GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF YIELD AND YIELD CONTRIBUTING CHARACTERS IN MAIZE (*Zea mays* L.)

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This is to certify that the thesis entitled "**GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF YIELD AND YIELD CONTRIBUTING CHARACTERS IN MAIZE (*Zea mays* L.)**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **LABIBA JAHAN,** Registration number: **17-08276** 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.

Date: December, 2018
Place: Dhaka, Bangladesh

_____
Prof. Dr. Mohammad Saiful Islam
Supervisor

DEDICATED

TO

MY BELOVED PARENTS

AND

TO THE FARMERS WHO FEED THE NATION

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ABSTRACT

Thirty maize genotypes were studied in RCBD with three replication for the variability and character association of yield and yield related traits at Sher-e-Bangla Agricultural University, Dhaka during January to May, 2019. Significant variations were observed among the genotypes for all the traits studied. Among the genetic parameters, high GCV values were observed for kernels per cob (13.20) and yield per plant (15.49). High heritability values with high genetic advances in percent mean were obtained for kernel per cob (22.83), 1000 seeds weight (20.17) and grain yield per plant (31.69) indicating these traits are controlled by additive gene action. Correlation studies revealed significant positive association of yield per plant with cob length (0.273), cob diameter (0.346), kernel per row (0.232) and kernel per cob (0.395) at both genotypic and phenotypic levels. Path coefficient analysis indicated positive direct contribution towards yield per plant through plant height (0.282), leaves per plant (0.939), days to first female flowering (0.197), cob height (0.425), cob diameter (0.935), rows per cob (0.315) and kernel per row (1.107). The genotypes were grouped into five different clusters by D^2 analysis and cluster III consist of highest eight genotypes. The maximum inter-cluster divergence was observed between cluster I and V (10.747) indicated that the varieties belonging to cluster I was far diverged from those of cluster V. Considering diversity pattern, genetic status and other agronomic performance G6 (PAC-399), G12 (Deklab-30B07), G25 (Cornell) and G26 (Kaveri) would be selected from cluster II for the highest grain yield per plant, kernels per cob, cob length and leaves per plant. For early flowering and early maturity, genotypes G5 (BHM-7) G15 (Krishibid-102) andG18 (Uttoron) would be selected from cluster I. Other genotypes G1 (BM-5) and G9 (Pacific) could be considered suitable genotypes from cluster IV for dwarf plant. So, genotypes could be selected from advance segregating generations for developing inbred line development and use as open pollinated variety.

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SOME COMMONLY USED ABBREVIATIONS

ABBREVIATIONS	FULL WORD
AEZ	Agro-Ecological Zone
et al.	And others
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Co-efficient of variation
etc.	Etcetera
Fig.	Figure

G	Genotype
GA	Genetic Advance
GCV	Genotypic Co-efficient of Variation
$\dagger^2{}_g$	Genotypic Variance
g	Gram
h^2b	Heritability in broad sense
J.	Journal
kg	Kilogram
m	Meter
MSS	Mean Sum of Square
mm	Millimeter
MOP	Muriate of potash
No.	Number
%	Percent
PCV	Phenotypic Co-efficient of Variation
$\dagger^2{}_e$	Phenotypic Variance
RCBD	Randomized Complete Block Design
R	Replication
Res.	Research
SAU	Sher-e-Bangla Agricultural University

CHAPTER I

INTRODUCTION

Maize is considered the third most important cereal crop after rice and wheat in the world (FAO, 2014). This cereal is referred as miracle crop and queen of the cereals due to its high productivity potential compared to other *Poaceae* family members. Globally 67% of maize is used for livestock feed, 25% human consumption, industrial purposes and balance is used as seed and demand for grain is increasing worldwide (Reddy *et al.*, 2013). Top corn producing countries include the United States, China, Brazil, Mexico, Indonesia, India,

France and Argentina. Among them the United States produces 40% of the world's harvest. Like as India climate condition of Bangladesh favors maize cultivation.

Maize (*Zea mays* L.) (2n = 20) has been originated from teosinte. It 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. It is a tall, determinate annual C_4 plant and mostly photo-insensitive, cross pollinated crop. The Mesoamerican region is known to the center of origin for *Zea mays* (Matsuoka *et al.,* 2002).

Maize grain has high nutritive value containing 66.2%, starch 11.1% protein, 7.12% oil, 1.5% minerals and 2.7 % fiber (Gopalan *et al.,* 1981). 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). It's oil is used as the best quality edible oil. Green 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, maize cultivation was started in the late 19th century and its production has an increasing tendency with the introduction of hybrid and adoption improved technology since 1993. Recently, it ranked 2nd position next to rice (DAE, 2012) and occupied of 4.8% of the total cropped land area (Ahmad *et al*., 2011). Total cultivated area about 152 thousand hectares and total annual production was 887 thousand MT with an average yield of 5.83 tha[-1] (BBS, 2014). The yield of maize is low in Bangladesh as compared to the other maize growing countries, even though, it is well adapted to the climate and soils of our country. Every day the country is losing about 200 hectares of crop land owing to industrialization, urbanization and river erosion. Therefore to face this challenge cultivation of high productive crop like maize breeding

is necessity. Previously sporadic attempts were made to accelerate maize production.

Since grain yield in maize is quantitative in nature and polygenically controlled. To enhance the yield productivity, genetic parameters and correlation studies between yield and yield components are prerequisite to plan a meaningful breeding program for developing high yielding inbreeds as well as hybrids.

Genetic variability is marked as a heritable difference among cultivars and required in an optimal level within a population. 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 segregating population that represents different climatic, geographical regions (Ilarslan*et al.,* 2002). Abayi *et al*. (2004) observed significant genetic variation in important agronomic traits like earliness, cob height and grains per cob 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 trait in maize controlled by numerous genes (Zdunic *et al*., 2008). Different yield contributing components like ear height, plant height and 1000-grain weight influences yield (Rahman *et al*., 1995). Grain yield is proportionately associated with ear weight. Therefore, Yield can be improved by selection for grain yield, plant height and ear height (Prodhan and Rai, 1997).

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

- to study the variability among the maize varieties;

- to study the correlation and path coefficient analysis among the yield contributing traits of maize varieties;
- to estimate the nature and magnitude of genetic diversity and selection of superior maize variety.

CHAPTER II

REVIEW OF LITERATURE

Various investigators at worked with different maize genotypes and studied their performance regarding the characterization. Many studies on the growth, yield, variability, correlation, path analysis and genetic diversity 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 Reproductive biology

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

Silking stage involving the formation of the female flowers or cobs is the first reproductive stage and occurs 2-3 days after tasseling stage. This stage begins when any silks are visible outside the husk. These are auxiliary flowers unlike tassels that are terminal ones. Pollination occurs when these new moist silks catch the falling pollen grains. Maize is a monoecious plant, that is, the sexes are partitioned into separate pistillate (ear), the female flower and staminate (tassel), the male flower. It has determinate growth habit and the shoot terminates into the inflorescences bearing staminate or pistillate flowers (Dhillon and Prasanna, 2001).

Maize is generally protandrous, that is, the male flower matures earlier than the female flower. Within each male flower spikelet, there are usually two functional florets, although development of the lower floret may be delayed slightly in comparison to the upper floret. Each floret contains a pair of thin scales i.e. lemma and palea, three anthers, two lodicules and rudimentary pistil. Pollen grains per anther have been reported to range from 2000 to 7500 (Kiesselbach,1949). Kiesselbach (1949) estimated that 42,500 pollen grains are produced per square inch of cornfield. The pollen grains are very small, barely

visible to the naked eye, light in weight, and easily carried by wind. The wind borne nature of the pollen and protandry lead to cross-pollination, but there may be about five percent self-pollination. In maize, the pollen shed is not a continuous process and usually begins two to three days prior to silk emergence and continues for five to eight days. The silks are covered with fine, sticky hairs which serve to catch and anchor the pollen grains. Pollen shed stops when the tassel is too wet or too dry and begins again when temperature conditions are favourable. Under favourable conditions, pollen grain remains viable for only 18 to 24 hours. Cool temperatures and high humidity favor pollen longevity. Under optimal conditions the interval between anthesis and silking is one to two days. Fertilization occurs after the pollen grain is caught by the silk and germinates by growth of the pollen tube down the silk channel within minutes of coming in contact with a silk and the pollen tube grows the length of the silk and enters the embryo sac in 12 to 28 hours. Pollen is light and is often carried considerable distances by the wind. Under field conditions 97% or more of the kernels produced by each plant are pollinated by other plants in the field. Fertilization of ovules begins about one third of the way up from the base of the ear.

2.2 Mean performance of maize

Chowdhury and Islam (1993) reported that maize varieties Barnali. Khoibhutta, Mohor and Shuvra were 200, 160, 210 and 175 cm tall respectively.

Akhtar and Mitra (1990) found that plant height was significantly different among the 6 CIMMYT entries and one local cheek.

Jotshi *et al.* (1988) working with 25 varieties of maize and observed that leaves per plant differed significantly among the varieties. Lee et al. (1986) studying with 28 maize hybrids also observed significant differences in number of leaves per plant among the varieties.

Singh *et al.* (1991) conducted an experiment with varieties Ganga 5 and HLL and found that Ganga 5 was significantly superior to HLL with regard to growth and yield which was due to ear length. In an experiment with 5 maize cultivars (R2, Ganga 5, Ganga 11, HH 216 and D765).

Ear length is an important yield component for maize and had a direct effect on grain yield (Subramanin *et al.*, 198l). BARI (1990), reported that cv. Bamali gave more ear per plant than Khaibhutta.

Paradkar and Sharma (1993) observed that out of 5 maize varieties (R1, Ganga 5, Ganga 1l, HH2l6 and D765), Ganga 1l gave increased grain rows per ear. Ganga 11 gave more ear length followed by Gonga 5 and D 7654.

Kamen (1983) observed that early maturity hybrids had fewer grain rows per ear than late maruriting hybrids. Number of grains per row may differ among the varieties. Grains per ear, one of the important yield contributing characters, varied with variety.

Khaibhutta produced significantly higher (432.5) number of grains per ear than Barnali (343.5) as reported by Anonymous (1988). On the other hand, Khoibhutta produced the highest number of grains per ear when compared with variety Pirsabak 8l46, Lamaquina 7827 and Guaira 8045 (Anonymous, l987).

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).

Viola *et al.* (2004) reported that maize display an orderly sequence of development of yield components namely number of ear per plant, number of kernel per row, number of kernel row per ear and hundred kernel weights.

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

Hossain (2015) studied in Sher-e-Bangla Agricultural University in 2015 with white maize. The results revealed that highest grains per row ((33.98) and rows per cob (13.67) were recorded from variety PSC 121. KS 510 showed maximum 100 grain weight (37.20 g). PSC-121 showed the tallest plant (204.73 cm at harvest) and KS-510 showed the shortest plant (198.82 cm at harvest). KS 510 and PSC 121 showed the highest (274.11 cm^2) and lowest (188.42 cm^2) leaf area, respectively. PSC 121 showed the highest base diameter (9.02 cm) and KS 510 showed the lowest base diameter (8.87 cm).

2.3 Genetic variability

Grzesiak (2001) observed that considerable variability among maize genotypes for different traits.

An experiment was conducted by Sola *et al.* (2004) under the field conditions using two-factor factorial arrangement in RCBD with four replications. Significant variations in plant height, ear height, stalk diameter, number of days to 50% silking and tasseling, maturity, percentage of barren plants, percent ear fill, ear length, ear diameter and 1000-seed weight were attributed to the independent effects of generation and nitrogen application.

Ihsan *et al.* (2005) 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 weight, grain moisture content, 300-grains weight and grain yield, 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.

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.

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 indicating the genetic variances for these traits.

Hussain *et al.* (2011) observed that the maize varieties significantly differed in days to 50% pollen shedding. The highest (81) days taken to 50% pollen shedding were recorded in maize variety Islamabad White and the lowest (67) in Soan-3. Other varieties, except for EV-1097, EV-1098, Soan-3 and Agaiti 2002, showed statistically similar days to pollen shedding.

Idris and Mohammed (2012) made a study to develop a suitable procedure for selecting the most sustainable maize genotype to grow by considering genetic variability for vegetative, yield and yield components under irrigated farming. Significant variability was observed for plant height, stem diameter, number of rows per cob and ear length during the first season 2007/08 and for days to 50% flowering and 100-seed weight during the second season 2008/09. Frantic genotype scored maximum seed weight (81.0g) while Baladi had least seed weight (57.48g). Frantic genotype had maximum grain yield (0.577 t/ha), while minimum grain yield ton/ha was recorded in Baladi (0.473 t/ha).

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.

Ogunniyan and Olakojo (2014) found significant variation existed in all the characters. The coefficients of variation were low except 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.

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 to moderate genotypic and phenotypic coefficient of variation.

Breeders are interested in screening and development of open pollinated population in maize. Ishaq *et al.* (2015) showed highly significant differences (P 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. The study revealed a considerable amount of genetic variation that could be manipulated for further improvement in maize breeding.

Present study was an attempt in this direction to assess the genetic variability of 100 homozygous maize inbred lines during kharif 2013 and 2014 by Asim Gazal *et al.* (2017) Inbred lines were evaluated for obtaining information on genetic variability for yield attribute and quality traits. A wide range of variability revealing significant response was observed. Medium to high values of genetic coefficient of variability was exhibited for anthesis-silking interval, leaf relative water content, stomatal count, chlorophyll content before flowering, chlorophyll content before maturity, ears per plant, grain yield per plot.

Matin *et al.* (2017) studied with twenty one locally developed maize hybrids for ten characters to access variability and found that high genotypic coefficient of variation (GCV) was obtained from thousand seed weight, days to 50% silking, cob diameter and anthesis silking interval. The highest phenotypic coefficient of variation (PCV) was observed in thousand seed weight followed by days to 50% silking and cob diameter.

Pandey *et al.* (2017) studied on genetic parameters included the mean performance, genotypic variances, phenotypic variances, genotype by environment variances, broad sense heritability in maize. Significant differences were recorded for all traits studied thereby revealing the variability

of the maize genotypes. Grain yield per plant, shelling%, and 100 seed weight (g) showed high heritability and high genotypic variances suggesting the involvement of additive gene action. Days to 50% tasseling, days to 50% silking and physiological maturity showed the highest heritability but low genotypic variance suggesting the preponderance of non-additive gene action.

Barua *et al.* (2017) studied on genetic variability in maize (*Zea mays* L.) genotypes for grain yield and yield contributing traits. High heritability exertion along with high genetic advance was recorded for plant height (95.00, 44.07), ear height (95.00, 30.42) and grain yield (90.00, 4484.69), indicating that these traits were controlled by additive genes and suggesting hybridization to be effective.

Singh *et al.* (2017) studied and revealed highly significant differences for all the characters studied in maize, indicating the presence of substantial genetic variability. The phenotypic and genotypic coefficient of variation (PCV and GCV) was high for days to 50% tasseling followed by kernel rows per year and 100 grains weight, respectively.

Kumar *et al*. (2017) studied on genetic variability parameters in Quality Protein Maize (QPM) genotypes with 18 lines and 4 standard checks. In the present investigation significant differences were observed for all the yield and yield contributing traits and quality parameters.

Asim Gazal *et al.* (2017) studied heritability on 100 homozygous maize inbred lines during kharif 2013 and 2014. High heritability and high genetic gain (as % of mean) were exhibited for anthesis-silking interval, leaf relative water content, stomatal count, chlorophyll content before flowering, chlorophyll content before maturity, ears per plant, grain yield per plot, protein content all confirming that these traits can be given more weightage while applying selection for improvement of these traits and in identifying elite drought tolerant lines.

Bhiusal *et al.* (2017); estimated the extent of genetic variability in maize with fifty five genotypes during rabi 2013-14. Analysis of variance revealed

significant differences for 18 characters studied among the genotypes. High genotypic and phenotypic coefficient of variation was recorded for grain yield/plant, biological yield/plant and cob weight coupled with high heritability and genetic advance. Thus, traits showing variability need to be paid attention while formulating breeding strategies for improvement of grain yield of maize.

2.4 Heritability and genetic advance

Benjamin (2001) studied 13 reciprocal full-sib recurrent selection cycles in two maize populations, BS10 and BS11 in a 8 x 8 simple lattice on 9 locations, in Iowa and one location in USA. Relatively high estimates of heritability were observed in both the populations for days to mid-anthesis, days to mid-silk, plant height, ear height, grain moisture percentage and grain yield.

