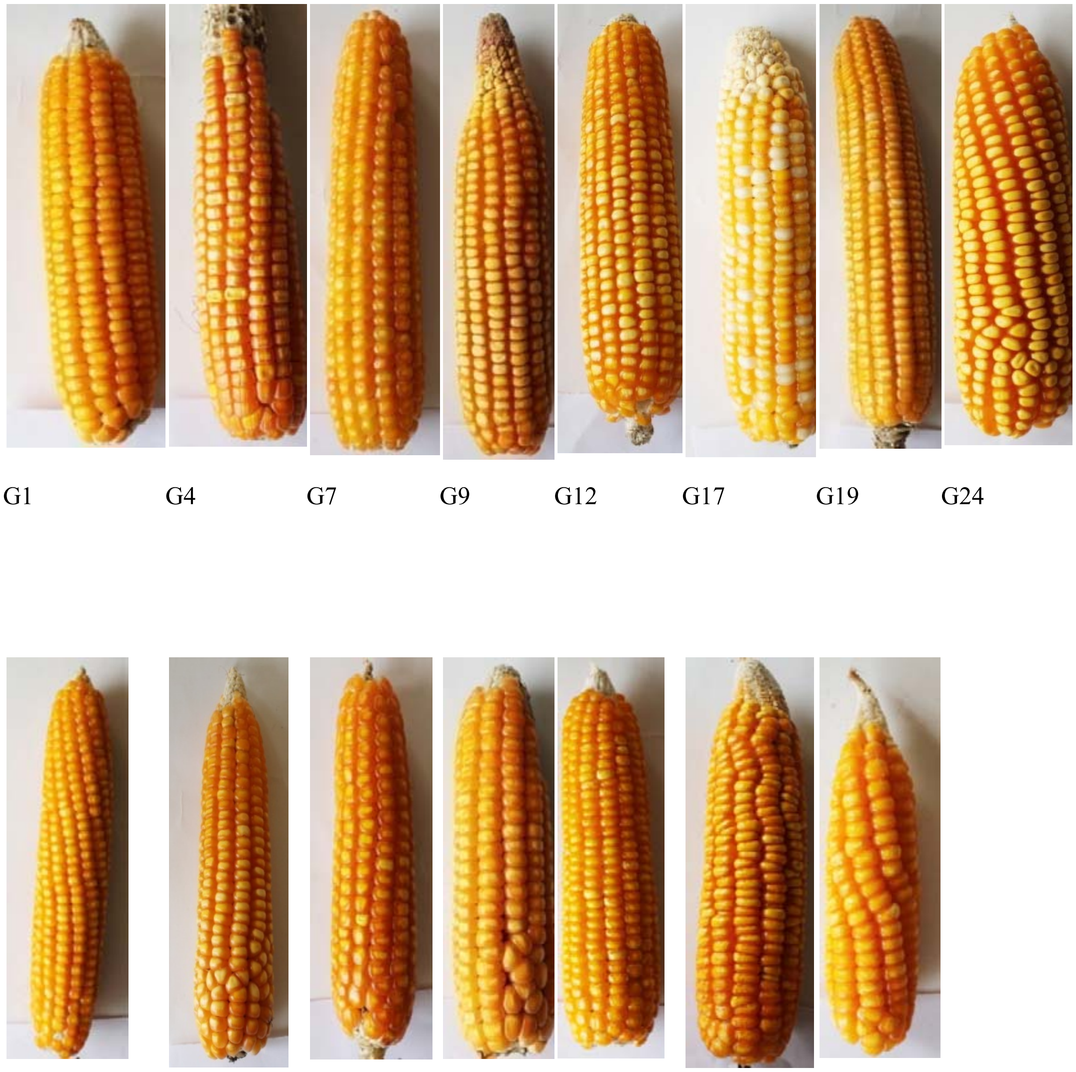
Highly significant positive association was recorded for number of leaves of maize genotypes with plant height and diameter of leaf for both genotypic and phenotypic level. The insignificant positive association was recorded for leaf length, row per cob and cob weight (Table 5a & 5b). On the other hand, significant negative association was not recorded for any significant level whereas insignificant negative association was observed with leaf length, cob length and 100 seed weight (Table 5a & 5b).

4.3.3 Leaf length

Highly significant positive association was recorded for leaf length of maize genotypes with diameter of leaf, cob length, cob breadth and yield per plant for both genotypic and phenotypic level. The insignificant positive association was recorded for seed per row, cob weight and 100-seed weight (Table 5a & 5b). On the other hand, significant negative association was not observed for any significant level as well as insignificant negative association was not also observed (Table 5a & 5b).

4.3.4 Leaf diameter

Highly significant positive association was recorded for diameter of leaf of maize genotypes with cob length for both genotypic and phenotypic level (Table 5a & 5b). The insignificant positive association was recorded for seed



G1 G4 G7 G9 G12 G17 G19 G24

G25 G28 G30 G31 G34 G36 G37

Plate: 6 Photograph showing different cob of maize genotypes

per row, cob breadth and cob weight (Table 5a & 5b). On the other hand, significant negative association was observed with row per cob for genotypic significant level as well as insignificant negative association was also observed in seed per cob, 100- seed weight and total yield per plant (Table 5a & 5b).

4.3.5 Cob length

Highly significant positive correlation was recorded for cob length of maize genotypes with cob breadth, seed per row, seed per cob, cob weight, 100- seed weight and total yield per plant for both the genotypic and phenotypic level (Table 5a & 5b). The insignificant positive association was recorded for row per cob. On the other hand, significant negative association was not found for any significant level (Plate 6).

4.3.6 Cob breadth

Significant positive association was recorded for cob breadth of maize genotypes with roe per cob, cob weight and total yield per plant for both significant level (Table 5a & 5b). The insignificant positive association was recorded for seed per cob and 100-seed weight. On the other hand, insignificant negative association was recorded for seed per row at phenotypic level (Table 5a & 5b).

4.3.7 Number of seed row per cob

Number of seed row per cob showed highly significant positive correlation with plant height, leaf length, cob length and cob breadth at the genotypic level. It showed non-significant positive correlation with seed per row (0.081) at genotypic level. It showed highly significant negative correlation with diameter of leaf (-0.362) at genotypic level and (-0.132) at phenotypic level. Our results disagree with EL-Hosary *et al.* (1989); Amin *et al.* (2003); EL-Beially (2003) and Mohammadi *et al.*(2003) who found number of rows per cob showed significant and negative correlations with 100-seed weights and number of seed per row.

4.3.8 Number of seed per row

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

4.3.9 Number of seed per cob

Number of seed per cob showed highly significant positive correlation with leaf length, cob length and seed per row for both the genotypic and phenotypic level (Table 5a & 5b). It showed highly significant negative correlation with leaf per plant and diameter of leaf at both the genotypic and phenotypic level (Table 5a & 5b). It showed non-significant positive correlation with plant height and cob weight for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with leaf per plant and diameter of leaf (Table 5a & 5b). Alvi *et al.* (2003) and Sofi and Rather (2007) also found strong association between grain yield and seed row number.

4.3.10 100-seed weight

Highly significant positive correlation were observed between 100-seed weight with cob length, row per cob, seed per row, seed per cob, cob weight and total yield per plant at both the genotypic and phenotypic level (Table 5a & 5b). It showed non-significant positive correlation with plant height, leaf length and cob breadth for both genotypic and phenotypic levels. Non-significant negative phenotypic and genotypic correlation was also observed with leaf per plant and diameter of leaf (Table 5a & 5b). Grain yield is considered to have positive

Table 5a. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of Maize

	LPP	LL	LD	CL	CB	RPC	SPR	SPC	CW	HSW	YPP
PH	0.621**	0.042	0.036	-0.059	0.338**	0.367**	0.100	0.205	0.289**	0.234*	-0.188*
LPP		-0.018	0.419**	-0.139	0.375**	0.242**	-0.175	-0.084	0.242**	-0.078	-0.114
LL			0.251**	0.357**	0.400**	0.430**	0.172	0.225*	0.093	0.176	0.199*
LD				0.283**	0.212	-0.362**	0.155	-0.050	0.220	-0.163	-0.167
CL					0.478**	0.339	0.567**	0.595**	0.667**	0.505**	0.502**
CB						0.527**	0.001	0.185	0.348**	0.152	0.196*
RPC							0.081	0.438**	0.244**	0.422**	0.524**
SPR								0.936**	0.716**	0.906**	0.882**
SPC									0.724**	0.969**	0.986**
CW										0.642**	0.642**
HSW											0.994**

** = Significant at 1%, * = Significant at 5%.

PH = Plant height (cm), LPP = Leaf per plant, LL = Leaf length (cm), LD = Diameter of leaf (cm), CL = Cob length (cm), CB = Cob Breadth (cm), RPC = Row per cob, SPR = Seed per row, SPC = Seed per cob, CW = Cob weight (g), HSW = 100 seeds weight (g) and YPP = Yield per plant (g).

Table 5b. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of Maize

	LPP	LL	LD	CL	CB	RPC	SPR	SPC	CW	HSW	YPP
PH	0.475**	0.078	0.086	-0.048	0.299**	0.105	0.063	0.124	0.242**	0.124	-0.126
LPP		-0.025	0.271**	0.099	0.203*	0.047	0.068	-0.035	0.108	-0.080	-0.096
LL			0.297**	0.318**	0.354**	0.110	0.138	0.143	0.083	0.138	0.154*
LD				0.218*	0.171	0.132	0.091	-0.058	0.135	-0.132	-0.147
CL					0.481**	0.066	0.497**	0.428**	0.577**	0.363**	0.386**
CB						0.183	0.001	0.128	0.307**	0.106	0.152
RPC							0.048	0.578**	0.335**	0.522**	0.520**
SPR								0.745**	0.604**	0.714**	0.718**
SPC									0.718**	0.943**	0.949**
CW										0.642**	0.643**
HSW											0.972**

** = Significant at 1%.

* = Significant at 5%.

PH = Plant height (cm), LPP = Leaf per plant, LL = Leaf length (cm), LD = Diameter of leaf (cm), CL = Cob length (cm), CB = Cob Breadth (cm), RPC = Row per cob, SPR = Seed per row, SPC = Seed per cob, CW = Cob weight (g), HSW = 100 seeds weight (g) and YPP = Yield per plant (g).

correlation with plant height and hundred seed 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-seed weight.

4.4 Path coefficient analysis

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

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

4.4.1 Direct effect

Five out of eleven characters had positive direct effect on grain yield per plant. The characters which had positive direct effect are leaf per plant (0.74), leaf length (0.23), cob length (0.39), cob breadth (0.13) and seed per cob (2.26). However, character *viz.,* plant height (-0.12), diameter of leaf (-0.81), row per cob (-0.73), seed per row (-0.06), cob weight (-0.57) and 100-seed weight (-0.77) had negative direct effect on grain yield (Table 6). Path coefficient analysis revealed that grain yield per plant was directly influenced by leaf per

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

	Direct effect	Indirect effect via											Genotypic correlation with yield
		PH	LPP	LL	LD	CL	CB	RPC	SPR	SPC	CW	HSW	
PH	-0.12	-	0.46	0.01	-0.03	-0.02	0.04	-0.27	-0.01	0.46	-0.17	-0.18	0.188*
LPP	0.74	-0.07	-	0.00	-0.34	-0.05	0.05	-0.18	0.01	-0.19	-0.14	0.06	-0.114
LL	0.23	0.00	-0.01	-	-0.20	0.14	0.05	-0.31	-0.01	0.51	-0.05	-0.13	0.199*
LD	-0.81	0.00	0.31	0.06	-	0.11	0.03	0.26	-0.01	-0.11	-0.13	0.12	-0.167
CL	0.39	0.01	-0.10	0.08	-0.23	-	0.06	-0.25	-0.03	1.34	-0.38	-0.39	0.502**
CB	0.13	-0.04	0.28	0.09	-0.17	0.18	-	-0.38	0.00	0.42	-0.20	-0.12	0.196*
RPC	-0.73	-0.04	0.18	0.10	0.29	0.13	0.07	-	0.00	0.99	-0.14	-0.32	0.524**
SPR	-0.06	-0.01	-0.13	0.04	-0.13	0.22	0.00	-0.06	-	2.11	-0.41	-0.69	0.882**
SPC	2.26	-0.02	-0.06	0.05	0.04	0.23	0.02	-0.32	-0.06	-	-0.41	-0.74	0.986**
CW	-0.57	-0.03	0.18	0.02	-0.18	0.26	0.05	-0.18	-0.04	1.63	-	-0.49	0.642**
HSW	-0.77	-0.03	-0.06	0.04	0.13	0.19	0.02	-0.31	-0.05	2.19	-0.37	-	0.994**

Residual effect: 0.207

* = Significant at 5%.