A series of tropical maize hybrids, involving 10 single, 4 double and 4 three-way crosses, were examined along with their parental inbred lines and three local varieties as check entries at University Putra Malaysia, Serdang, Malaysia by Saleh *et al.* (2002). Broad sense heritability estimates varied with characters, Moderate heritability estimates were observed for grain yield indicating a substantial amount of genetic variation in the hybrids. They further added that low and negligible heritability estimates for days to silking and 100- grain weight indicated that these traits were highly influenced by environmental factors.

Presterl *et al.* (2003); conducted experiments in a series of 21 in different locations in typical maize growing regions of Germany and France on 48 to 144 entries derived from maize inbred lines of dent and flint gene pools in various combinations under low and high nitrogen levels. They observed moderate to high levels of heritability for grain yield and grain dry matter content under both the low nitrogen (LN) and high nitrogen (HN) levels in all the experiments. The estimates of heritability ranged from 35.9% to 94.1% under low nitrogen level while under high nitrogen level, it varied from 40.7% to 88.0%.

A total of 66 cross combinations evaluated by Sujiprihati *et al*. (2003) in two locations in a randomized complete block design (RCBD) in Malaysia. They observed heritability estimates of 0.3-54.0% for gain yield and number of kernel rows per ear at one location while a range of 0.3 to 36.7% was observed for ear length and number of kernel rows per ear, respectively at the other location.

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.

In a study of heritability among grain yield and its components in 49 maize hybrids and 14 parental lines by Rafique *et al*. (2004) and observed that heritability estimates higher than 80% for plant height, ear height, ear length, ear diameter, kernels per row and grain yield.

Thirty six F_1s with 9 parental inbred lines and a commercial hybrid were evaluated at the Agriculture Faculty Experiment Station, Adnan Menderes University Andin, Turkey in 4 replications by Unay *et al*. (2004). They observed heritability estimate for grain yield in broad sense (0.97) and in narrow sense (0.24) from their study.

Beyene (2005) evaluated 180 maize accessions in a randomized complete block design in Alemaya University, Ethiopia. He observed heritability estimates of high levels for days to tasselling (78.5%), days to silking (77.8%), plant height (70.1), number of leaves per plant (86.9%), days to maturity (84.1%) and kernels per row (69.5%), moderate for ear height (53.0%), leaf length (45.8%) ear diameter (44.7%) and rows per ear (46.4), while low levels of 17.0%, 17.7%, 18.1% and 21.6%, respectively for grain yield, leaf width, 1000- seed weight and ear length.

Two hundred and thirty four F_2 families were evaluated along with their parents for drought response (Xiao *et al*., 2005). They observed high estimates of heritability under well water regime as compared to water stress regime for

ear weight, kernel weight per ear, kernel numbers per ear, 100-kernel weight and grain yield. The estimates of heritability ranged from 0.49–0.71 and 0.31–0.64, respectively under well water and water stress regimes.

High levels of heritability estimates of 96.8%, 98.5%, 94.5%, 97.2%, 89.4%, 97.0%, 98.8%, 88.1%, 99.2% and 98.7% were observed, respectively for days to 50% flowering, days to 50% silking, plant height, ear height, number of kernel rows per ear, number of kernels per row, number kernels per ear, 100-seed weight, grain yield and shelling percentage in a set of 47 diverse maize genotypes collected from CIMMYT, Mexico (Sumathi *et al*., 2005).

Abdelmula and Sabiel (2007) estimated genetic parameters including heritability in 15 maize genotypes during evaluation at two locations in Sudan. They observed moderate levels of heritability estimates for days to 95% anthesis (26%), leaf area index (27%), days to 95% silking (29%), stem diameter (36%), grain yield (40%), number of leaves per plant (41%) and plant height (56%).

Twenty diverse maize cultivars obtained from various locations within the Ekiti State were evaluated at Teaching and Research Farm, University of Ado-Ekiti, Nigeria for various plant traits (Salami *et al*., 2007). They estimated low levels of heritability in broad sense for days to 50% anthesis, days to 50% silking (0.20), plant height (0.35) and grain yield (0.24). From these low levels of heritability they noticed that perhaps the heritability estimates would have been improved if the evaluation had been conducted in multiple environments.

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 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.

Data recorded by Idris and Mohammed (2012) for heritability showed that days to 50% flowering had maximum heritability (79.1%) while the minimum heritability (4.46%) was recorded for 100 seed weight.

Ogunniyan and Olakojo (2014) studied with heritability was greater than 80% for all characters whereas expected genetic advance ranged from low (8.91) in days to silk emergence to high (72.03) in number of ear per plant.

Praveen *et al*. (2014) revealed that traits yield per plant, plant height, ear height, number of seeds per row, 100-seed weight were shown high heritability accompanied with 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.

Ishaq *et al.* (2015) reported that broad sense heritability (h^2_b) ranged from 0.29 to 0.95 for various traits. The study revealed a considerable amount of heritability estimates that could be manipulated for further improvement in maize breeding.

Alhussein and Idris (2017) studied that heritability for all the traits except ear height and grain yield had non additive type of gene action with high heritability. The exploitation of these traits would be effective in hybrid maize breeding. Ear height and grain yield showed both additive and non additive type of gene action with environmental influence due to high environmental variance. These traits can be utilized effectively through selection in varietal development.

Higher values of broad sense heritability were obtained for almost all the characters except days to 50% tasseling which is moderate. High heritability coupled with high genetic advance as per cent of mean was reported for plant height, grain yield per plant and ear height (Singh *et al.*, 2017).

Matin *et al.* (2017) studied with twenty one locally developed maize hybrids for ten characters to access heritability. The highest heritability (h^2b) was observed for cob diameter (95.25) followed by days to 50% silking (94.15), days to maturity (93.85) and ear height (93.06). The characters with high GCV and higher values of heritability indicated high potential for selection.

2.5 Correlation co-efficient

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).

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

Pande *et al*. (1971) observed that 100-seed weight was positively correlated with grain yield.

Experiment conducted by Debnath (1991) 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.

AL-Ahmad (2004) 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.

Aydin *et al.* (2007) 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.

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.

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).

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.

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.

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.

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.

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.

Pandey *et al.* (2017) studied on phenotypic and genotypic correlation coefficients and revealed that the grain yield was positively and strongly correlated with 100 seed weight, shelling%, cob length, plant height, kernels per row and kernel rows per cob.

Barua *et al.* (2017) studied on correlation in maize genotypes for grain yield and yield contributing traits. Grain yield showed highly significant positive genotypic correlation with plant height (0.767) and ear height (0.823) indicating these characters, can be strategically used to improve grain yield of maize. Thus, selection can be exercised on these traits in improving maize population for high grain yield.

Alhussein and Idris (2017) studied to investigate the genotypic association among grain yield components and yield. Correlation studies revealed significant positive phenotypic relationship of grain yield with plant and ear height, ear length and diameter and hundred kernel weight.

Singh *et al.* (2017) reported on correlation studies showed that grain yield per plant had significant phenotypic correlation with ear length.

Matin *et al.* (2017) studied with twenty one locally developed maize hybrids for ten characters to access correlation and found that positive and significant genotypic, phenotypic correlation coefficient were recorded for yield with anthesis silking interval ($r_g = 1.00^{**}$, $r_p = 0.96^{**}$), cob diameter ($r_g = 0.99^{**}$ and $r_p = 0.95^{**}$) and ear height ($r_g = 0.98^{**}$ and $r_p = 0.94^{**}$). But days to 50% tasseling had moderate but significant positive correlation at both phenotypic and genotypic level.

Kumar *et al.* (2017) studied on genetic correlations on parameters in Quality Protein Maize (QPM) genotypes with 18 lines and 4 standard checks. The grain yield per plant had highly significant and positive correlations both at genotypic and phenotypic levels with 100-grain weight ($r_g=0.863$, $r_p=0.829$), starch content ($r_g=0.657$, $r_p=0.649$), harvest index ($r_g=0.529$, $r_p=0.504$), lysine Content ($r_g=0.518$, $r_p=0.486$), ear length ($r_g=0.476$, $r_p=0.463$), tryptophan content ($r_g=0.468$, $r_p=0.457$) and ear height ($r_g=0.351$, $r_p=0.339$).

Bhiusal *et al.* (2017) estimated the traits association in maize with fifty five genotypes during rabi 2013-14. Strong positive associations were exhibited to grain yield per plant with plant height, ear height, leaf area index, cobs/plant, cob weight, cob length, cob girth, grains/row and biological yield/plant both at genotypic and phenotypic levels. Thus, traits showing variability and strong positive correlation both at genotypic and phenotypic levels need to be paid attention while formulating breeding strategies for improvement of grain yield of maize.

2.6 Path analysis

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.

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.

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.

Venugopal *et al.* (2003) reported that 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.

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.

Khazaei *et al*. (2010) reported that 100-grains weight and number of seed had the highest direct effect on grain yield.

Bello *et al*. (2010) studied on path analysis and 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)

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.

Kumar *et al*. (2014) revealed that path analysis showed days to 50% tassel had highest magnitude directly effect on grain yield per plant followed by ear height, 100 seeds weight and ear circumference.

Pandey *et al.* (2017) studied on path analysis of maize. Path analysis was used to partition the genetic correlations between grain yield and related characters. Days to 50% silking, physiological maturity, shelling% and 100-seed weight showed positive direct effect on grain yield. The highest direct effect belonged to days to 50% silking the highest direct effect (0.3032), followed by physiological yield (0.1586).

Jakhar *et al.* (2017) studied the path analysis and revealed that it provides an effective measure of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product. Direct and positive effect on yield was exhibited by days to 75% brown husk, tassel length, cob length without husk, days to 50% tasselling, leaf width, plant height, 100 seed weight, cob length with husk, cob diameter indicating the

effectiveness of direct selection, where as direct and negative effects were exhibited by days to 50% silking and ear height indicating the effectiveness of indirect selection.

Barua *et al.* (2017) studied on path analysis in maize genotypes for grain yield and yield contributing traits. Path analysis revealed that days to 50% silk (1.918) had shown the highest positive direct effect on grain yield followed by days to 50% pollen shed (1.779), days to 75% dry husk (0.840), plant height (0.753) and number of kernels per row (0.600) indicating these characters, can be strategically used to improve grain yield of maize. Thus, selection can be exercised on these traits in improving maize population for high grain yield.

Alhussein and Idris (2017) studied to investigate the path analysis of grain yield components on yield. Therefore ear length and diameter and hundred kernel weight had high positive direct effects on grain yield. Flowering day such as days tasseling had high negative direct effect on yield. These result depicted that ear length and diameter may be used as reliable criteria for improving grain yield.

Singh *et al.* (2017) studied on path analysis and revealed that high positive direct effect on grain yield per plant for days to maturity followed by kernel rows per ear, grains per ear revealing that these are the major yield contributing traits in maize.

Matin *et al.* (2017) studied with twenty one locally developed maize hybrids for ten characters to access path analysis. Anthesis silking interval (0.79) had the highest positive direct effect on yield followed by cob diameter (0.31), cob length (0.31) and plant height (0.04) indicating the effectiveness of direct selection. While some other characters such as days to 50% tasseling (−0.12), days to 50% silking (−1.78), ear height (−1.16), days to maturity (−0.64) exhibited indirect negative effect on yield indicating the effectiveness of indirect selection.

Kumar *et al*. (2017) studied on path analysis on parameters in Quality Protein Maize (QPM) genotypes with 18 lines and 4 standard checks. The highest

positive and direct effect was found for days to 50% tasseling (5.559) followed by lysine content (0.710) and starch content (0.439). The negative and direct effect was found for days to 50% silking (-5.774) and plant height (-0.331).

2.7 Genetic diversity

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

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

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

analysis, 5 dent and 4 flint inbreds were selected for evaluation of the performance of 36 single crosses.

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

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

Brkic *et al.* (2003) used one hundred simple sequence repeats (SSR) as molecular markers to analyze the genetic relationship among nine maize inbred lines. Genetic variation was also examined between the inbred lines B73 and M017 obtained from two different sources. Genetic dissimilarity ranged from 8 (between the M017 lines obtained from different sources) to 92 (between M017 and Os438-95). Mean heterozygosity values within samples were relatively low (with an average of 2.l8% across all samples), however, B73 from the Agrogene source showed a much higher level of within sample heterozygosity at 14%. The relationship among samples determined by the SSR markers and UPGMA clustering agreed with the pedigree of these lines. The results showed

that different seed sources of the same inbred line did not vary considerably. Different sources of the same lines were tightly clustered in the UPGMA dendogram.

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

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

Characterization of genetic diversity of maize (*Zea mays* L.) germplasm is of great importance in hybrid maize breeding (Melchinger *et al.,* 2005). Inbreds included in the study were assayed with 79 SSR markers. The CIMMYT inbred

lines originated from 35 mostly broad-based populations and pools with mixed origins. A total of 566 alleles were scored, (averaging 7.2 and ranging from 2 to 16 alleles per locus).

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).

An experiment was conducted by Singh *et al*. (2005) to study genetic divergence of 23 genotypes of maize using D^2 analysis. The genotypes fell into six clusters. The inter-cluster distances were higher than intra-cluster distances, suggesting wide genetic maximum distance between clusters III and VI and the lowest distance between clusters I and IV. The cluster means were higher for 50% tasselling, 50% silking, plant height, cob height, ear length, number of grains per row and 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 seven clusters using Mahalanobis D^2 statistics. Cluster II was the largest with 25 genotypes followed by cluster III with 11 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.

Gautam (2008) accomplished genetic divergence using D2 statistic of 135 populations of maize from different agro climatic situations of Himachal Pradesh revealed existence of considerable diversity. The populations were grouped into 15 clusters. The cluster II was the largest containing 24 populations followed by cluster IV and I with 22 and 20 entries, respectively.

The grouping of population in cluster did not show any relationship between genetic divergence and geographic diversity.

Clustering of maize inbred lines based upon several qualitative and quantitative traits have been of prime importance for heterotic grouping and exploitation of heterosis. Ranatunga *et al.* (2009) performed the genetic diversity analysis of 45 maize inbreds based on eight qualitative traits, 10 quantitative traits and 42 SSR primer pairs. Among the eight qualitative traits, leaf pubescence did not show any variation across the genotypes. Traits viz., silk colour at emergence, ear shape, kernel colour, grain texture and grain shape were the predominant phenotypic variants. Ten quantitative traits observed across the 43 maize inbreds showed wide variation. Cluster analysis using 8 different qualitative traits across 43 maize genotypes resulted in grouping of genotypes into two major clusters of 19 and 24 genotypes where as cluster analysis based on 10 quantitative traits resulted in 2 major clusters, one with 39 genotypes and the other with 4 genotypes.

Yadav *et al.* (2010) also studied on different morphometric traits using distinguishabilty measures of UPOV guidelines and found that the traits tassel branching, plant height, kernels/row, ear height, ear length and ear width were holding the top position in discriminating the inbreds among themselves. All the inbred lines were confirmed as morphologically and physiologically distinct. At morphological level, the maximum genetic distance (10.8) and least genetic distance (1.6) were found. For physiological characters, distance varied from 0.35 to 1.92 and results from dendrogram, which was made on the basis of dissimilarity matrix, were grouped into five major clusters. From RAPD, random primers provide polymorphic amplification products; the distance varying 0.42 to 0.65 and dendrogram showed that these lines formed close clusters due to the less variation in these lines at molecular level.

Ahmad *et al.* (2011) showed that the results of diversity analysis for 14 maize genotypes revealed that all the characters like days to 50% pollen shedding,

days to 50% silking, plant height, ear height, 100 grain weight, harvest index and grain yield were significantly affected due to various maize genotypes.

Dagne *et al.* (2012) studied 15 parents for 17 morphological traits and also examined for DNA polymorphism using 40 SSR markers. SSR markers and morphological methods of genetic distance estimates showed moderately high genetic distance among the inbred lines studied. Cluster analysis based on the two distance measures grouped the 15 parental lines differently. The SSR marker-based genetic distance was positively and highly significantly correlated with grain yield (r = 0.37), and negatively and highly significantly with days to anthesis (r = −0.40) and days to silking (r = −0.42). These relationships suggested that high grain yield and earliness of QPM hybrids can be predicted from SSR marker determined distances of the parents.

Azad *et al.* (2012) were also able to produce the greater contribution of plant height, ear length, ear diameter, no. of grains/ear, thousand kernels weight and kernel yield/plant to the existing variability among 30 inbred lines in the study of the genetic divergence using multivariate analysis. The lines were evaluated for thirteen parameters (viz. Plant height, ear height, 50% tasseling, 50% silking, maturity and other yield traits) for the study of principal component analysis and by application of non-hierarchical clustering using co-variance matrix; 30 maize inbreds were grouped into six different clusters. The intra-cluster distances in all the six clusters were more or less low, indicating that the genotypes within the same cluster were closely related. Days to maturity and ear diameter showed maximum contribution towards total divergence among different characters. Based on medium to high inter-cluster distances, they concluded the existence of diverse inbred lines would produce the chance of development of highly heterotic and high performing crosses.

Shukla *et al.* (2014) carried a diversity analysis in 64 maize genotypes using Mahalanobis's generalized distance D^2 analysis and found that biological yield per plant contributed most towards genetic divergence. Total 64 genotypes were grouped into 5 clusters with maximum number of 60 genotypes within a

same cluster which bear maximum intra cluster D^2 value. They suggested for selection of parents from the diverse genotypes.

Sharma *et al.* (2014) assessed the genetic variability, heritability, genetic advance for yield and kernel quality traits in twenty diverse maize genotypes. Genetic variability parameters showed that phenotypic coefficient of variation (PCV) was higher than the respective genotypic coefficient of variation (GCV) and heritability was high for most of the traits under study. Test weight, grain yield per plant, grains per cob, cob length, grains per row and harvest index were found important in selection programs aiming to maize yield improvement.

CHAPTER III

MATERIALS AND METHODS

An experiment was carried out during late *Rabi* to *Kharif-1* season 2019 to study the genetic variability, character association of yield and yield contributing characters in maize. The details of material and methods applied and the experimental procedure adopted during the course of research are described below.

3.1 Location of the experiment

The study was carried out at the research farm of Sher-e-Bangla Agricultural University, Dhaka-1207 during the period from January to May, 2019. The location belongs to the sub-tropical climate and AEZ No. 28 called "Madhupur Tract". It is situated at 23°41 N latitude and 90°22 E longitude with an elevation of 8.6 meter from the sea level (Appendix-I). It is characterized by high temperature accompanied by moderate high rainfall during Kharif season (April to September) and low temperature in the Rabi season (October to March).

3.2 Climate and soil

The geographical situation of the experimental site was under the subtropical climate, characterized by three distinct seasons, the monsoon or rainy season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October (Edris *et al.,* 1979) and also characterized by heavy precipitation during the month of May to August and scanty precipitation during the period from October to March. The record of air, temperature, humidity and rainfall during the period of experiment were recorded from the Bangladesh Metrological Department, Agargaon, Dhaka (Appendix-III). The experimental site was situated in the subtropical zone. The soil of the experimental site lies in Agro-ecological region of Madhupur Tract (AEZ no. 28) of Noda soil series. The soil was loam in texture. The experimental site was medium high land and the pH was 5.6 to 5.8 and organic carbon content was 0.82%. The physical and chemical characteristics of the soil have been presented in Appendix-II.

3.3 Experimental material

The experimental material for this study consisted of 30 maize genotypes. The seeds were collected from the Department of Genetics and Plant Breeding, SAU, Dhaka. The details of genotypes were presented in Table 1.

3.4 Details of the experiment

The experiment was conducted during late Rabi to Kharif-1 season of 2019. Seeds were sown in main field on 20th January 2019. The experiment was laid out in a Randomized Complete Block Design (RCBD). Three replications were performed in this experiment. Block to block distance was 1m, Plant to plant distance was 30 cm and Row to row distance was 50 cm. The genotypes were distributed to each row in each block randomly.

3.5 Cultural practices

3.5.1 Land preparation

The experimental plot was opened in the second week of January 2019 with a power tiller and was exposed to the sun for a weak. After a week the land was prepared by several ploughing and cross ploughing followed by laddering and harrowing with power tiller and country plough to bring about good tilth. This was carried out to manage the weeds, provide good soil aeration and to obtain good seedling emergence and root penetration. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on 19th January, 2019. Special care was taken to remove the rhizomes of mutha grass.

3.5.2 Manure and fertilizers application

Generally cow dung, Urea, TSP and MP fertilizers are required for maize cultivation. The field was fertilized with 6 ton cow dung per ha. The field was also fertilized with Urea, TSP, MOP, Gypsum, Boric acid and Zinc sulphate 50-195-35-100-10-10 and 10 kg/ha, respectively. The entire amount of cow dung was applied seven days before sowing. TSP, MOP, Gypsum and Boron were applied during final land preparation and incorporated into the soil. The total amount of urea was divided by three splits. One third of the urea was applied after 25 days of seed germination and the rest two splits of the urea applied after 45 and 65 days of seed germination (before flowering) of the plants, respectively. At the time of third dressing of Urea 35 kg of MOP(rest) was also used. The dose and method of application of fertilizers are shown in the Table 2.

Table 1. List of experimental materials of maize used in the experiment

Code	Genotypes
G1	BM-5
G2	BHM-5
G3	BHM-6
G4	BM-6
G5	BHM-7
G6	PAC-399
G7	PAC-984
G8	PAC-60

G9	Pacific
G10	Pacific 98
G11	HP-222
G12	Deklab-30B07
G13	Deklab Super Gold
G14	Deklab Super
G15	Krishibid-102
G16	Shuvra
G17	AS-999
G18	Uttoron
G19	Mishty
G20	NK-40
G21	Bioseed
G22	Pioneer-30B07
G23	PAC-559
G24	Duranta-202
G25	Cornell
G26	Kaveri(218+)
G27	Kohinor1820
G28	Kohinor
G29	Chomak-07
G30	Golden 984

Source: Genetics and Plant Breeding Department, SAU

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

Manures and Fertilizers	Dose per ha	Application (Kg)			
		Basal	25DAP	45DAP	65DAP
Cowdung	06 tons	06tons	--	--	--
Urea	170 Kg	50Kg	40Kg	40kg	40kg
TSP	195 Kg	195Kg	--	--	--
MOP	70 Kg	35Kg	--	--	35kg

Gypsum	100 Kg	100Kg	--	--	--
Zinc Sulphate	10 Kg	10Kg	--	--	--
Magnesium	10 Kg	10Kg	--	--	--
Boric acid	10 Kg	10Kg	--	--	--

Plate 1. Photograph showing seed sowing

3.5.3 Seed sowing

After the lay out, the maize genotypes seeds were assigned to different plots in each replication by using random numbers. The seeds of each replication were sown by dibbling two seeds per hill. The gap filling was done by re-sowing within a week after germination. Seeds were sown in main field on 20th

January, 2019. Before sown the seeds they were treated with Sevin 75 WP @ 2 g per Kg of seeds for controlling ant.

3.5.4 Thinning of excess seedlings

The weak seedlings were thinned out leaving only one vigorous seedling per hill after 25 days of sowing. The first one third dose of nitrogen was top dressed at 30 days after sowing. All recommended cultural practices were followed to raise a good white maize crop.

3.5.5 Other operations

The 1st and 2nd weeding were done respectively after 20 and 40 days of sowing to keep the soil free from weed. Irrigation was given when it is necessary during the crop period. Earthling up was done twice during growing period. The first earthling up was done at 45 days after sowing (DAS) and the second earthling up was done after 65 DAS. Field was covered by net on 28th January 2019.

3.5.6 Plant protection

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

3.5.7 Harvesting, threshing and cleaning

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

3.6 Observations recorded

Observations were recorded from the selected plants at random from each unit plot. Data were collected in respect of the following parameters.
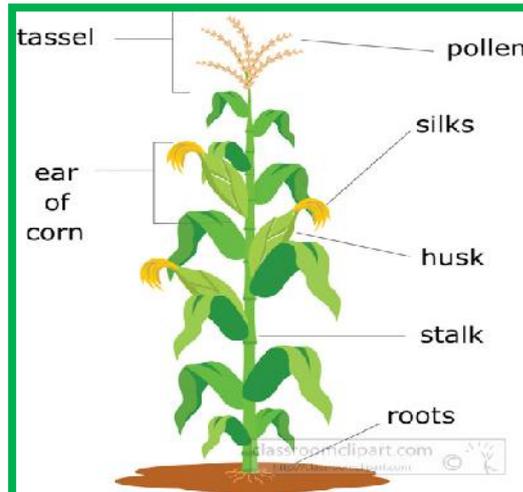
Figure 1: Different parts of a maize plant (https://corn-plant- structure-clipart-illustration-6818_jpg.htm**.)**

3.6.1 Plant height (cm)

Plant height refers to the length of the plant from ground level up to the last node (base of the tassel/flag leaf node) of the plant. Height of randomly selected plants of each unit plot was measured and the mean was calculated. It was measured in cm with a graduated measuring stick.

3.6.2 Leaves per plant

Number of leaves per plant was recorded by counting all the leaves from the selected plants of each unit plot and the mean was calculated
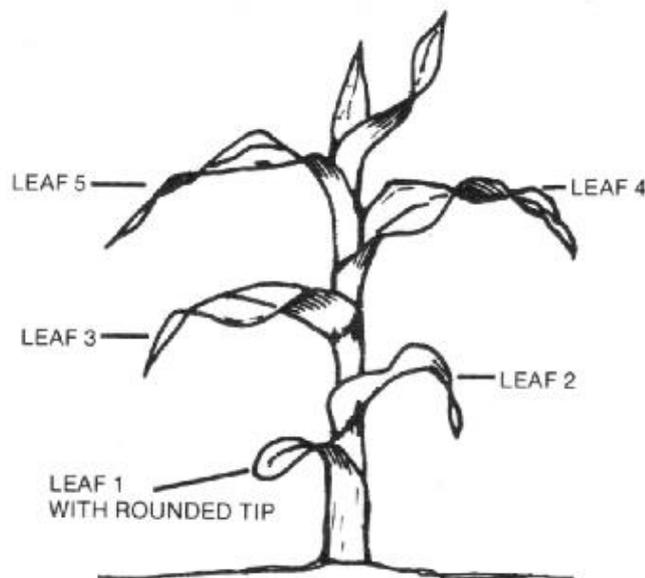
Figure 2: Measuring of the leaves per plant in maize

(https://www.extension.purdue.edu/extmedia/nch/nch-1.html.)

3.6.3 Days first male flowering

Days to first male flowering were documented as number of days from planting to the time 5% of plants had fully emerged tassels.

3.6.4 Days to first female flowering

Days to silking were recorded as number of days from planting to the time 5% of plants had completely extruded silks.

3.6.5 Days to 75% maturity

Days to maturity were recorded as number of days from planting to the time cob cover turn in straw colour and base of kernel in black colour.

Plate 2: Photograph showing data collection in experimental field

3.6.6 Cob height (cm)

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

3.6.7 Cob length (cm)

The lengths of cobs were measured from the cob base to the apex in centimeter by using measuring scale.

3.6.8 Cob diameter (cm)

The diameter of cobs at the top, basal and central part was measured in centimeter by using a measuring tape and the average was recorded.

Cob length
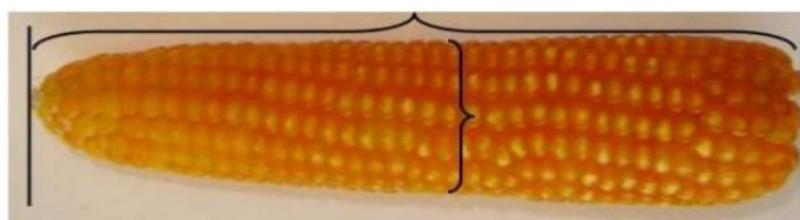
Cob diameter

Figure 3: Cob length and diameter measurement
(https://www.slideshare.net/SatishKhadia2/dus-test-guidelines-for-maize)

3.6.9 Rows per cob

The total number of rows each cob were counted and the average was recorded.

Figure 4: Measurement of rows per cob

(https://extension.udel.edu.com.)

3.6.10 Kernel per row

The total number of kernels from each row of a cob was counted and the average was recorded.

3.6.11 Kernel per cob

Number of kernels per cob was recorded from each cob was counted and the average was recorded.

3.6.12 1000 seeds weight (g)

A sample of 1000 seeds were taken at random and weighed to the nearest 1/10 gram.

3.6.13 Yield per plant (g)

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

3.7 Statistical analysis

The mean replicated data collected on 13 traits were subjected to biometrical analysis following appropriate biometrical procedures.

3.7.1 Analysis of variance

Analysis of Variance was carried out as per the procedure given by Panse and Sukhatme (1985). The structure of analysis of variance is as follows.

Source of variation	Degrees of freedom	Sum of squares	Expected MSS
Replication	r-1	M_1	$\sigma^2_e + t\,\sigma^2_r$
Treatment	t-1	M_2	$\sigma^2_e + r\,\sigma^2_g$
Error	(r-1) (v-1)	M_3	σ^2_e
Total	rv-1	$(M_1 + M_2 + M_3)$	

Where,

r = Number of replications

v = Number of genotypes (treatments)

σ^2_e = Error variance

σ^2_g = Genotypic variance

Statistical significance of variation due to genotype was tested by comparing calculated values to F-table values at one per cent and five per cent level of probability, respectively.

Data on the 13 characters, namely plant height (cm), leaves per plant, days to first male flowering, days to first female flowering, days to 75% maturity, cob height (cm), cob length (cm), cob diameter (cm), rows per cob, kernel per row, kernel per cob, 1000 seeds weight (g) and yield per plant (g) were recorded from five randomly selected plants from each plot.

3.7.2 Genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

Genotypic variance $(\sigma^2_g) = \dfrac{GMS - EMS}{r}$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

Phenotypic variance $(\sigma^2_p) = \sigma^2_g + \sigma_e^{\ 2}$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

σ^2_e = Error variance

3.7.3 Genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952).

Genotypic co-efficient of variation (GCV %) $= \sqrt{\dfrac{\sigma^2_g}{\bar{x}}} \times 100$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) $= \sqrt{\dfrac{\sigma^2_{ph}}{\bar{x}}} \times 100$

Where,

σ^2_p = Phenotypic variance

$\bar{x}$ = Population mean

3.7.4 Heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

Heritability, $\quad h^2{}_b\% = \dfrac{\sigma^2{}_g}{\sigma^2{}_p} \times 100$

Where,

$h^2{}_b$ = Heritability in broad sense

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

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

3.7.5 Genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, $GA = K. h^2. \sigma_p$

Or Genetic advance, $GA = K. \dfrac{\sigma^2{}_g}{\sigma^2{}_p} . \sigma_p$

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

$h^2{}_b$= Heritability in broad sense

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

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

3.7.6 Genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

$$\text{Genetic advance (\% of mean)} = \frac{\text{Genetic Advance (GA)}}{\text{Population mean (x)}} \times 100$$

3.8 Genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation,}(r_{gxy}) = \frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$$

Where,

$\sigma_{gxy} =$ Genotypic co-variance between the traits x and y

$\sigma^2_{gx} =$ Genotypic variance of the trait x

$\sigma^2_{gy} =$ Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{PCOVxy}{\sqrt{PVxPVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{py})}}$$

Where,

$\sigma_{pxy} =$ Phenotypic covariance between the trait x and y

$\sigma^2_{px} =$ Phenotypic variance of the trait x

$\sigma^2_{py} =$ Phenotypic variance of the trait y

3.9 Path Coefficient Analysis

To establish a cause and effect relationship the first step used was to partition genotypic and phenotypic correlation coefficient into direct and indirect effects by path analysis as suggested by Dewey and Lu (1959) and developed by Wright (1921).

The second step in path analysis is to prepare path diagram based on cause and effect relationship. In the present study, path diagram was prepared by taking yield as the effect i.e. function of various components like X_1, X_2, X_3 and these component showed following type of association with each other.

In path diagram the yield is the result of X_1, X_2, X_3…..X_n and some other undefined factors designated by R. The double arrow lines indicated mutual association as measured by correlation coefficient. The single arrow represents direct influence as measured by path coefficient P_{ij}.

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

$$r_{ny} = P_{ny} + r_{n2} \, P_{2y} + r_{n3}P_{3y} + \text{……………}$$

Where,

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

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

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

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

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 $\sum D^2/n$, where $\sum D^2$ is the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the average D^2 values represents the distance (D) within cluster.

3.10.6 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 '^'.

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

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

58

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.

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

Where,

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

N = All possible combinations

Plate 3: Photograph showing visiting experimental field with supervisor

CHAPTER IV
RESULTS AND DISCUSSION

The experiment was conducted for achieving the objectives. The results of the research work are presented as follows:

4.1 Mean performance

Analysis of variance and mean performance was presented in Table 3-4 and Appendix IV. 'F' test revealed highly significant variation among 30 maize genotypes in terms of all the yield contributing characters and yield under studied. It revealed the possibilities of improving the genetic yield potential of maize genotypes.