** = Significant at 1%.

PH = Plant height (cm), LPP = Leaf per plant, LL = Leaf length (cm), LD = Diameter of leaf (cm), CL = Cob length (cm), CB = Cob Breadth (cm), RPC = Row per cob, SPR = Seed per row, SPC = Seed per cob, CW = Cob weight (g), HSW = 100 seeds weight (g) and YPP = Yield per plant (g).

plant, leaf length, cob length, cob breadth and seed per cob. Hence, selection for any of these independent traits leads to improving the genotypes for grain yield per plant.

4.4.2 Indirect effects

Plant height had negative indirect effect through diameter of leaf (-0.03), cob length (-0.02), row per cob (-0.27), seed per row (-0.01), cob weight (-0.17) and 100-seed weight (-0.18) (Table 6). However, its positive indirect effects through leaf per plant (0.46), leaf length (0.01), cob breadth (0.04) and seed per cob (0.46).The effect of leaf per plant to grain yield per plant through cob breadth (0.05), seed per row (0.01) and 100-seed weight (0.06) was remarkable, its contribution through other traits was low. Leaf length influenced the grain yield per plant indirectly through cob length (0.14), cob breadth (0.05) and seed per cob (0.51) (Table 6). The indirect and positive effect on grain yield per plant was exhibited by diameter of leaf via leaf per plant (0.31), leaf length (0.06), cob length (0.11), cob breadth (0.03), row per cob (0.26) and 100-seed weight (0.12) Whereas, through other traits it had also negative indirect effects. Cob length showed positive indirect effect to grain yield per plant via leaf length (0.08), cob breadth (0.06) and seed per cob (0.134) (Table 6). It had a negative indirect effect through leaf per plant (-0.10), diameter of leaf (-0.23), row per cob (-0.25), seed per row (-0.03), cob weight (-0.38) and 100-seed weight (-0.39). Cob breadth showed indirect effect on grain yield per plant had positive through leaf per plant (0.28), leaf length (0.09), cob length (0.18) and seed per cob (0.42)(Table 6). Row per cob had positive indirect effect through leaf per plant (0.18), leaf length (0.10), diameter of leaf (0.29), cob length (0.13), cob breadth (0.07) and seed per cob (0.99) (table 6). This trait showed negative indirect effect via plant height (-0.04), cob weight (-0.14) and 100-seed weight (-0.32) (Table 8).Seed per row showed indirect positive effects on grain yield per plant by leaf length (0.04), cob length (0.22) and seed per cob (2.11) (Table 6). It showed indirect negative effect on grain yield per plant through leaf per plant (-0.13), diameter of leaf (-0.13), cob weight (-0.41) and

100-seed weight (-0.69) (Table 6). Seed per cob showed indirect positive effects on grain yield per plant by leaf length (0.04), cob length (0.22) and seed per cob (2.11) (Table 6). It showed indirect negative effect on grain yield per plant through leaf per plant (-0.06), row per cob (-0.32), seed per row (-0.06), cob weight (-0.41) and 100-seed weight (-0.74) (Table 6). The indirect and positive effect on grain yield per plant was exhibited by cob weight via diameter of leaf (-0.18), row per cob (-0.18) and 100-seed weight (-0.49).It had also negative indirect effects through other traits. It has also indirect and positive effect on grain yield per plant via leaf per plant (0.18), cob length (0.26) and seed per cob (1.63) (Table 6). 100-seed weight showed indirect positive effects on grain yield per plant by diameter of leaf (0.13), cob length (0.19) and seed per cob (2.19) (Table 6). It showed indirect negative effect on grain yield per plant through leaf per plant (-0.06), plant height (-0.03), row per cob (-0.31) and cob weight (-0.37) (Table 6).

4.5 Genetic diversity

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

4.5.1 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 37 maize genotypes were grouped into six different clusters. It is stated that highest 40% genotypes were included in cluster V and it was followed by 30% in cluster VI, 18% genotypes in both cluster I and IV and the remaining 12% genotypes were in cluster II and III. The composition of clusters with different genotypes is presented in Table 7.

From Table 7 cluster V had the maximum 13 genotypes (G1, G2, G3, G4, G8, G13, G14,G19, G21, G32, G34, G35, G36) followed by cluster VI which had 10 genotypes (G7, G12, G17, G18, G24, G25, G26, G28, G29, G33), cluster I and IV also had 8 genotypes (G5, G6, G27, G37,G20, G22, G23, G30) and cluster II and III had 6 genotypes (G9, G11, G31, G10, G15, G16).

4.5.2 Principal component analysis (PCA)

Eigen values of principal component axis, percent of total variation and cumulative variation accounted for them obtained from principal component analysis are presented in Table 8. The results showed that the first principal axis, plant height (cm) largely accounted for the variation among the genotypes which alone contributed 41.57% of the total variation among the genotypes.

The first eight characters of the principal component axes with eigen values above unity accounted for 97.89% of the total variation among the twelve characters. The rest four characters contributed remaining 2.11% of total variation. Based on principal component scores I and II obtained from the principal component analysis, a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed which has been presented in figure 3.