4.1.1 Plant height (cm)

Plant height is an important agronomic character for selecting desirable genotype for breeding program (Ali *et al*., 2014). Plant height varied significantly indicated considerable difference among the genotypes studied (Table 3). The lowest plant height was recorded in G1 (152.47 cm) and the highest in G14 (250.20 cm)(Fig. 5). The average plant height was recorded 214.15 cm and ranged from 152.47 cm to 250.20 cm (Table 4). Tahir *et al. (*2008) reported that maximum (206.00) plant height was found in Pioneer-32B33 which was followed by FSH-421 (200.00), HG-3740 (196.75) and pioneer-3062 (195.00); and the minimum plant height was observed in Rafhan-2303(173.75). These results are also in accordance with the results of Ali (1994) who also reported difference of plant height in different hybrids.

4.1.2 Leaf per Plant

Significant variation was observed for number of leaves per plant among different maize genotypes (Table 3). The average number of leaves per plant was 13.83 which range from 11.67 to 16.00 (Table 4). The maximum number of leaves per plant was recorded in G21(16.00) minimum followed by G20 (15.00) and G17 (15.00) (Appendix IV) whereas the minimum number was

observed from the genotypes G3, G5, G7 (11.67) . These results are in line with those of Dijk *et al.* (1999) who observed significant differences while evaluating maize genotypes for different morphological and yield traits. Jotshi *et al.* (1988) worked with 25 varieties of maize and observed that leaves per plant differed significantly among the varieties.

4.1.3 Days to first male flowering

Days to first flowering showed significant variation for different maize genotypes under study (Table 3).The results revealed that the average days to first flowering was recorded around 64.44 with a range from 62.00 to 65.67 (Table 4 & Appendix IV). The highest days to first flowering was found in G18 (65.67) whereas the lowest days was found in G5(62.00). The result revealed that different variety required different days to first flowering and it was might be due to genetical factor of the genotype.

4.1.4 Days to first female flowering

Significant variation was observed for days to first female flowering among the maize genotypes under investigation (Table 3). The average days to first female flowering was 66.39 days with a range from 64.67 to 67.67 (Table 4). The minimum days to first flowering was observed in G5 (64.67). The highest days to first female flowering was found in the G11 (67.67). The differences in days to first female flowering might be due to genetical factor of the genotype concerned.

Table 3. Analysis of variance for different characters in maize genotypes

Characters	Mean sum of square		
	Replication **(r-1) = 2**	**Genotype** **(g-1) = 29**	**Error** **(r-1)(g-1) = 58**
Plant height (cm)	228.88	1429.16**	124.46
Leaves per plant	0.53	3.26**	1.15
Days to first male flowering	6.54	1.32**	0.40
Days to first female flowering	3.88	0.90*	0.44
Days to 75% maturity	0.28	1.83**	0.31
Cob height (cm)	122.92	219.19**	102.95
Cob length (cm)	0.11	4.36**	0.76
Cob diameter (cm)	8.02	1.93**	0.34
Rows per cob	1.18	2.25**	0.89
Kernel per row	1.35	32.08**	2.45
Kernel per cob	16142.22	14295.75**	1752.77
1000 seeds weight (g)	134.46	3564.76**	12.55
Yield per plant (g)	17.28	1958.65**	9.22

* Denotes significant at 5% level of probability   ** Denotes significant at 1% level of probability

Table 4. Range, mean and CV (%) of 30 maize genotypes

Parameters	Range		Mean	CV (%)
	Min.	Max.		
Plant height (cm)	G1 (152.47)	G14 (250.20)	214.15	5.21
Leaves per plant	G3 (11.67)	G21 (16.00)	13.83	7.77
Days to first male flowering	G5 (62.00)	G18 (65.67)	64.44	0.98
Days to first female flowering	G5 (64.67)	G11 (67.67)	66.39	1.00
Days to 75% maturity	G4 (103.00)	G11 (105.67)	104.19	0.54
Cob height (cm)	G9 (63.68)	G14 (99.67)	86.22	11.77
Cob length (cm)	G11 (15.57)	G26 (20.80)	17.91	4.88
Cob diameter (cm)	G19 (13.28)	G17 (16.37)	14.96	3.91
Rows per cob	G4 (12.77)	G15 (15.50)	14.24	6.64
Kernel per row	G6 (28.77)	G24 (39.33)	34.89	4.49
Kernel per cob	G3 (369.33)	G24 (602.27)	489.69	8.55
1000 seeds weight (g)	G19 (287.85)	G28 (429.67)	349.55	1.01
Yield per plant (g)	G15 (120.33)	G25 (213.00)	164.52	1.85

CV (%) = coefficient of variation
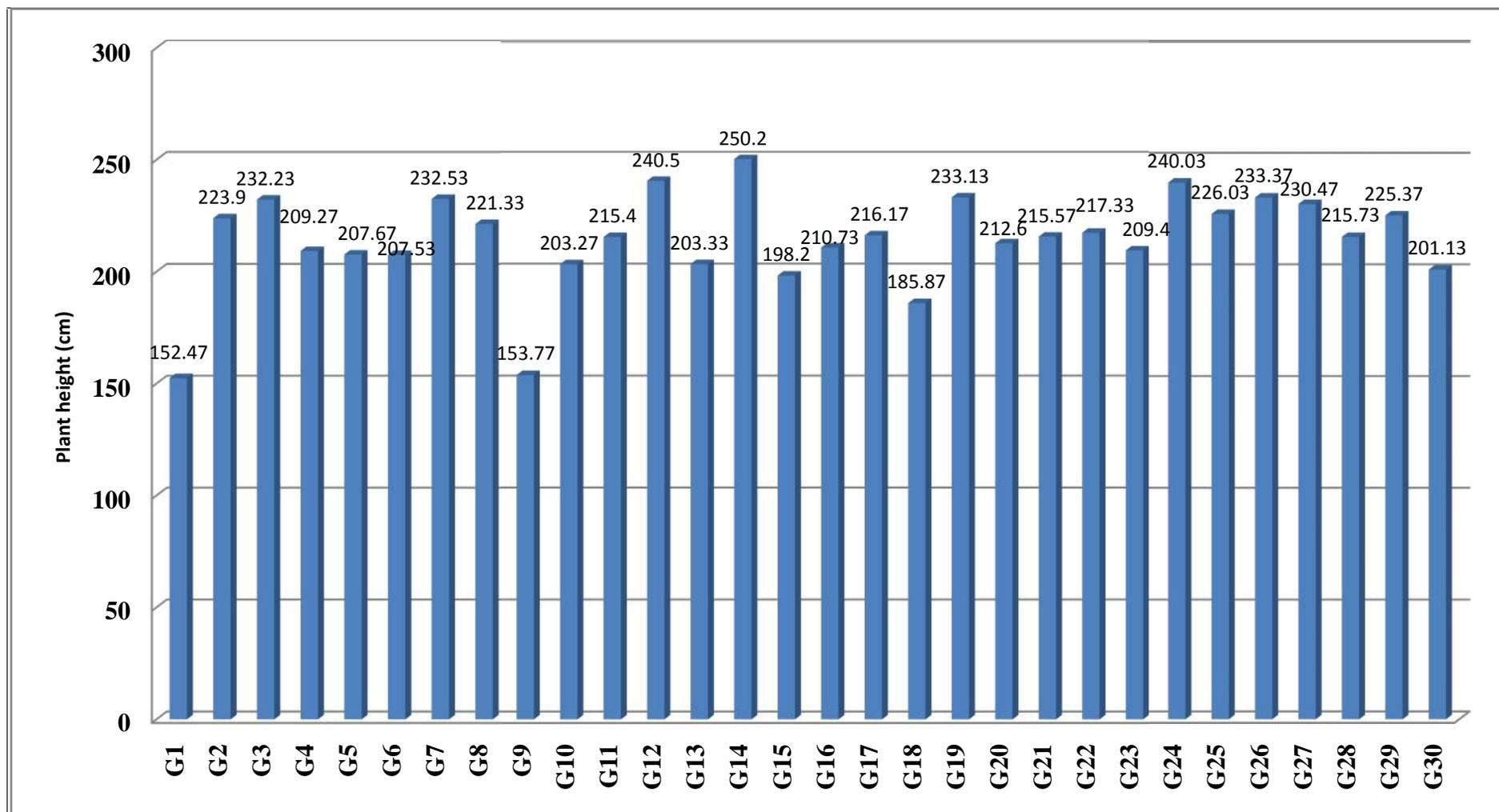
Figure 5. Mean performance of plant height of 30 maize genotypes

4.1.5 Days to 75% maturity

Statistically significant variation was recorded for days to 75% maturity for different maize genotypes (Table 3). The average days to 75% maturity was recorded 104.19 with a range from 103.00 to 105.67 (Table 4). The highest days to maturity was found in the genotype G11(105.67). The minimum days to maturation was found in G4 (103.00) followed by G5, G16, G19 and G25 (103.33).

4.1.6 Cob height (cm)

Cob height varied significantly among the genotypes (Table 3). This result are in line with those of Dijak *et al*. (1999) who observed significant differences while evaluating maize genotypes for this trait. The average cob height was 86.22 cm with a range from 63.68 cm to 99.67 cm (Table 4). The lowest cob height was recorded in G9 (63.68 cm). The highest cob height was observed in G14 (99.67 cm).

4.1.7 Cob length (cm)

Significant variation was exhibited in respect of cob length among different varieties under studied (Table 3). The average cob length was recorded 17.91 with a range from 15.57 to 20.80. The longest cob was observed in G26 (20.80), whereas the shortest in G11 (15.57).

4.1.8 Cob diameter (cm)

Cob diameter varied significantly in different maize genotypes (Table 3). The average cob diameter was recorded 14.96 cm with a range from 13.28 cm to 16.37 cm (Table 4). The highest cob diameter was recorded in G17 (16.37) which was followed by G1 (16.10 cm), whereas the lowest cob diameter was observed G19(13.28 cm).

Plate 4: Maturity sign of maize for days to maturity parameter

4.1.9 Number of rows per cob

Number of rows per cob is a genetically controlled factor but environmental and nutritional level may also influence the number of rows per cob (Tahir *et al.,* 2008). The more number of rows per cob results in more grain yield. Row per cob varied significantly among the genotypes (Table 3). The average rows per cob was 14.24. The highest row per cob was in G15 (15.50) and followed by the G13 (15.47) and G6 (15.43), while the lowest number of row per cob was observed in G4 (12.77). These results were in line with Ahmad *et al.* (1978) in maize.

4.1.10 Kernels per row

Number of kernels per row varied significantly due to different maize genotypes (Table 3). The average number of kernels per row was recorded around 34.89 with a range from 28.77 to 39.33 (Table 3 & Appendix IV). The highest number of kernels per row was recorded in G24 (39.33) which was followed by G23 (39.07) and G9 (38.97), whereas the lowest number was observed in G6 (28.77).

4.1.11 1000-seed weight (g)

1000-seed weight is an important factor directly contributing to final seed yield. There was a prominent effect of different genotype on 1000-grain weight. This was due to genetically controlled factor that 1000-grain weight of different hybrids was different. As for the effect of environment factors on 1000-grain weight is concerned it could it could not be neglected but the selection of suitable genotype can manage the influence of environment. Data indicated that highly significant due to 1000-grain weight among different maize genotypes (Table 3). The average 1000-grain weight was 349.55 g with a range from 287.85 g to 429.67 g (Table 4 & Appendix IV). The highest 1000-grain weight was recorded in G28 (429.67 g) while the lowest was in G19 (287.85 g).Similar results were also reported by Jing *et al.* (2003) and Ali (1994).

Plate 5: Photograph showing different cob among maize genotypes (Representative)

4.1.12 Grain yield per plant (g)

Grain yield varied significantly due to different maize genotypes under the present study (Table 3). The results showed that the average grain yield per plant was recorded 164.52 g with a range from 120.33 g to 213.00 gm (Table 4 & Appendix IV). The highest grain yield per plant was recorded in G25 (213.00 g) followed by G12 (210.70 g) and G26 (193.33 g). Tahir *et al. (*2008) observed that the maximum grain yield was obtained from HG-3740. The

lowest grain yield was observed in G15 (120.33g).
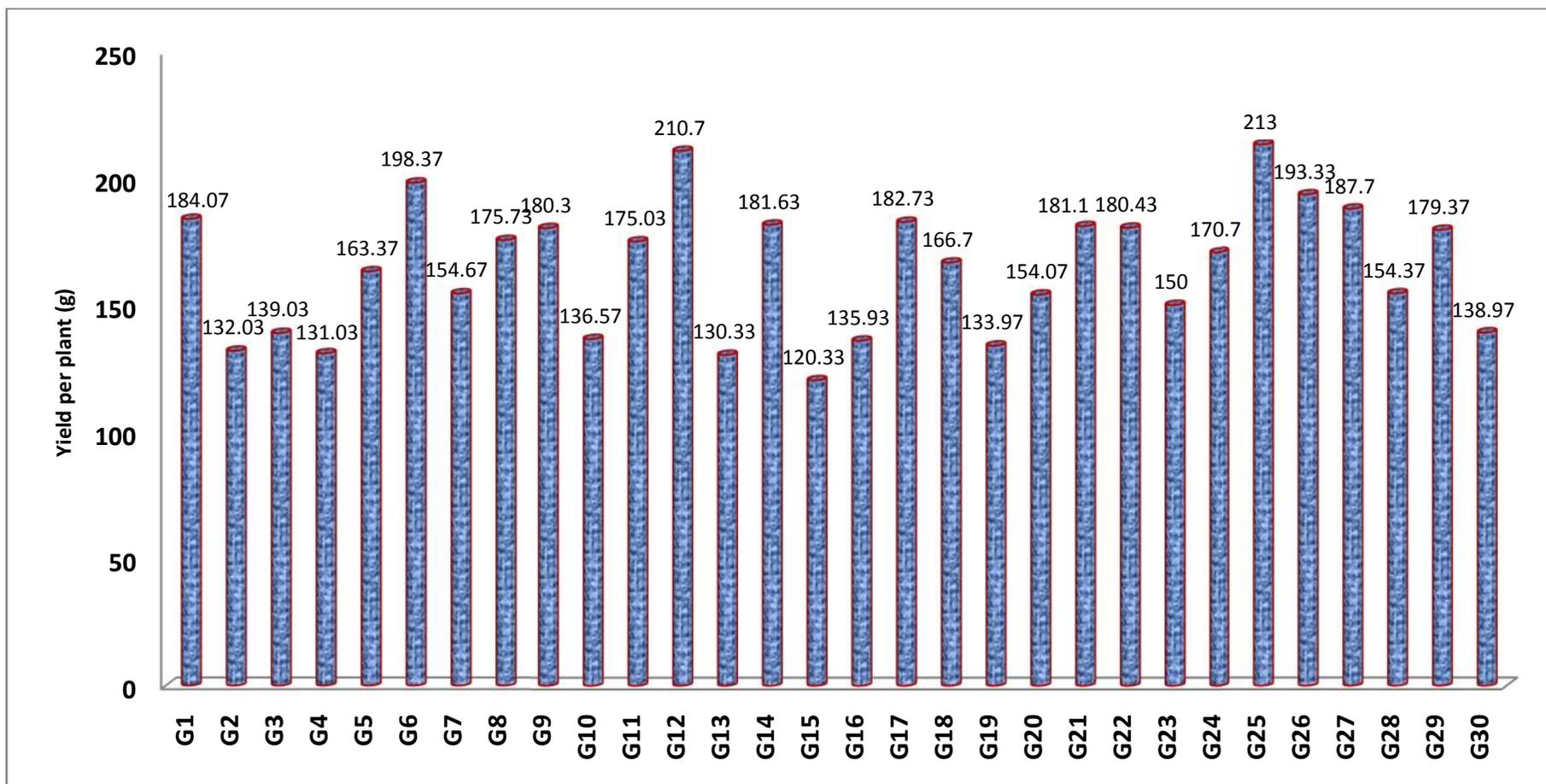
Figure 6. Mean performance of yield per plant of 30 maize genotypes

4.2 Genetic Variability, heritability and genetic advance

Genotypic and phenotypic variance, heritability and genetic advance in percentage of mean were estimated for 13 traits in 30 genotypes of maize and presented in Table 5.