4.5.3 Inter cluster distance

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

Table 7. Distribution of genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	5, 6, 27, 37	4	G5, G6, G27, G37
II	9, 11, 31	3	G9, G11, G31
III	10, 15, 16	3	G10, G15, G16
IV	20, 22, 23, 30	4	G20, G22, G23, G30
V	1, 2, 3, 4, 8, 13, 14, 19, 21, 32, 34, 35, 36	13	G1, G2, G3, G4, G8, G13, G14, G19, G21, G32, G34, G35, G36
VI	7, 12, 17, 18, 24, 25, 26, 28, 29, 33	10	G7, G12, G17, G18, G24, G25, G26, G28, G29, G33
	Total	37	

Table 8. Eigen values and yield percent contribution of 12 characters of 37 germplasm

Principal Component Axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	4.98	41.57	41.57
II	2.06	17.18	58.75
III	1.51	12.58	71.33
IV	1.24	10.39	81.72
V	0.74	6.20	87.92
VI	0.58	4.87	92.79
VII	0.32	2.69	95.48
VIII	0.28	2.41	97.89
IX	0.19	1.59	99.48
X	0.04	0.37	99.85
XI	0.01	0.09	99.94
XII	0.01	0.06	100.00

Z1-Z2 Graph

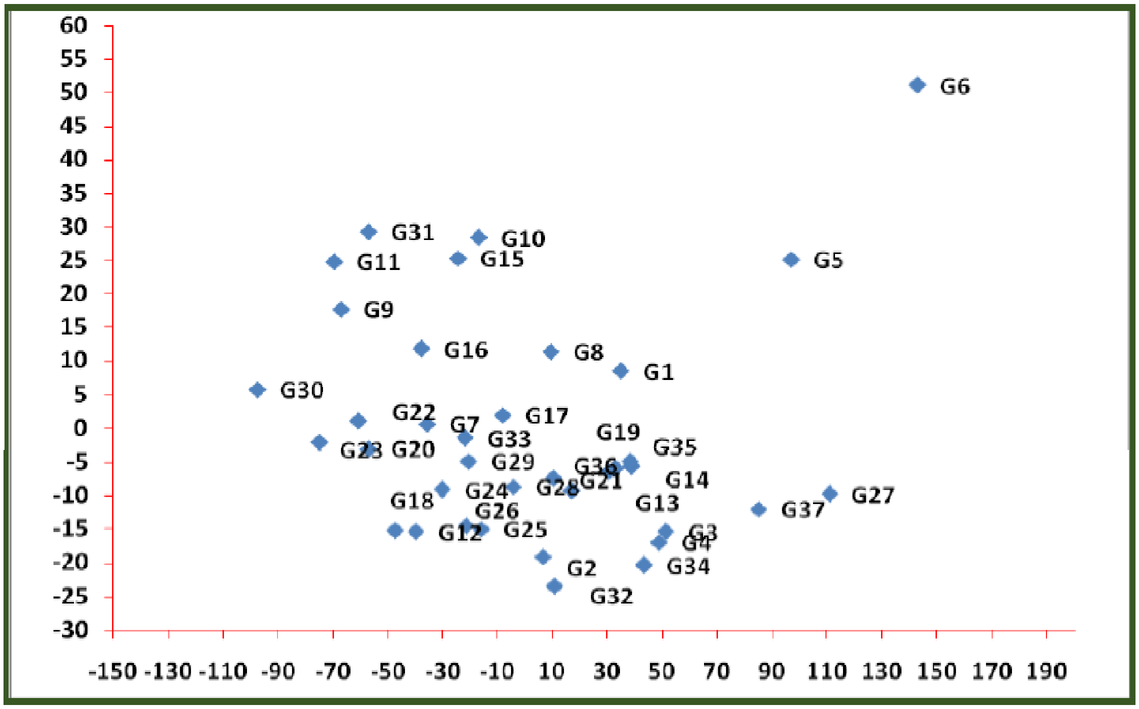


Fig 3. Scattered diagram of 37 Maize genotypes

Table 9. Intra (Bold) and inter cluster distances (D^2) for 37 genotypes

Cluster	I	II	III	IV	V	VI
I	**0.654**	14.57	10.08	13.09	6.27	9.67
II		**0.456**	6.03	5.07	10.53	6.50
III			**0.087**	5.11	6.00	3.30
IV				**0.132**	9.15	5.14
V					**0.221**	4.58
VI						**0.065**

Table 10. The nearest and farthest clusters from each cluster between D^2 values in Maize

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	**I**	**V (**6.27**)**	**II (**14.57)
2	**II**	**IV (**5.07**)**	**I (**14.57)
3	**III**	**VI (**3.30**)**	**IV (**13.09)
4	**IV**	**II (**5.07**)**	**I(**13.09)
5	**V**	**VI (**4.58**)**	**II (**10.53)
6	**VI**	**III (**3.30)	**I (**9.67)

4.5.4 Intra cluster distance

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

4.5.5 Cluster diagram

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

4.5.6 Cluster mean analysis

The cluster means of 12 different characters (Table 11) were compared and indicated considerable differences between clusters for all the characters studied. Maximum plant height was observed in cluster VI (147.53), whereas minimum plant height was observed in cluster I (137.87). Maximum (10.45) and minimum (9.56) leaf per plant were observed in cluster II and III respectively. Genotypes in cluster I showed the lowest leaf length (45.33) and cluster III had the highest mean (50.77). Maximum (5.69) and minimum (5.12) diameter of leaf were observed in cluster V and I respectively. Maximum cob length was observed in cluster IV (18.26), whereas minimum cob length was observed in cluster I (13.33). Cluster IV had the maximum cob breadth (14.32), cluster III had the minimum cob breadth (12.10). The maximum row per cob (14.00) was observed in the cluster II, whereas minimum row per cob (12.92) was observed in cluster I. Seed per row was the highest in cluster IV with a mean value of (34.08) and it was least in genotypes belongs to the cluster I (25.58). Seed per cob was the highest in cluster II with a mean value of (477.78) and it was least in genotypes belongs to the cluster I (333.83). Maximum cob weight was observed in cluster IV (180.91), whereas