4.2.1 Plant height (cm)

In case of plant height phenotypic variance (559.36) was higher than the genotypic variance (434.90) indicating highly environmental influence for expression of this character which was supported by difference between phenotypic (11.04%) and genotypic (9.74%) co-efficient of variation (Table 5). High heritability (77.75%) along with high genetic advance (37.88%) and medium genetic advance in percent of mean (17.69%) revealed the possibility of predominance of additive and non additive gene action in the inheritance of this trait. So, selection based on this trait would be effective. Similar findings were also reported by Alvi*et al.* (2003). Mihaljevic *et al.* (2005) obtained high heritability values (0.90) for plant height. The greater the heritability of a particular trait, the lesser will be the environmental effect on its expression.

4.2.2 Leaves per plant

The differences between phenotypic variances (1.86) and genotypic variances (0.70) were relatively low for leaves per plant indicating low environmental influence on these characters (Table 5). The value of PCV and GCV were 9.85% and 6.05%, respectively for this trait which indicating less variation exists among the genotypes. Leaves per plant showed medium heritability (37.81%) along with low genetic advance (1.06%) and low genetic advance in percent of mean (7.67%) revealed that non additive gene action in the inheritance of this trait. So, selection based on this trait was not effective.

4.2.3 Days to first male flowering

Days to first male flowering refers to phenotypic variance (0.70) was higher than the genotypic variance (0.31) that indicating environmental influence on this characters which was supported by narrow difference between phenotypic

(1.30%) and genotypic (0.86%) co-efficient of variation (Table 5). Medium heritability (43.78%) in days to first male flowering attached with low genetic advance in percentage of mean (1.17%). Medium estimate of heritability and low genetic advance for days to first male flowering suggested that this character was controlled by both additive and non-additive gene action and selection on the basis of this would not be rewarded.

4.2.4 Days to first female flowering

Days to first female flowering refers to phenotypic variance (0.59) was higher than the genotypic variance (0.15) that indicating environmental influence on this characters which was supported by narrow difference between phenotypic (1.16%) and genotypic (0.59%) co-efficient of variation (Table 5). Low heritability and low genetic advance revealed the major role of non-additive gene action in the transmission of this character from parents to off springs.

Tasseling **Silking**
Plate 6: Representing of male (L) and female (R) flowering of maize

Table 5. Estimation of genetic parameters for different characters in maize

Parameters	$\dagger^2$p	$\dagger^2$g	$\dagger^2$e	PCV	GCV	ECV	Heritability	GA (5%)	GAM
Plant height (cm)	559.36	434.90	124.46	11.04	9.74	5.21	77.75	37.88	17.69
Leaves per plant	1.86	0.70	1.15	9.85	6.05	7.77	37.81	1.06	7.67
Days to first male flowering	0.70	0.31	0.40	1.30	0.86	0.98	43.78	0.76	1.17
Days to first female flowering	0.59	0.15	0.44	1.16	0.59	1.00	25.69	0.41	0.61
Days to 75% maturity	0.82	0.51	0.31	0.87	0.68	0.54	61.86	1.15	1.11
Cob height (cm)	141.70	38.75	102.95	13.81	7.22	11.77	27.34	6.71	7.78
Cob length (cm)	1.96	1.20	0.76	7.82	6.11	4.88	61.09	1.76	9.84
Cob diameter (cm)	0.87	0.53	0.34	6.25	4.87	3.91	60.73	1.17	7.81
Rows per cob	1.34	0.45	0.89	8.14	4.72	6.64	33.55	0.80	5.63
Kernel per row	12.33	9.88	2.45	10.06	9.01	4.49	80.10	5.79	16.61
Kernel per cob	5933.76	4180.99	1752.77	15.73	13.20	8.55	70.46	111.81	22.83
1000 seeds weight (g)	1196.62	1184.07	12.55	9.90	9.84	1.01	98.95	70.51	20.17
Yield per plant (g)	659.03	649.81	9.22	15.60	15.49	1.85	98.60	52.14	31.69

σ^2p: Phenotypic variance   PCV: Phenotypic coefficient of variation   GA (5%): Genetic advance
σ^2g: Genotypic variance   GCV: Genotypic coefficient of variation   GAM: Genetic advance (% of mean)
σ^2e: Environmental variance   ECV: Environmental coefficient of variation
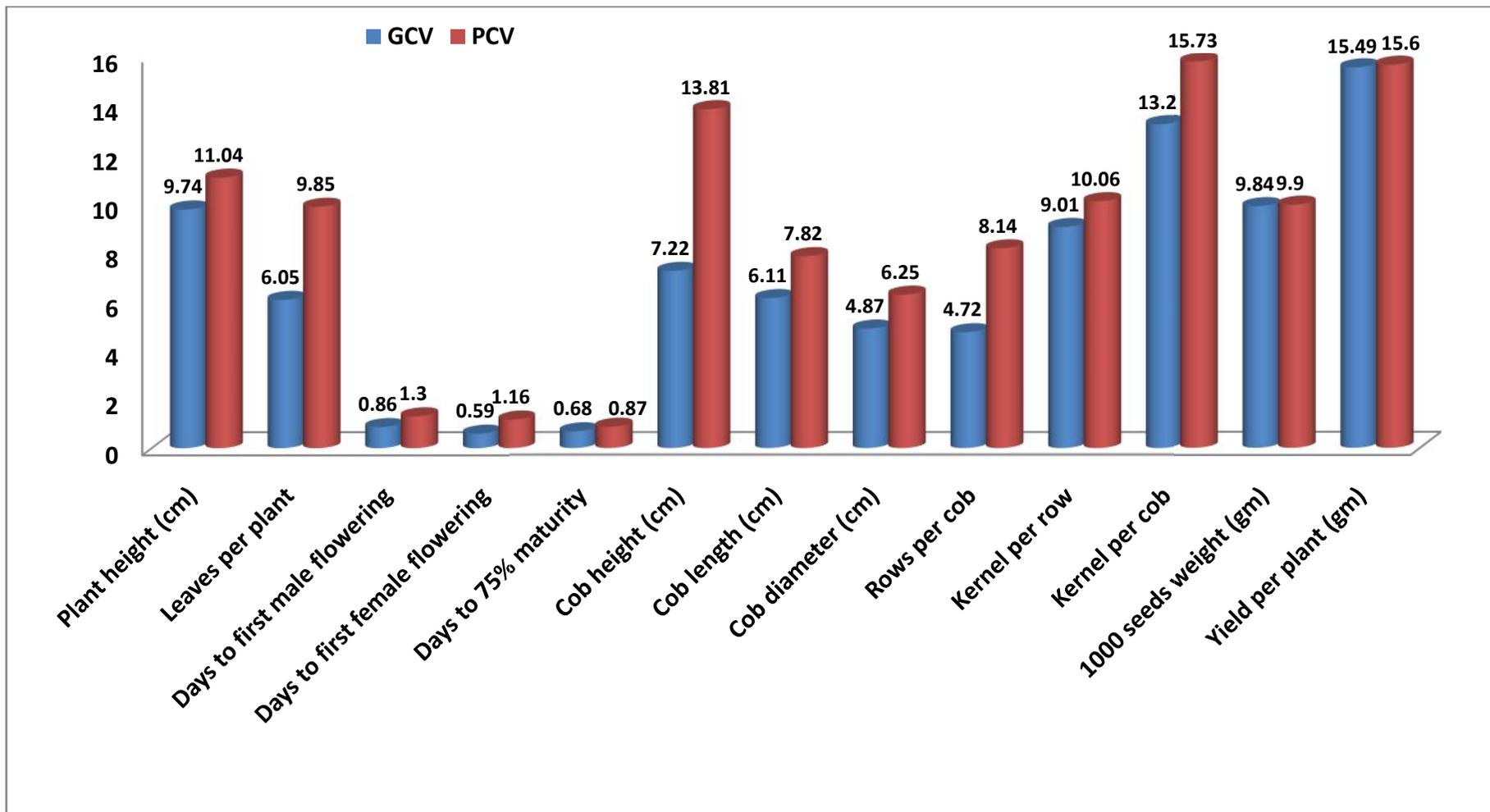
Figure 7: Genotypic and phenotypic coefficient of variation
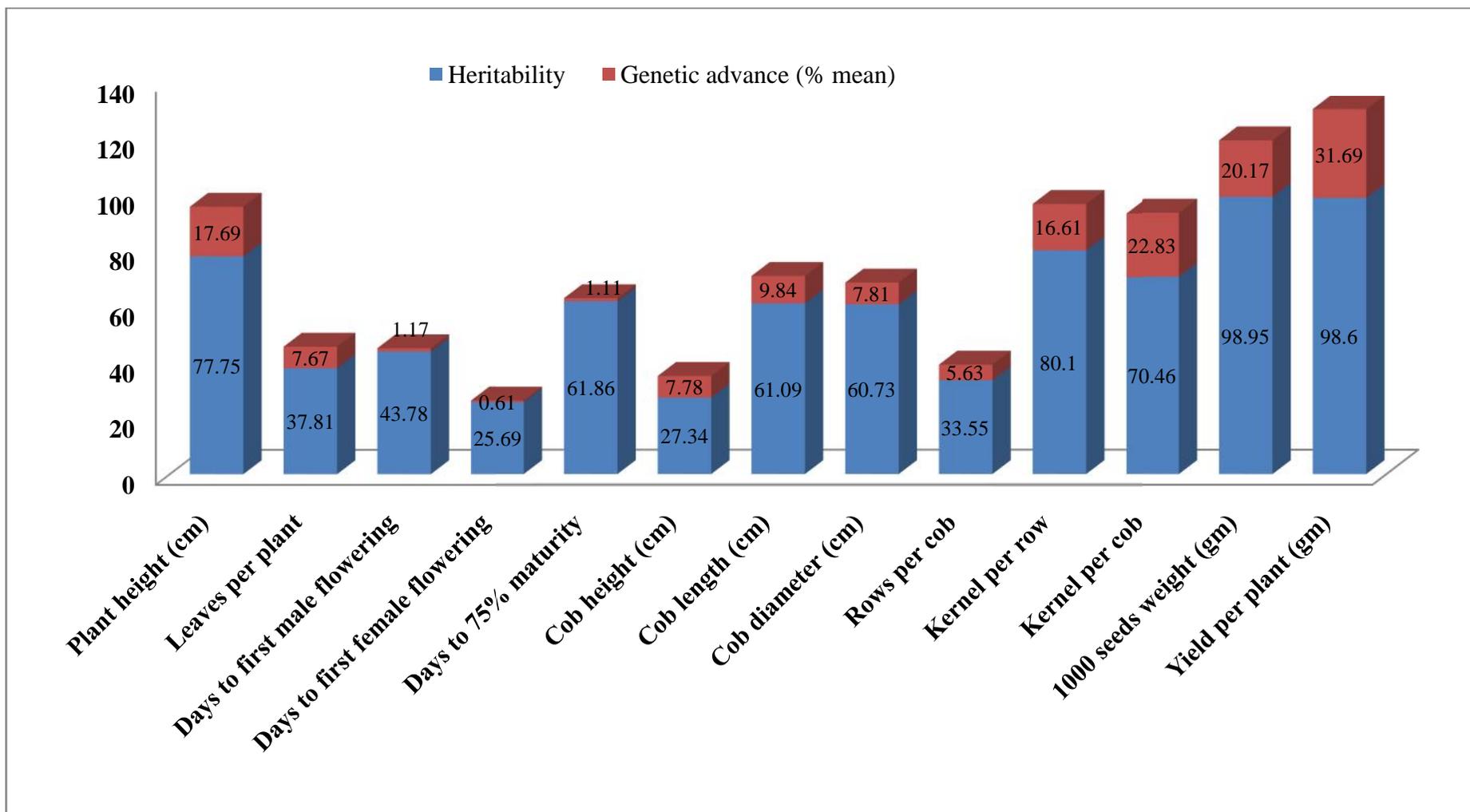
Figure 8: Heritability and Genetic advance in percent of mean

4.2.5 Days to 75% maturity

Days to 75% maturity refers to low phenotypic variance (0.82) was less higher than the genotypic variance (0.51) that indicating less environmental influence on expression of this character which was supported by narrow difference between phenotypic (0.87%) and genotypic (0.68%) co-efficient of variation (Table 5). High heritability (61.86%) along with low genetic advance in percentage of mean (1.11%). This trait is most probably controlled by both additive and non additive gene action.

4.2.6 Cob height (cm)

Cob height refers to high phenotypic variance (141.70) was higher than the genotypic variance (38.75) indicating that highly environmental influence for expression of this character (Table 5). The phenotypic coefficient of variation (13.81%) was higher than the genotypic coefficient of variation (7.22%), which suggested that environment has a significant role on the expression of this trait. Low heritability (27.34%) coupled with low genetic advance as percent of mean (7.78) was observed for this trait. These traits are most probably controlled by non additive gene action.

4.2.7 Cob length (cm)

Cob length showed less differences between phenotypic variance (1.96) and genotypic variance (1.20) indicating less environmental influence on this character and relatively moderate difference between PCV (7.82%) and GCV (6.11%) value indicating the apparent variation not only due to genotypes but also due to the moderate influence of environment (Table 5). The high heritability estimates of 61.09% with an expected genetic advance as percent of mean of 9.84 percent. High heritability coupled with low genetic advance was observed for this character, indicating limited scope for the selection upon this character due to the non-additive gene action.

4.2.8 Cob diameter (cm)

Cob diameter refers to phenotypic variance (0.87) was less higher than the genotypic variance (0.53) that indicating less environmental influence on this characters where moderate difference between phenotypic (6.25%) and genotypic (4.87%) co-efficient of variation (Table 5). High heritability (60.73%) along with low genetic advance in percentage of mean (7.81%) indicating moderate scope for the selection upon this character due to the non-additive gene action.

4.2.9 Rows per cob

Phenotypic and genotypic variance for row per cob was observed 1.34 and 0.45, respectively with moderate differences between them, suggested moderate influence of environment on the expression of the genes controlling of this trait. The phenotypic coefficient of variation (8.14%) was higher than the genotypic coefficient of variation (4.72%) (Table 5), which suggested that environment has a significant role on the expression of this trait. Low heritability (33.55%) coupled with low genetic advance in percent of mean (5.63%) attributed non-additive gene action. Similar results were reported by Chen *et al*. (1996), Satyanarayan and Kumar (1995) and Ojo*et al*. (2006).

4.2.10 Kernel per row

Kernel per row showed 12.33 and 9.88, respectively the phenotypic and genotypic variance with more differences between them indicating more environmental influences on expression of this character as well as PCV (10.06%) and GCV (9.01%) indicating presence of considerable variability among the genotypes (Table 5). High heritability (80.10%) coupled with moderate genetic advance in percent of mean (16.61) attributed to additive and non-additive gene actions. Similar results were reported by Abd El-Sattar (2003). In the contrary low heritability estimates for number of kernel per row were also reported by Rather *et al.* (2003) and Rajesh *et al.* (2013).

4.2.11 Kernel per cob

The differences between phenotypic variances (5933.76) and genotypic variances (4180.99) were high for kernel per cob indicating high environmental influence on these characters (Table 5). The value of PCV and GCV were 15.73% and 13.20% respectively for this trait which indicating that less variation exists among different genotypes. High heritability (70.46%) coupled with moderate genetic advance in percent of mean (22.83) attributed to additive gene actions indicating greater scope for the selection upon this character.

4.2.12 1000 seeds weight (g)

1000 seeds weight showed moderate phenotypic (1196.62) and genotypic (1184.07) variance with high differences indicating that they were high responsive to environmental factors and the values of GCV and PCV were 9.90% and 9.84% indicating that the genotype has considerable variation for this trait (Table 5). Similar results of PCV and GCV values for this trait were reported by Abirami *et al.* (2005). High heritability (98.95%) along with high genetic advance in percentage of mean (20.17%) revealed the possibility of predominance of additive gene action in the inheritance of this trait. Anshuman *et al.* (2013) found the high heritability and high genetic advance in percent of mean.

4.2.13 Yield per plant (g)

The phenotypic variance (659.03) appeared high difference with the genotypic variance (649.81), suggested high influence of environment on the expression of the genes controlling this trait. The phenotypic co-efficient of variation (15.60%) was little higher than the genotypic co-efficient of variation (15.49%) which suggested that environment has a little influence on the expression of this trait (Table 5). High heritability (98.60%) coupled with high genetic advance as percent of mean (31.69%) was observed for indicating that this trait is controlled by additive gene action which is very useful in selection. The higher value of heritability for grain yield per plant indicates that this character can be used as the genetic parameter for the improvement and selection of

higher yielding genotype. Crop improvement could be possible by simple selection because high heritability coupled with high genotypic variation revealed the presence of an additive gene effect.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was observed for kernel per cob, 1000 seeds weight and yield per plant. These traits are most probably controlled by additive gene action which is very useful in selection.