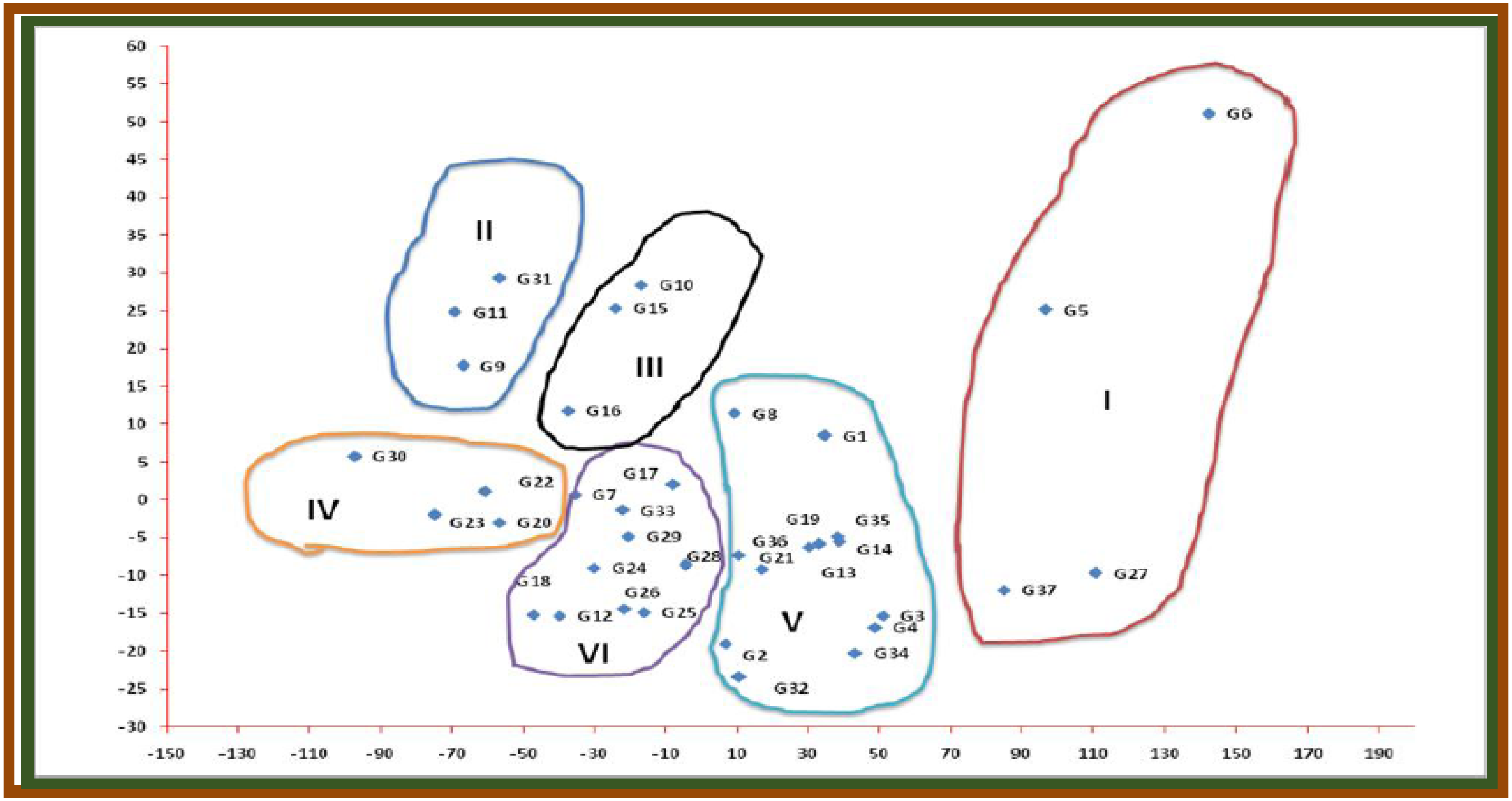


Fig 4 Intra and inter cluster distances of 37 genotypes in Maize

Table 11. Cluster mean values of 12 different characters of 37 genotypes

Characters	**I**	**II**	**III**	**IV**	**V**	**VI**
Plant height(cm)	137.87	**140.45**	142.34	143.66	140.26	147.53
Leaf per plant	10.00	10.45	9.56	9.75	10.28	10.43
Leaf length (cm)	45.33	47.88	50.77	48.47	46.82	45.79
Diameter of leaf (cm)	5.12	5.16	5.21	5.14	5.69	5.56
Cob length (cm)	13.33	16.76	17.03	18.26	16.73	16.96
Cob Breadth (cm)	12.27	12.52	12.10	14.32	12.79	12.70
Row per cob	12.92	14.00	13.89	13.67	13.03	13.37
Seed per row	25.58	33.11	32.44	34.08	30.36	32.37
Seed per cob	333.83	477.78	446.89	472.75	397.41	437.93
Cob weight (g)	104.50	155.00	143.00	180.91	152.64	169.90
100 seeds weight (g)	19.25	31.00	28.11	31.05	22.95	27.33
Yield per plant (g)	66.49	148.25	129.19	153.71	91.66	120.88

minimum cob weight was observed in cluster I (104.50). Maximum 100-seed weight was observed in cluster IV (31.05), whereas minimum 100-seed weight was observed in cluster I (19.25). Highest yield per plant was recorded by the cluster IV (153.71) while cluster I (66.49) showed the least yield per plant.

4.5.7 Contribution of characters towards divergence

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

In vector (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were plant height (0.001), leaf per plant (0.143), leaf length (0.043), diameter of leaf (0.110), cob length (0.124) and yield per plant (0.257) were important because all these characters had positive signs.

On the other hand cob breadth, row per cob, seed per row, seed per cob, cob weight and 100-seed weight possessed the negative sign in the first axis of differentiation and plant height, diameter of leaf, cob breadth, seed per row, row per cob and cob possessed negative signs in the second axis of differentiation that means it had minor role in the genetic diverse. Leaf per plant, leaf length, cob length and yield per had positive signs in both the vectors, which indicated they were the important component characters having higher contribution to the genetic divergence among the materials studied.