Plate 7: Photograph showing seed variation among different maize genotypes (Representative)

4.3 Correlation analysis

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 would surely help to identify the characters to make selection for higher yield with a view to determine the extent and nature of relationship prevailing among yield contributing characters. Hence, an attempt has been made to study the character association in the maize genotype at both the levels.

For clear understanding correlation coefficients are separated into genotypic and phenotypic level in Table 7. The genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the genetic reason of association. In some cases phenotypic correlation coefficient were higher than genotypic correlation coefficient indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level.

Table 6. Genotypic (G) and phenotypic (P) correlations among different pairs of traits for different genotype of maize

		PH	LPP	DFMF	DFFF	DM	CH	CL	CD	RPC	KPR	KPC	TSW
LPP	G	-0.119											
	P	-0.119											
DFMF	G	-0.066	0.495**										
	P	-0.104	0.292**										
DFFF	G	-0.134	0.649**	0.909**									
	P	-0.116	0.203	0.898**									
DM	G	-0.109	0.177	0.240*	0.121								
	P	-0.139	0.048	0.013	-0.077								
CH	G	0.923**	-0.100	-0.037	-0.073	-0.162							
	P	0.888**	-0.077	-0.020	-0.035	-0.110							
CL	G	0.164	0.686**	0.030	0.061	0.122	0.184						
	P	0.111	0.332**	0.037	0.048	0.077	0.160						
CD	G	-0.386**	0.278**	0.141	0.103	0.290**	-0.386**	0.184					
	P	-0.262*	0.086	0.116	0.053	0.149	-0.309**	0.135					
RPC	G	0.133	0.069	0.464**	0.426**	0.132	0.076	0.232*	0.334**				
	P	0.028	0.101	0.259*	0.129	0.153	0.041	0.066	0.328**				
KPR	G	0.214*	0.214*	0.125	0.072	0.395**	0.196	0.716**	0.155	0.274**			
	P	0.185	0.136	0.040	-0.007	0.263*	0.187	0.521**	0.048	0.139			
KPC	G	0.360**	0.347**	0.183	0.081	0.261*	0.290**	0.374**	0.443**	0.498**	0.637**		
	P	0.249*	0.266*	0.122	0.016	0.233*	0.247*	0.301**	0.334**	0.457**	0.449**		
TSW	G	-0.323**	0.475**	0.038	0.201	0.082	-0.278**	0.320**	0.359**	-0.189	0.003	-0.112	
	P	-0.282**	0.283**	0.029	0.100	0.075	-0.274**	0.266*	0.285**	-0.097	0.004	-0.091	
YPP	G	0.126	0.036	0.093	0.091	0.162	0.129	0.343**	0.492**	0.151	0.247*	0.481**	0.162
	P	0.110	0.038	0.082	0.059	0.115	0.126	0.273**	0.371**	0.093	0.234*	0.413**	0.162

** = Significant at 1% level, * = Significant at 5% level, PH: plant height (cm), LPP: leaves per plant, DFMF: days to first male flowering, DFFF: days to first female flowering, DM: days to 75% maturity, CH: cob height (cm), CL: cob length (cm), CD: cob diameter (cm), RPC: rows per cob, KPR: kernel per row, KPC: kernel per cob, TSW: 1000 seeds weight (g) and YPP: yield per plant (g).
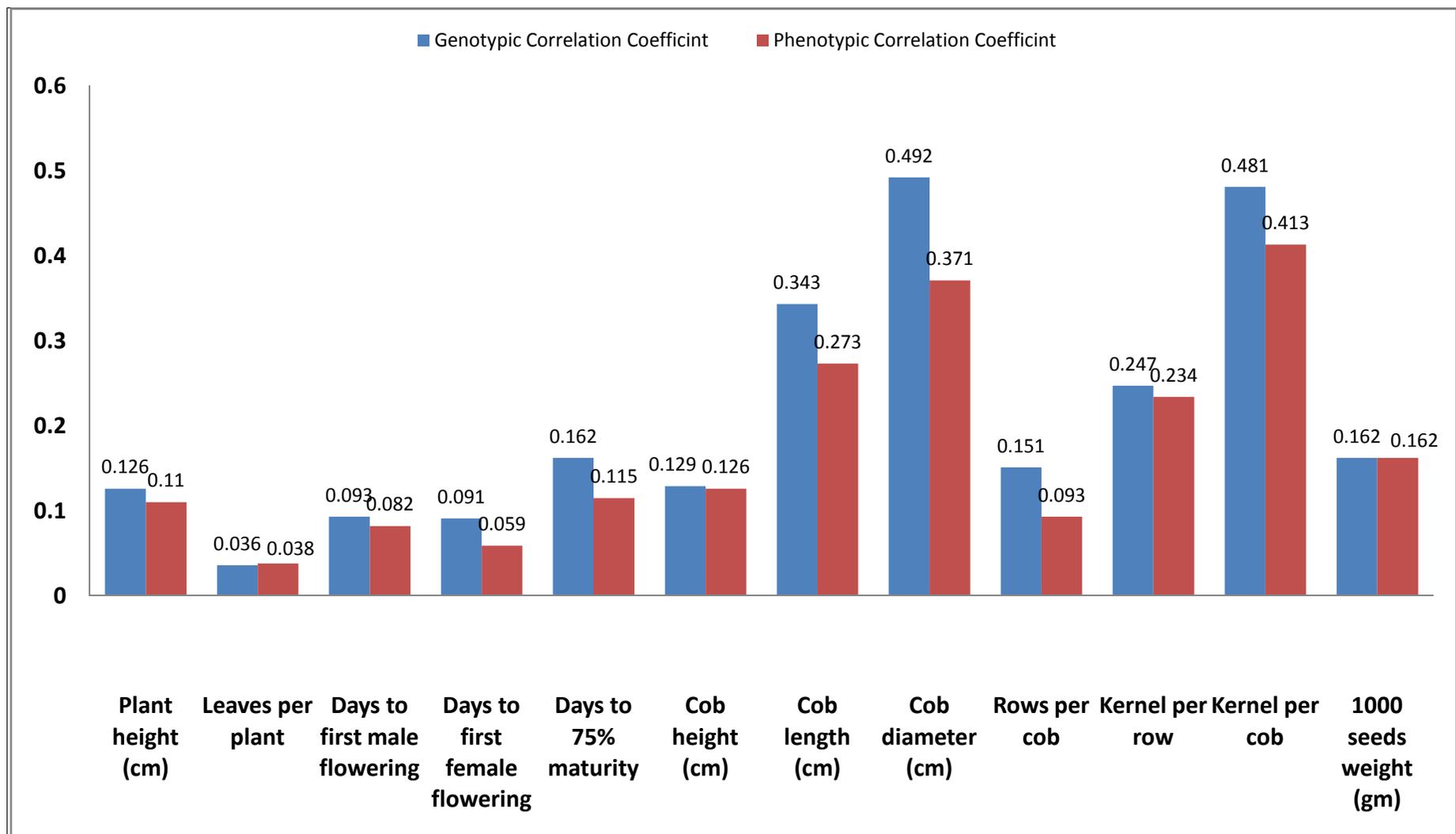
Figure 9: Genotypic and phenotypic correlation of different yield contributing traits with yield

4.3.1 Plant height

Plant height had highly significant and positive correlation with cob height (0.923 and 0.888), kernel per cob (0.360 and 0.249) at both genotypic and phenotypic levels. 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 diameter. Plant height has positive correlation with yield (0.126 and 0.110). Plant height (0.586) was positively and significantly correlated with grain yield per plant (Triveni *et al.*, 2014). In the contrary, Srekove *et al.* (2011) reported a negative correlation between grain yield and plant height. It was negatively significant correlation with cob diameter (-0.386 and -0.262) and 1000 seeds weight (-0.323 and -0.282) at both levels.

4.3.2 Leaves per plant

Number of leaves per plant showed positive significant interaction with days to first male flowering (0.495 and 0.292), days to first female flowering (0.649 and 0.203), cob length (0.686 and 0.332), kernel per cob (0.347 and 0.266) and 1000 seeds weight (0.475 and 0.283) (Table 6). Leaves per plant had positive correlation with grain yield (0.036 and 0.038). Triveni *et al.* (2014) found that the number of leaf per plant of maize was highly significantly and positively correlated with grain yield which is in agreement with where support the present findings. Results of this study imply that maize grain yield could be improved by considering number of leaf per plant.

4.3.3 Days to first male flowering

Highly significant positive association was recorded for days to first male flowering of maize genotypes with days to first female flowering (0.909 and 0.898) and rows per cob (0.464 and 0.259) at both levels (Table 6).

4.3.4 Days to first female flowering

Days to first female flowering was observed highly significant positive association with rows per cob (0.426) at genotypic level (Table 6). It was positively correlated with grain yield (0.091 and 0.059).

4.3.5 Days to 75% maturity

Significant positive correlation was observed for days to 75% maturity with kernel per row (0.395 and 0.263), kernel per cob (0.261 and 0.233) at both levels (Table 6). It had significant positive correlation with cob diameter (0.290) at genotypic level. Positive correlation was observed of days to 75% maturity with grain yield (0.162 and 0.115) at both genotypic and phenotypic levels.

4.3.6 Cob height (cm)

Cob height had highly significant and positive correlation with kernel per cob (0.290 and 0.247) at both the levels. It had positive correlation with cob length (0.184 and 0.160), kernel per row (0.196 and 0.187) and yield per plant (0.129 and 0.126) at both levels. Cob height had negatively highly significant correlation with cob diameter (-0.386 and -0.309) and 1000 seeds weight (-0.278 and -0.274).

4.3.7 Cob length (cm)

Cob length showed highly significant and positive correlation with kernel per row (0.716 and 0.521), kernel per cob (0.374 and 0.301), 1000 seeds weight (0.320 and 0.266), yield per plant (0.343 and 0.273) at both levels. The result indicated that grain yield was positively and significantly associated with cob length (0.618) and plant height with cob length (0.471) reported by Pandey*et al.* (2017).

4.3.8 Cob diameter (cm)

Cob diameter exhibited significant and positive association with rows per cob (0.334 and 0.328), kernel per cob (0.443 and 0.334), 1000 seeds weight (0.359 and 0.285) and grain yield per plant (0.492 and 0.371) at both levels.

4.3.9 Rows per cob

The number of row per cob had a positive and significant correlation with kernel per cob (0.498 and 0.457) at both levels. Significant positive correlation observed with kernel per rows (0.274) at genotypic level. Number of rows per cob negatively correlated with 1000 grain weight (-0.189 and -0.097) at both levels. This results supported by Amin *et al.* (2003) and Mohammadi *et al.* (2003) who found number of rows per cob showed significant and negative correlations with 1000-seed weights.

4.3.10 Kernel per row

The number of kernel per row had positive and highly significant correlation with kernel per cob (0.637 and 0.449) and significant correlation with yield per plant (0.247 and 0.234) at both levels. Amin *et al.* (2003) indicated that number of kernels per row was the highest contributors to variation in grain yield directly or indirectly. Kernels per row (0.656) were positively and significantly associated grain yield per plant reported by Pandey *et al.* (2017).

4.3.11 Kernel per cob

Kernel per cob had positively and significantly correlated with yield per plant (0.481 and 0.413) at both genotypic and phenotypic levels.

4.3.12 1000 seeds weight (g)

Positive correlations were observed of 1000 seeds weight with yield per plant (0.162 and 0.161) at both the genotypic and phenotypic level (Table 6). Grain yield is considered to have positive correlation with hundred seed weight (Ajmal *et al.*,2000). Sumathi *et al.* (2005) also found medium strong correlative relation between hundred grain weight and grain yield per plant, 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 co-efficient analysis

Association of character determined by correlation co-efficient might not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on total yield per plant. As a matter of fact, in order to find out a clear picture of the inter-relationship between total yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at genotypic level which also measured the relative importance of each component. Grain yield per plant was considered as reluctant (dependent) variable and plant height, leaves per plant, days to first male flowering, days to first female flowering, days to 75% maturity, cob height, cob length, cob diameter, rows per cob, kernel per row, kernel per cob and 1000 seeds weight were casual (independent) variables. Estimation of direct and indirect effect of path co-efficient analysis for maize was presented in Table 7.

4.4.1 Plant height (cm)

Plant height had positive direct effect (0.282) on grain yield per plant (Table 8) and it was contrary with the results of Pandey *et al.* (2017) and they found negative direct effect of plant height on grain yield. Plant height is an important trait that effect grain yield. Taller plants need more plant nutrients to complete more vegetative growth than reproductive phase that results in late maturation of cob. It showed highly positive indirect effect through cob height (0.434) and kernel per rows (0.237) and negligible positive indirect effect via days to first male flowering (0.049), days to maturity (0.017), rows per cob (0.042) and 1000 seeds weight (0.026). The plant height showed highly positive indirect effect for cob height (0.1421) (Jakhar *et al.*, 2017). It showed negative indirect effect through kernel per cob (-0.280), cob diameter (-0.361), cob length (-0.183), leaves per plant (-0.111) and days to first female flowering (-0.026). The results indicated that plant height had positive direct effect (0.282) on yield because of its positive indirect effect through cob height and kernel per row (Emer, 2011 and Mohan *et al.* 2002).

4.4.2 Leaves per plant

Number of leaves per plant had positive direct effect (0.939) on grain yield. It was found that number of leaves per plant had positive indirect effect on grain yield through cob diameter (0.260) and kernel per row (0.237), whereas negligible positive indirect effect via days to first female flowering (0.128) and rows per cob (0.022) (Table 7).

4.4.3 Days to first male flowering

Path analysis revealed that days to first male flowering had negative direct effect (-0.746) on grain yield per plant (Table 7). It showed positive indirect effect through leaves per plant (0.465) and days to first female flowering (0.208) and it was negligible positive indirect effect through rows per cob (0.146), kernel per rows (0.138) and cob diameter (0.132), whereas it showed negative indirect effect via kernel per cob (-0.142), days to maturity (-0.036), cob height (-0.016) and cob length (-0.033).

4.4.4 Days to first female flowering

Path analysis revealed those days to first female flowering had positive direct effect (0.197) on grain yield per plant (Table 7) and it was supported by Pandel *et al.* (2017) and Lingaiah *et al.* (2014). It showed more positive indirect effect through leaves per plant (0.609) and negligible positive effect via row per cob (0.134), cob diameter (0.097), and kernel per row (0.079). On the other hand days to first female flowering showed negative indirect effect through days to first male flowering (-0.790), cob length (-0.069), kernel per cob (-0.063), cob height (-0.031), plant height (-0.038) and days to maturity (-0.018).

4.4.5 Days to 75% maturity

Path analysis revealed that days to 75% maturity had negative direct effect (-0.152) on grain yield per plant (Table 7). It showed positive indirect effect through kernel per row (0.437), cob diameter (0.271), leaves per plant (0.166), rows per cob (0.042) and days to first female flowering (0.024).On the other hand, days to maturity represented negative indirect effect via days to first male

Table 7. Partitioning of genotypic correlations into direct (bold and underline) and indirect effects of different traits by path analysis of maize

	PH	LPP	DFMF	DFFF	DM	CH	CL	CD	RPC	KPR	KPC	TSW	Genotypic Correlation with YPP
PH	**0.282**	-0.111	0.049	-0.026	0.017	0.434	-0.183	-0.361	0.042	0.237	-0.280	0.026	0.126
LPP	-0.033	**0.939**	-0.369	0.128	-0.027	-0.042	-0.768	0.260	0.022	0.237	-0.270	-0.039	0.036
DFMF	-0.019	0.465	**-0.746**	0.208	-0.036	-0.016	-0.033	0.132	0.146	0.138	-0.142	-0.003	0.093
DFFF	-0.038	0.609	-0.790	**0.197**	-0.018	-0.031	-0.069	0.097	0.134	0.079	-0.063	-0.016	0.091
DM	-0.031	0.166	-0.179	0.024	**-0.152**	-0.069	-0.137	0.271	0.042	0.437	-0.203	-0.007	0.162
CH	0.289	-0.094	0.028	-0.014	0.025	**0.425**	-0.205	-0.361	0.024	0.217	-0.225	0.023	0.129
CL	0.046	0.645	-0.022	0.012	-0.019	0.078	**-1.119**	0.172	0.073	0.793	-0.290	-0.026	0.343**
CD	-0.109	0.261	-0.105	0.020	-0.044	-0.164	-0.205	**0.935**	0.105	0.172	-0.345	-0.029	0.492**
RPC	0.038	0.065	-0.347	0.084	-0.020	0.032	-0.260	0.312	**0.315**	0.303	-0.387	0.015	0.151
KPR	0.060	0.201	-0.093	0.014	-0.060	0.083	-0.801	0.145	0.086	**1.107**	-0.495	0.000	0.247*
KPC	0.102	0.326	-0.137	0.016	-0.040	0.123	-0.418	0.414	0.157	0.706	**-0.778**	0.009	0.481**
TSW	-0.091	0.446	-0.028	0.039	-0.012	-0.118	-0.358	0.335	-0.059	0.003	0.087	**-0.081**	0.162

Residual effect: 0.251   ** = Significant at 1% level.   * = Significant at 5% level.