Table 12. Relative contributions of the twelve characters of 37 varieties to the total divergence

Characters	Vector-1	Vector-2
Plant height(cm)	-0.015	0.001
Leaf per plant	0.571	0.143
Leaf length (cm)	0.004	0.043
Diameter of leaf (cm)	-0.189	0.110
Cob length (cm)	0.148	0.124
Cob Breadth (cm)	-0.032	-0.218
Row per cob	-2.357	-1.104
Seed per row	-1.019	-0.771
Seed per cob	0.118	-0.074
Cob weight (g)	-0.022	-0.033
100 seeds weight (g)	0.422	-0.369
Yield per plant (g)	0.034	0.257

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted in the experimental area of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka during January to May, 2015 to study the genetic diversity, correlation and path co-efficient analysis for yield and yield contributing characters of commercial maize varieties. In this experiment 37 maize genotypes were used as experimental materials. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Mean performance, variability, correlation matrix and path analysis on different yield contributing characters and yield of maize genotypes were estimated.

Analysis of variance revealed highly significant difference among the accessions for all the characters. The maximum number of leaves per plant was 12 recorded in the genotype PAC-60 and minimum was 8 recorded in the genotype Dekalb- 9120. The maximum leaf length was recorded in Khaivutta (57.87 cm) and minimum in BARI Mishty-1 (37.10 cm). Maximum leaf diameter was noted in PAC-60 (6.53 cm) while minimum in Dekalb- 9120 (3.87 cm). The minimum and maximum plant height was observed in the genotype Bio seed (93.33cm) and Mirakkel Super (154.77 cm) respectively. The minimum cob length was in BHM-7 (8.03 cm) and maximum cob length was for Uttoron-2 (19.27 cm). Maximum cob breadth was recorded in genotype PAC-399 (15.17 cm) while minimum was BARI Mishty-1 (7.37 cm).The lowest number of seed row per cob was observed in genotype BARI Mishty-1 (11.16 cm) while highest was PAC-60 (14.67 cm). The lowest number of seed per row was observed in genotype 4536 (24.33 cm) while highest was Uttoron-2 (37.33 cm).The lowest number of seed per cob was observed in genotype BHM-7 (316.00cm) while highest was DEKALB-9120 (496.33 cm).

100-seed weight ranged from 19.12 g to 34.00 g which was observed in NK-40 and DEKALB-9120 respectively. The highest total yield per plant was observed in the genotype DEKALB-9120 (163.84 g). The lowest total yield per plant was observed in the genotype BHM-7 (60.00 g).

Characters like plant height, leaf per plant, leaf length, diameter of breadth, cob length, cob breadth, seed per row, seed per cob, 100-seed weight and 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 28.21 and 23.37 respectively, which indicated that yield per plant was mostly dependent on the environment condition. Amongst the characters, the highest genotypic co-efficient of variation was recorded for total yield per plant (23.37 g) followed by cob weight (15.31) and 100-seed weight (13.85 g). The maximum genotypic and phenotypic variations were 2557.30and 1542.67 respectively in seed per cob.

The highest estimated heritability amongst twelve characters of maize was 97.97% for cob breadth and the lowest was 16.47% for row per cob. The highest genetic advance amongst twelve characters was found in number of seed per cob is 62.84 and the lowest genetic advance was carried out in row per cob (0.35). The maximum genetic advance in percent of mean was observed for total yield per plant (39.87 g), followed by cob weight (28.51), cob length (24.54 g) and cob breadth (23.86). 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 37 maize genotypes, total yield per plant was positively and significantly correlated with plant height, leaf length, diameter of leaf, number of seed row per cob, number of seed per row, number of seed per cob and 100-seed weight. Path analysis revealed that leaf per plant, leaf length, cob length, cob breadth and seed per cob showed positive direct effects on yield per plant. On the other hand plant height, diameter of leaf, row per cob, seed per row, cob weight and 100-ssed weight showed negative direct effects on yield per plant.

To estimate genetic diversity, multivariate analysis was performed through principal component analysis, principal coordinate analysis and cluster analysis. As per principal component analysis, D^2 statistics and cluster analysis, the genotypes were grouped into six different clusters. Cluster V consist of highest 13 genotypes viz Bio seed, Barnali, Shuvra, BHM-6, BHM-8, Khaivutta, Krishibid-102, AS-99, PAC-984, Profit, PAC-536, Badsha and Dekalb Super Gold. Followed by cluster VI which had 10 genotypes viz BARI Mishty-1, Kaberi Profit, PAC-60, BHM-5, GP-901, Mirakkel super, PAC-740, DEKALB-962, VA-786 and Pacific-11. Cluster I and Cluster IV which had 4 genotype of each, Cluster II and cluster III comprises with three genotypes viz BHM-9, BM-5, Pacific-98, BM-6, HP-222 and PAC-984.

The maximum inter-cluster divergence was observed between cluster I and II (14.57) followed by cluster I and IV (13.09), II and V (10.53), 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 I was far diverged from those of cluster II. The distance was minimum between cluster I and V (6.27) followed by cluster I and VI (9.67). The highest intra-cluster distances was computed for cluster I (0.654) composed of four genotypes followed by the cluster II (0.456) composed of three genotypes. However the lowest value (0.065) of intra-cluster distance in cluster VI indicated ten genotypes constituted this cluster might have diverged characters.

In respect of cluster mean performances of different cluster revealed that cluster IV can be selected for cob length, cob breadth, seed per row, cob weight, 100-seed weight and yield per plant. Cluster I was remarkable due to lowest plant height, leaf length, diameter of leaf, cob length, row per cob, seed per row, seed per cob, cob weight, 100-seed weight and total yield per. Considering diversity pattern, genetic status and other agronomic performance, Khai vutta, PAC-984 and DEKALB Super Gold from cluster V; BARI Mishty-1 and DEKALB-962, from cluster VI; Pacific-984, BM-5 and HP-22 , from cluster II and III might be considered better parents for efficient hybridization program. Result of present study revealed that the characters; plant height, leaf per plant, leaf length, number of seed per row and 100-seed weight contributed maximum divergence among the maize genotypes. Involvement of such diverse genotypes in crossing program may produce desirable sergeants. So, divergent genotypes are recommended to use as parent in hybridization program.