PH: plant height (cm), LPP: leaves per plant, DFMF: days to first male flowering, DFFF: days to first female flowering, DM: days to 75% maturity, CH: cob height (cm), CL: cob length (cm), CD: cob diameter (cm), RPC: rows per cob, KPR: kernel per row, KPC: kernel per cob, TSW: 1000 seeds weight (g) and YPP: yield per plant (g).

flowering (-0.179), cob length (-0.137), kernel per cob (-0.203) and cob height (-0.069).

4.4.6 Cob height (cm)

Cob height had positively direct effect (0.425) on grain yield per plant (Table 8). Cob height is an important trait that effect grain yield. Taller cob height denoted late maturation of cob. It showed positive indirect effect through plant height (0.289), kernel per row (0.217), days to first male flowering (0.028) and days to maturity (0.025). It showed negative indirect effect through cob diameter (-0.361), kernel per cob (-0.225) and cob length (-0.205). In the contrary, cob height showed highly negative indirect effect for plant height (-0.0852) reported by Jakhar *et al.* (2017).

4.4.7 Cob length (cm)

Cob length had negative direct effect (-1.119) on grain yield. It was found that cob length had positive indirect effect on grain yield through leaves per plant (0.645), kernel per row (0.793) and cob diameter (0.172) (Table 7). Wannows *et al.* (2010) reported similar findings. These results coincide with those obtained by Amin *et al.* (2003); AL-Ahmad (2004) and Sadek *et al.* (2006). Its indirect effects via plant height and number of leaves per plant also negative (Parh *et al.*, 1986).

4.4.8 Cob diameter (cm)

Path analysis revealed that cob diameter had positive direct effect (0.935) on yield per plant (Table 7). It showed negligible positive indirect effect through leaves per plant (0.261), kernel per row (0.172), rows per cob (0.105) and days to first female flowering (0.020), whereas cob diameter showed negative indirect effect through kernel per cob (-0.345), cob length (-0.205), cob height (-0.164), days to first male flowering (-0.105) and plant height (-0.109). The cob diameter showed highly positive indirect effect for cob height (0.90) reported by Jakhar *et al.* (2017) and it was similar with this present experiment.

4.4.9 Rows per cob

Number of row per cob revealed positive direct effect (0.315) on grain yield per plant. It was positive indirect effect on grain yield through kernel per row (0.303), cob diameter (0.312), cob height (0.032) and days to first female flowering (0.084). These results were in agreement with results which Ahmad and Saleem (2003) and Najeeb *et al*. (2009) found in their research. Rafiq *et al*. (2010) also found positive direct effect of kernel row number on grain yield, but it wasn't significant.

4.4.10 Kernel per row

Path analysis revealed that number of kernels per row had highest positive direct effect (1.107) on yield per plant (Table 8). It showed negligible positive indirect effect through leaves per plant (0.201), cob diameter (0.145), rows per cob (0.086), plant height (0.060) and days to first female flowering (0.014), whereas number of kernels per row showed negative indirect effect through cob length (-0.801), kernel per cob (-0.495), days to maturity (-0.060) and days to first male flowering (-0.093). The number of kernels per row showed highly positive indirect effect for cob height (2.00) reported by Jakhar *et al.* (2017) and it was similar with this present experiment.

4.4.11 Kernel per cob

Number of kernel per cob had negative direct effect (-0.778) on grain yield. It was found that number of kernel per cob had high positive indirect effect on grain yield through kernel per row (0.706) and cob diameter (0.414), whereas negligible positive indirect effect via leaves per plant (0.326), cob height (0.123), rows per cob (0.157) and plant height (0.102) (Table 7).

4.4.12 1000 seeds weight (gm)

Path analysis revealed that weight of 1000-seeds weight had negative direct effect (-0.081) on yield per plant (Table 7). It showed high positive indirect effect through leaves per plant (0.446) and cob diameter (0.335) and negligible positive indirect effect through days to first female flowering (0.039) and

kernel per row (0.003). While this trait was showed negative indirect effect on yield via cob length (-0.358), cob height (-0.118), plant height (-0.091) and rows per cob (-0.059).

The estimation of correlation indicates only the extent and nature of association between yield and its attributes, but does not show the direct and indirect effects of different yield attributes on yield per se. Grain yield is dependent on several characters which are mutually associated; these will in turn impair the true association exiting between a component and grain yield. A change in any one component is likely to disturb the whole network of cause and effect. Thus, each component has two paths of action viz., the direct influence on grain yield, indirect effect through components which are not revealed from the correlation studies. The highly positive and direct effect on yield was exhibited by kernel per row (1.107), cob diameter (0.935), leaves per plant (0.939), cob height (0.425), rows per cob (0.315), plant height (0.282) and days to first female flowering (0.197) indicating the effectiveness of direct selection, where as direct and negative effects were exhibited by days to first male flowering (-0.746), cob length (-1.119), kernel per cob (-0.778) and days to maturity (-0.152) indicating the effectiveness of indirect selection.

4.5 Genetic diversity analysis

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 for desirable trait. Its magnitude in desirable direction is preferable.

4.5.1 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 30 maize genotypes were grouped into five different clusters. It is stated that highest eight (26.66%) genotypes were included in cluster III and it was followed by six (20%) in both clusters I and II, five (16.67%) genotypes were

in both clusters IV and V. The composition of clusters with different genotypes is presented in Table 8.

From Table 8 cluster III had the maximum eight genotypes (G2, G4, G7, G8, G11, G13, G19, G20) followed by cluster I with genotypes G3, G5, G15, G18, G28, G30 and cluster II with genotypes G6, G12, G14, G22, G25, G26 whose both had six genotypes each. Cluster IV (G1, G9, G16, G21, G29) and V (G10, G17, G23, G24, G27) had five genotypes each.

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 9. The results showed that the first principal axis (PCA I) was largely accounted for the variation among the genotypes which alone contributed 25.05% of the total variation among the genotypes. The first seven axes (PCA I-PCA XII) of the principal component with eigen values above unity accounted for 87.80% of the total variation among the thirteen characters. The rest five characters contributed remaining 12.20% 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 10.

4.5.3 Inter cluster distance

The inter cluster D^2 values are given in Table 10 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 11. The inter cluster D^2 values were maximum (10.747) between the cluster I and V, followed by I and II (8.025) & III and V (6.083) (Table 11). 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 V indicated the genotypes in these clusters were diversed than those clusters.

Table 8. Distribution of 30 genotypes in different clusters

Cluster no.	Genotypes	No. of populations	Percent
I	G3, G5, G15, G18, G28, G30	6	20
II	G6, G12, G14, G22, G25, G26	6	20
III	G2, G4, G7, G8, G11, G13, G19, G20	8	26.66
IV	G1, G9, G16, G21, G29	5	16.67
V	G10, G17, G23, G24, G27	5	16.67
	Total	30	100

Table 9. Eigen values and yield percent contribution of 13 characters of 30 genotypes

Principal component axes	Eigen values	Percent variation	Cumulative percent of % variation
I	2.345	25.05	25.05
II	2.281	20.34	45.39
III	2.212	15.33	60.72
IV	2.087	10.83	71.55
V	2.012	6.73	78.28
VI	1.985	5.9	84.18
VII	1.253	3.62	87.80
VIII	0.945	3.5	91.30
IX	0.657	2.3	93.60
X	0.414	2.6	96.20
XI	0.293	2.23	98.43
XII	0.211	1.33	99.76
XIII	0.025	0.24	100.00

Table 10. Intra (Bold) and inter cluster distances (D^2) for 30 genotypes

Cluster	I	II	III	IV	V
I	**2.12**	8.025	4.865	5.235	10.747
II		**0.46**	3.191	4.314	3.799
III			**1.87**	2.244	6.083
IV				**0.83**	5.767
V					**0.23**

Table 11. 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	III (4.865)	V (10.747)
2	II	III (3.191)	I (8.025)
3	III	IV (2.244)	V (6.083)
4	IV	III (2.244)	V (5.767)
5	V	II (3.799)	I (10.747)
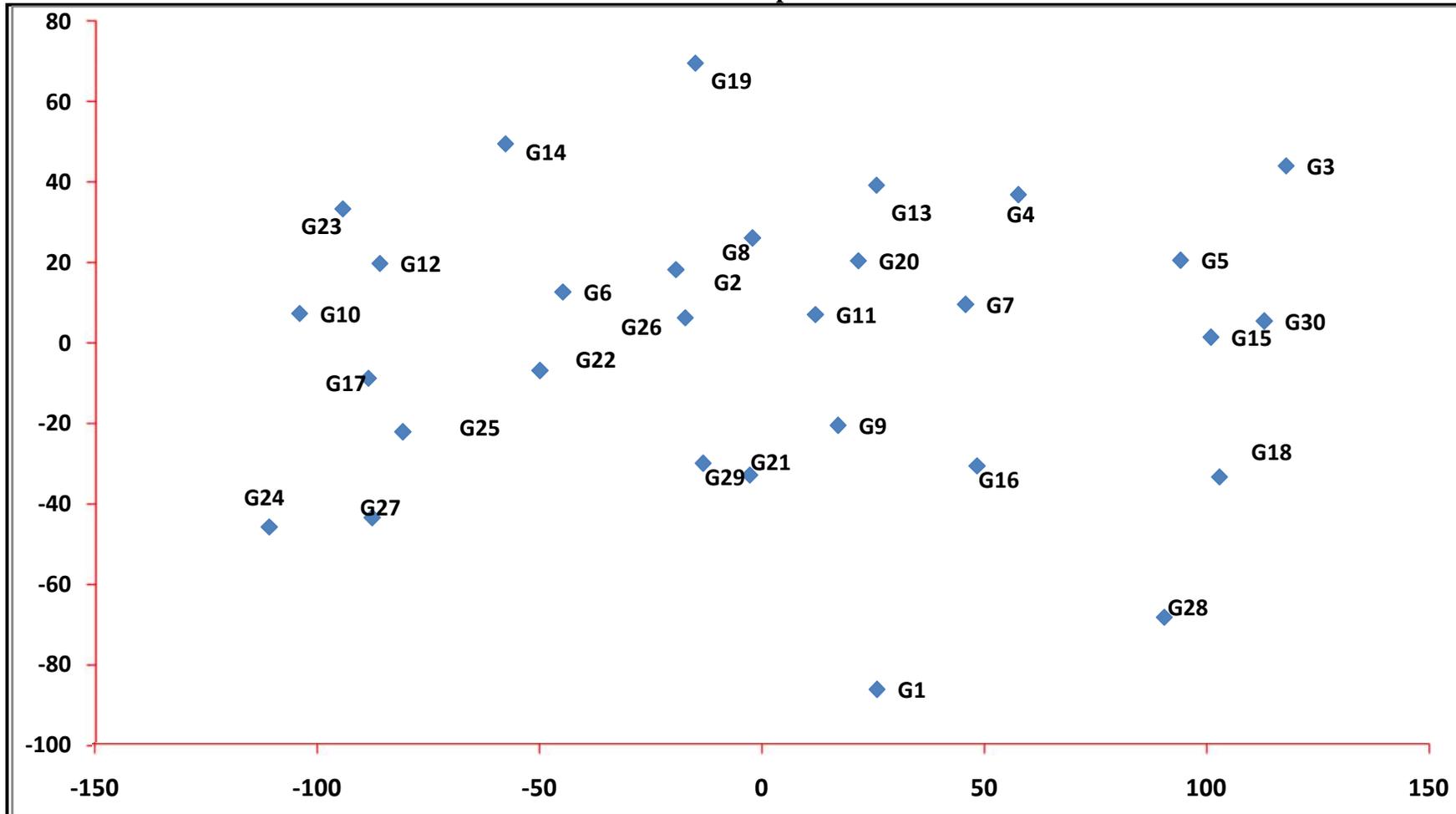
Figure 10: Scattered diagram of 30 maize genotypes
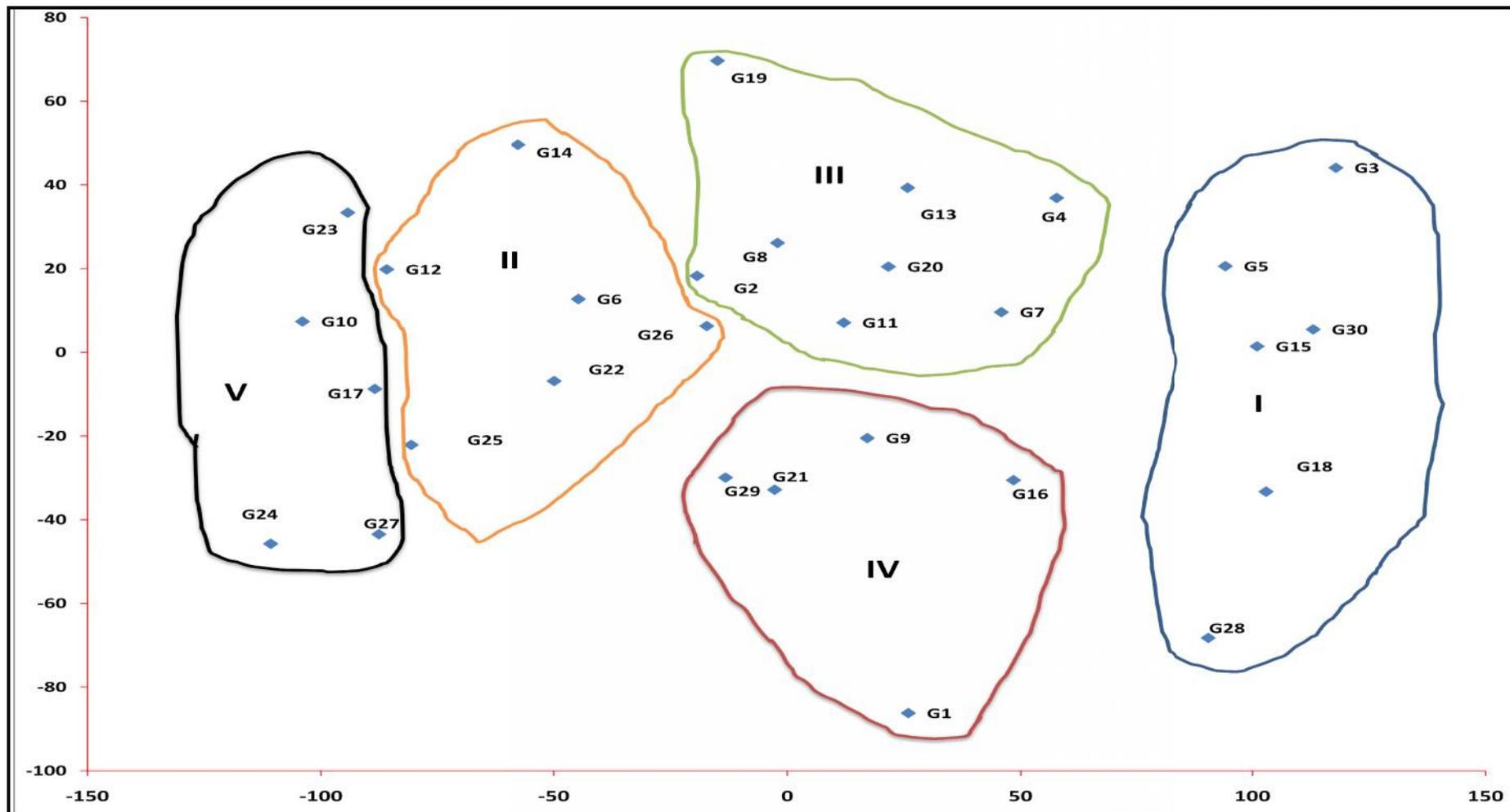
Figure 11.Cluster diagram showing genotypes grouping in different clusters of 30 genotypes of maize

Cluster V was the most diverse as many other clusters showed the maximum inter cluster distance with it (Table 11). The minimum distance observed between clusters III and IV (2.244) indicated close relationship among the genotypes included.