Considering the above findings of the present experiment, the following recommendations and suggestions may be made

- Selected maize genotypes are needed in different agro-ecological zones (AEZ) of Bangladesh for regional adaptability and other performance.
- More genotypes with different crosses may be included for further study.

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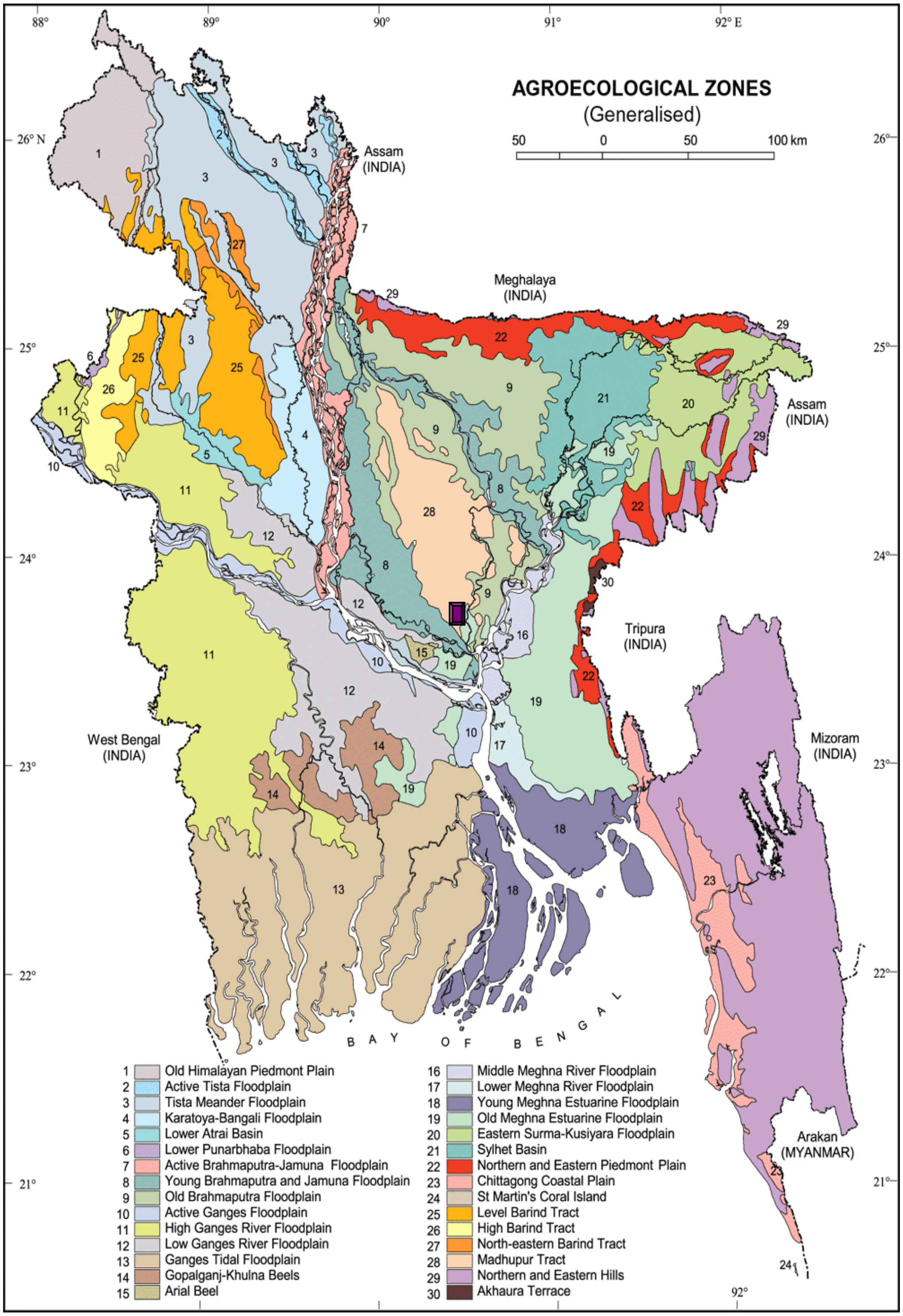
APPENDICES

Appendix 1. The map of the experimental site



Appendix 2. Monthly average of air temperature, relative humidity and total rainfall of the experimental site during the period from January to May, 2015

Month (2014)	*Air temperature (^oC)		*Relative humidity (%)	*Rainfall (mm)(total)
	Maximum	Minimum		
January	24.8	15.6	66	00
February	28.4	18.7	68	06
March	31.4	24.9	74	20
April	33.4	26.1	76	78
May	35.2	27.9	82	185

* Monthly average, **Source:** Bangladesh Meteorological Department, Agargoan, Dhaka – 1212

Appendix 3. Characteristics of the soil of experimental field

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Agronomy field , SAU, Dhaka
AEZ	Madhupur Tract (28)
General Soil Type	Shallow red brown terrace soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical and chemical properties of the initial soil

Characteristics	Value
% Sand	27
% Silt	43
% clay	30
Textural class	Silty-clay
pH	5.7
Organic matter (%)	1.13
Total N (%)	0.061
Available P (ppm)	5.46
Exchangeable K (me/100 g soil)	0.13
Available S (ppm)	12.7
Available B (ppm)	0.41