4.5.4 Intra cluster distance

The intra cluster D^2 values were given in Table 10. 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 (2.12) followed by cluster III (1.87), cluster IV (0.83), cluster II (0.46) and lowest in cluster V (0.23). The intra cluster distances in all the five 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 five groups, which indicated that considerable diversity existed among the genotypes (Fig. 11) .

4.5.6 Cluster mean analysis

The cluster means of 13 different characters (Table 12) were compared and indicated considerable differences between clusters for all the characters studied. Maximum plant height was observed in cluster II (229.2), whereas minimum plant height was observed in cluster IV (191.6). Maximum (14.60) and minimum (13.44) leaf per plant were observed in cluster V and I, respectively. Genotypes in cluster I showed the lowest days to first male flowering (64.06) and cluster III had the highest mean (64.63). Maximum (66.53) and minimum (66.17) days to first female flowering were observed in cluster IV and I, respectively. Maximum days to maturity were observed in cluster V (104.53), whereas minimum days to maturity were observed in cluster I (103.89).

Table 12. Cluster mean for 13 yield and yield related characters in 30 maize genotypes

Characters	I	II	III	IV	V
Plant height (cm)	206.8	229.2**	218.9	191.6*	219.9
Leaves per plant	13.44*	13.56	13.67	14.13	14.60**
Days to first male flowering	64.06*	64.56	64.63**	64.53	64.40
Days to first female flowering	66.17*	66.44	66.50	66.53**	66.27
Days to 75% maturity	103.89*	104.22	104.04	104.40	104.53**
Cob height (cm)	84.6	91.2**	87.4	78.4*	88.1
Cob length (cm)	17.7	18.4	17.2*	18.1	18.6**
Cob diameter (cm)	14.5*	15.0	14.7	15.1	15.7**
Rows per cob	13.8	14.6	14.2	13.7*	14.8**
Kernel per row	31.8*	36.3	34.2	35.9	37.1**
Kernel per cob	388.8*	538.3	474.3	477.9	588.9**
1000 seeds weight (gm)	362.4	332.5	325.5*	384.5**	358.2
Yield per plant (gm)	147.1*	196.2**	148.4	172.2	165.5

* Lower value
** Higher value

Cluster II had the maximum cob height (91.2), cluster IV had the minimum cob height (78.4). Maximum cob length was observed in the cluster V (18.6), whereas minimum cob length was observed in cluster III (17.2). Genotypes in cluster I showed the highest cob diameter (15.7) and cluster I had the lowest mean value (14.5). The maximum rows per cob (14.8) was observed in the cluster V, whereas minimum rows per cob (13.7) was observed in cluster IV. Kernels per row were the highest in cluster V with a mean value of (37.1) and it was least in genotypes belongs to the cluster I (31.8). Kernels per cob were the highest in cluster V with a mean value of (588.9) and it was least in genotypes belongs to the cluster I (388.8). Maximum 1000-seed weight was observed in cluster IV (384.5), whereas minimum 1000-seed weight was observed in cluster III (325.5). Highest yield per plant was recorded by the cluster II (196.2) while cluster I (147.1) 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 13. 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 (0.0211), leaf per plant (0.0554), days to first female flowering (0.5214), days to maturity (0.2456), cob diameter (0.4904), kernel per row (0.0869), kernel per cob (0.0514) and yield per plant (0.0035) were important because all these characters had positive signs. In vector (Z_2) obtained from PCA, the important

Table 13. Relative contributions of the thirteen characters of 30 genotypes to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Plant height (cm)	0.0211	0.0683
Leaves per plant	0.0554	0.1034
Days to first male flowering	-0.2874	0.1525
Days first female flowering	0.5214	0.3458
Days to 75% maturity	0.2456	0.2345
Cob height(cm)	-0.0506	-0.1022
Cob length(cm)	-0.2445	0.1126
Cob diameter(cm)	0.4904	-0.0038
Rows per cob	-0.4504	0.5209
Kernel per row	0.0869	-0.0684
Kernel per cob	0.0514	-0.0117
1000 seeds weight(g)	-0.0031	-0.0283
Yield per plant(g)	-0.0035	0.0301

characters responsible for genetic divergence in the axis of differentiation were plan height, leaves per plant, days to first female flowering, days to maturity, cob length, row per cob, kernel per row, kernel per cob and yield per plant were important because all these characters had positive signs.

On the other hand days to first male flowering, cob height, cob length, rows per cob and 1000 seeds weight possessed the negative sign in the first axis of differentiation and days to first male flowering, cob height, cob diameter 1000 seeds weight possessed negative signs in the second axis of differentiation that means it had minor role in the genetic diverse. Plant height, Leaf per plant, days to first female flowering, days to maturity, kernel per row, kernel per cob and yield per plant 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.

CHAPTER V

SUMMARY AND CONCLUSION

Analysis of variance revealed highly significant difference among the maize genotypes for all the characters studied. The minimum and maximum plant height was observed in the genotype G1 (152.47 cm) and G14 (250.20), respectively. The leaves per plant was maximum in the genotype G21 (16.00) and minimum in the genotype G3 (11.67). The minimum days to first male flowering was recorded in the genotype G5 (62.00) and maximum in G18 (65.67). Days to first female flowering as minimum were observed in G5 (64.67) and maximum in G11 (67.67). Minimum days to maturity were noted in G4 (103.00) while maximum in G11 (105.67). Minimum cob height was noted in G9 (63.68) while maximum in G14 (99.67). The cob length was maximum in G26 (20.80) and minimum in G11 (15.57) observed. The highest number of rows per cob was observed in genotype G15 (15.50) while lowest in genotype G4 (12.77). Genotype G24 (39.33) shown the highest number of kernels per row and the genotype G6 (28.77) represented the lowest value. 1000-seeds weight ranged from 287.85 g to 429.67 g which was observed in genotype G19 and G28, respectively. The highest grain yield per plant was observed in the genotype G25 (213.00). The lowest grain yield per plant was observed in the genotype G15 (120.33).

Characters like cob height (13.81 and 7.22), kernel per row (10.06 and 9.01), kernel per cob (15.73 and 13.20) and yield per plant (15.60 and 15.49) exhibited more 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 high differences between phenotypic and genotypic co-efficient of variation were leaves per plant, cob height and rows per cob which indicated these traits were mostly dependent on the environment condition. Amongst the characters, more genotypic co-efficient of

variation was recorded for number of kernels per cob (13.20) and yield per plant (15.49). The maximum genotypic and phenotypic variations were 4180.99 and 5933.76 respectively in kernels per cob.

The highest estimated heritability among the thirteen characters of maize was 98.95% for 1000 seeds weight and the lowest was 25.69% for days to first female flowering. The highest genetic advance among the thirteen characters was found in kernels per cob is 111.81 and the lowest genetic advance was carried out in days to first female flowering (0.41). The maximum genetic advance in percent of mean was observed for yield per plant (31.69), followed by kernels per cob (22.83), 1000 seeds weight (20.17) and kernel per row (16.61). In the present study, high heritability coupled with high genetic advance as per cent of mean was observed for kernel per cob (70.46 and 22.83), 1000 seeds weight (98.95 and 20.17) and grain yield per plant (98.60 and 31.69). These traits are most probably controlled by additive gene action which is very useful in selection. High heritability with medium genetic advance in percent of mean was observed in plant height (77.75 and 17.69) and kernel per row (80.10 and 16.61) indicating these traits are controlled by both additive and non additive gene action.

Considering both genotypic and phenotypic correlation co-efficient among thirteen yields contributing characters of 30 maize genotypes, yield per plant was positively and significantly correlated with cob length. cob diameter, kernel per row and kernel per cob. Path analysis revealed that plant height, leaves per plant, days to first female flowering, cob height, cob diameter, rows per cob and kernel per row showed positive direct effects on yield per plant indicating these traits effectiveness for direct selection. On the other hand days to first male flowering, days to maturity, cob length, kernel per cob and 1000 seeds weight showed negative direct effects on yield per plant indicating the effectiveness of indirect selection.

As per principal component analysis, D^2 statistics and cluster analysis, the genotypes were grouped into five different clusters. Cluster III consist of

highest eight genotypes followed by cluster I & II with six genotypes each. Cluster IV and V consisted five genotype of each. The maximum inter-cluster divergence was observed between cluster I and V (10.747) followed by cluster I and II (8.025) and III and V (6.083). The maximum values of inter-cluster distance indicated that the varieties belonging to cluster I was far diverged from those of cluster V. The inter cluster distance was minimum between cluster IV and V (5.767). The highest intra-cluster distances was computed for cluster I (2.12) composed of six genotypes followed by the cluster III (1.87) composed of eight genotypes.

In respect of cluster mean performances of different cluster revealed that cluster V can be selected for highest leaves per plant, days to maturity, cob length, cob diameter, rows per cob, kernel per rows and kernel per cob. Cluster II was remarkable due to highest, cob height and yield per plant. Considering variability, diversity pattern, genetic status and other agronomic performance, genotypes G25, G12, G6, G26 were selected from cluster II for high yield per plant; genotypes G1 and G9 selected from cluster IV for short plant type. Genotypes G5, G15 and G18 selected from cluster I for early maturity. These genotypes also might be considered better parents for efficient hybridization program. Involvement of such diverse genotypes in crossing program may produce desirable sergeants. So, divergent genotypes are recommended to use as parent in hybridization program.

Conclusion

Results of the present studies indicated significant variation among the genotypes for all the characters studied. Plant height, Leaf per plant, days to first female flowering, days to maturity, kernel per row, kernel per cob and yield per plant contributed maximum towards yield improvement. Considering yield and other agronomic performance the genotypes G25, G12, G6 were selection for highest value of grain yield per plant, number of kernels per cob, cob length and number of leaves per plant. G5 and G15 were selected for early flowering and early maturity. Genotypes G1 and G9 could be considered

suitable genotypes for dwarf plant. So, genotypes could be selected from advance segregating generations for inbred line development and use as open pollinated variety.

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APPENDICES

Appendix I. Map showing the experimental site under the study

★ The experimental site under the study

Appendix II: Physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1965)
Silt	26.40	Hydrometer method (Day, 1965)
Clay	36.66	Hydrometer method (Day, 1965)
Texture class	Clay loam	Hydrometer method (Day, 1965)

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1982
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix III. Monthly average temperature, relative humidity and total rainfall and sunshine of the experimental site during the period from December, 2018 to May, 2019.

Month	Air temperature (ºc)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
December,2018	32.4	16.3	69	0	7.9
January, 2019	29.1	13.0	79	0	3.9
February, 2019	28.1	11.1	72	1	5.7
March, 2019	35	21	74	88	8.3
April, 2019	34	23	76	200	7.5
May, 2019	35	24	79	580	4.0

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

Appendix IV.Mean performance of different characters of 30 maize genotypes

Code	PH (cm)	LPP	DFMF	DFFF	DM	CH	CL	CD	RPC	KPR	KPC	TSW	YPP
G1	152.47	13.67	65.00	67.00	104.67	65.90	17.43	16.10	15.23	32.10	471.87	420.07	184.07
G2	223.90	13.67	64.33	66.33	103.67	89.34	17.46	14.27	14.33	32.67	513.73	340.07	132.03
G3	232.23	11.67	63.67	65.67	104.00	93.17	16.70	13.63	13.90	31.47	369.33	320.17	139.03
G4	209.27	14.00	64.00	66.00	103.00	83.77	16.17	14.07	12.77	33.13	435.47	320.07	131.03
G5	207.67	11.67	62.00	64.67	103.33	84.40	17.50	15.00	13.67	31.03	392.97	330.80	163.37
G6	207.53	13.67	65.00	66.67	104.00	80.67	16.30	15.40	15.43	28.77	528.73	323.13	198.37
G7	232.53	11.67	64.33	66.33	104.00	91.13	16.34	14.42	13.23	36.27	442.20	349.27	154.67
G8	221.33	14.00	65.00	66.67	104.67	86.72	18.60	15.50	14.23	35.87	487.03	320.67	175.73
G9	153.77	13.00	64.00	66.00	104.67	63.68	18.23	15.70	12.90	38.97	476.77	350.67	180.30
G10	203.27	14.00	64.00	66.00	105.67	80.00	17.50	15.53	14.77	38.73	602.27	340.11	136.57
G11	215.40	13.00	65.00	66.67	105.67	86.77	15.57	15.33	14.63	31.73	474.70	340.37	175.03
G12	240.50	13.00	65.00	66.67	103.67	95.31	18.51	15.33	15.40	38.57	564.00	320.10	210.70
G13	203.33	14.00	65.00	66.67	103.67	81.58	17.63	15.55	15.47	34.93	468.63	314.33	130.33
G14	250.20	12.00	64.67	66.67	104.33	99.67	16.51	13.97	14.43	36.07	537.90	300.03	181.63
G15	198.20	14.00	65.00	67.00	103.67	80.03	19.22	14.07	15.50	36.17	396.87	359.47	120.33
G16	210.73	14.00	64.67	66.67	103.33	84.40	17.33	14.87	13.50	34.37	448.47	390.67	135.93
G17	216.17	15.00	64.33	66.33	103.00	85.48	17.54	16.37	14.00	30.50	577.10	350.33	182.73
G18	185.87	14.67	65.67	67.67	103.33	83.38	17.55	15.30	13.33	30.67	389.23	382.07	166.70
G19	233.13	14.00	64.33	66.33	103.33	94.20	17.93	13.28	14.10	32.47	504.27	287.85	133.97
G20	212.60	15.00	65.00	67.00	104.33	85.50	18.01	15.07	15.20	36.17	468.33	330.97	154.07
G21	215.57	16.00	64.67	66.67	104.67	87.27	19.30	13.28	13.23	37.70	491.20	380.67	181.10
G22	217.33	14.67	64.33	66.33	105.33	86.73	18.65	15.30	14.10	37.40	537.63	351.18	180.43
G23	209.40	14.67	64.67	66.00	105.67	87.32	18.62	15.40	15.43	39.07	586.97	311.73	150.00
G24	240.03	14.67	64.67	66.67	103.67	95.55	19.53	15.47	15.07	39.33	602.07	398.63	170.70
G25	226.03	14.00	63.67	65.67	103.33	90.90	19.38	15.10	14.83	38.87	562.67	360.33	213.00
G26	233.37	14.00	64.67	66.67	104.67	93.73	20.80	15.07	13.40	37.83	498.93	340.33	193.33
G27	230.47	14.67	64.33	66.33	104.67	92.20	19.58	15.53	14.57	38.07	575.87	390.33	187.70
G28	215.73	14.67	63.67	65.67	104.67	85.42	18.43	15.33	13.67	30.97	403.93	429.67	154.37
G29	225.37	14.00	64.33	66.33	104.67	91.00	18.37	15.60	13.83	36.57	501.07	380.33	179.37
G30	201.13	14.00	64.33	66.33	104.33	81.38	16.64	13.93	12.90	30.37	380.40	352.03	138.97

PH: plant height (cm), LPP: leaves per plant, DFMF: days to first male flowering, DFFF: days to first female flowering, DM: days to 75% maturity, CH: cob height (cm), CL: cob length (cm), CD: cob diameter (cm), RPC: rows per cob, KPR: kernel per row, KPC: kernel per cob, TSW:1000seeds weight (gm) and YPP: yield per plant(gm).

Appendix V. Principal component score I and II

Genotypes	PCA 1	PCA 2
1	25.89	-86.19
2	-19.31	18.28
3	117.87	44.11
4	57.65	36.91
5	94.13	20.59
6	-44.75	12.72
7	45.82	9.61
8	-2.11	26.14
9	17.12	-20.48
10	-103.98	7.39
11	12.06	7.09
12	-85.92	19.84
13	25.75	39.31
14	-57.67	49.60
15	100.95	1.45
16	48.40	-30.56
17	-88.49	-8.74
18	102.90	-33.29
19	-14.95	69.68
20	21.66	20.48
21	-2.72	-32.83
22	-49.91	-6.83
23	-94.25	33.39
24	-110.77	-45.73
25	-80.73	-22.10
26	-17.23	6.29
27	-87.63	-43.45
28	90.48	-68.24
29	-13.23	-29.92
30	112.98	5.48