Source: Soil Resources Development Institute (SRDI), Farmgate, Dhaka

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

	PH	LPP	LL	LD	CL	CB	RPC	SPR	SPC	CW	HSW	YPP
G1	99.33	8.33	41.57	6.10	18.97	11.60	13.00	30.67	398.00	142.33	22.33	89.09
G2	133.27	10.67	51.77	5.63	17.97	13.20	13.00	31.00	413.00	171.67	23.67	97.83
G3	126.53	10.00	55.50	5.77	16.87	12.77	13.00	29.00	377.67	154.00	22.00	77.81
G4	139.07	10.33	44.23	4.80	17.17	11.40	13.00	29.00	377.00	154.00	22.67	82.82
G5	138.07	10.00	49.13	5.30	16.23	12.97	13.67	25.33	346.00	97.67	20.33	75.58
G6	127.90	9.00	42.83	4.23	8.03	10.27	12.00	25.67	316.00	59.00	18.33	60.00
G7	121.93	9.00	37.10	5.50	16.47	7.37	12.00	36.33	448.67	171.00	27.67	127.28
G8	136.37	9.00	57.87	5.73	16.90	11.87	13.00	33.00	417.00	141.33	24.67	106.82
G9	126.97	10.00	51.67	5.30	18.07	13.90	14.00	33.33	477.33	165.00	31.00	148.07
G10	135.93	10.00	47.83	5.37	15.80	11.20	14.00	32.33	441.67	134.67	28.33	125.32
G11	149.80	10.67	52.00	5.20	16.27	11.30	14.00	33.67	482.00	154.00	31.33	151.27
G12	143.80	9.00	50.63	6.00	18.47	13.63	13.00	33.67	447.33	183.33	28.33	127.25
G13	146.43	11.00	51.47	5.90	18.80	14.17	13.67	28.67	399.33	147.67	22.00	88.33
G14	139.17	9.33	41.73	5.10	17.53	13.87	13.00	29.33	392.00	145.67	21.00	85.55
G15	146.73	10.00	51.20	5.37	16.17	11.30	14.00	32.00	447.67	137.67	28.33	127.21
G16	144.37	8.67	53.27	4.90	19.13	13.80	13.67	33.00	451.33	156.67	27.67	135.03
G17	153.67	10.67	44.23	4.97	16.17	12.97	14.00	30.33	424.33	153.67	28.33	119.96
G18	154.00	12.00	52.30	6.53	16.50	14.00	14.00	32.67	457.33	182.67	27.33	125.95
G19	148.90	10.67	50.13	6.40	16.30	12.73	13.00	30.33	393.67	146.67	23.33	92.09
G20	153.83	10.00	48.97	6.00	19.27	13.27	12.00	37.33	459.67	176.33	31.33	145.27
G21	154.60	10.00	50.73	5.53	16.13	13.37	13.00	31.33	407.33	154.00	23.67	96.93
G22	141.67	10.00	50.07	5.33	16.80	15.07	14.00	32.00	460.67	177.33	29.33	152.27
G23	138.03	11.00	51.23	5.37	17.87	15.17	14.67	32.33	474.33	185.33	30.33	153.45
G24	151.00	9.00	42.97	5.40	16.30	12.57	14.00	30.67	439.00	173.00	29.00	128.49
G25	154.77	11.00	40.07	5.07	16.40	12.70	14.00	30.33	432.67	171.00	25.67	111.32
G26	153.17	11.00	49.40	5.03	17.53	13.00	13.00	33.33	434.00	173.67	26.67	117.85
G27	141.53	11.00	46.13	5.73	16.73	14.57	12.00	27.00	324.33	125.67	19.00	62.22
G28	152.03	11.00	50.33	5.77	17.80	14.50	13.67	31.00	424.00	161.67	25.33	108.03
G29	139.73	11.00	43.10	5.43	18.20	14.07	13.00	32.33	432.33	167.67	28.00	123.93

Appendix 4. Continued

	PH	LPP	LL	LD	CL	CB	RPC	SPR	SPC	CW	HSW	YPP
G30	141.10	8.00	43.60	3.87	19.10	13.77	14.00	34.67	496.33	184.67	33.00	163.84
G31	144.57	10.67	39.97	4.97	15.93	12.37	14.00	32.33	474.00	146.00	30.67	145.40
G32	151.17	12.00	39.27	5.13	13.53	12.03	13.00	31.00	404.33	171.67	25.00	102.60
G33	151.20	10.67	47.73	5.93	15.77	12.23	13.00	33.00	439.67	161.33	27.00	118.77
G34	150.17	10.67	39.47	5.27	15.17	11.90	13.00	28.67	382.67	156.33	21.33	82.80
G35	151.13	11.00	39.20	6.33	15.20	13.00	12.67	31.00	392.67	142.67	22.00	86.68
G36	147.27	10.67	45.73	6.30	16.93	14.30	13.00	31.67	411.67	156.33	24.67	102.21
G37	144.00	10.00	43.23	5.23	12.33	11.27	14.00	24.33	349.00	135.67	19.33	68.16

PH = Plant height (cm), LPP = Leaf per plant, LL = Leaf length (cm), LD = Diameter of leaf (cm), CL = Cob length (cm), CB = Cob Breadth (cm), RPC = Row per cob, SPR = Seed per row, SPC = Seed per cob, CW = Cob weight (g), HSW = 100 seeds weight (g) and YPP = Yield per plant (g).

Appendix 5. Principal component score 1 & 2.

Genotypes	Z_1	Z_2
1	34.82	8.52
2	6.71	-19.05
3	51.14	-15.32
4	48.81	-16.85
5	96.84	25.19
6	142.61	51.12
7	-35.52	0.71
8	9.34	11.48
9	-66.99	17.77
10	-16.99	28.47
11	-69.36	24.88
12	-39.91	-15.28
13	30.24	-6.26
14	38.65	-5.5
15	-24.21	25.38
16	-37.62	11.85
17	-7.89	2.04
18	-47.24	-15.13
19	33.02	-5.82
20	-56.9	-2.96
21	16.96	-9.18
22	-60.62	1.13
23	-74.76	-1.98
24	-30.38	-8.99
25	-16.04	-14.85
26	-21.57	-14.42
27	110.7	-9.71
28	-4.41	-8.61
29	-20.57	-4.79
30	-97.35	5.85
31	-56.81	29.36
32	10.67	-23.39
33	-22.05	-1.34
34	43.3	-20.24
35	38.07	-4.86
36	10.39	-7.32
37	84.93	-11.89