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

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BY

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CERTIFICATE

This is to certify that thesis entitled,**"GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF YIELD COMPONENTS IN MAIZE (*Zea mays* L.)"** submitted to the Faculty of Agriculture,Sher-e- BanglaAgricultural University, Dhaka, in partial fulfillment of the requirements for the degreeof **Master of Science in Genetics and Plant Breeding**, embodies the result of a piece of bona fide research work carried out by **MST. SUMAYEA KHAN**, Reg. No. **12-04948** under my supervision and guidance. No part of the thesis has been submitted for any other degreeordiploma.

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

Dated:June,2018

Prof. Dr. FirozMahmud
Supervisor

Dedicated to My Beloved Family

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ABSTRACT

The research investigation was carried out in the experimental area of Sher-e-Bangla Agricultural university, Sher-e-Bangla Nagar, Dhaka-1207, during the late Rabi season Mid December to May 2018 to study the genetic variability and character association of yield components in Maize with35 maize genotypes as experimental materials that was laid out in Randomized Complete Block Design (RCBD) with three replications. The research work was oriented to calculate and estimate the yield factor through analyzingthe mean performances, variability, heritability, genetic advance, correlation coefficient, path analysis and genetic diversity involving the yield contributing characters. The maximum yield per plant (117.51 g) was estimated inthe genotype G12 (Pacific) and the minimum yield per plant (51.89 g) was recorded in the genotype G17 (Dekalb Super). The phenotypic coefficient of variation was observed higher than the genotypic coefficient of variation for all yield contributing characters. Heritability was also showed higher compared to genetic advance in comparative mean study for all the characters involved. Significant and positive correlation was observed for grain yield per plant with plant height (0.774), cob length (0.956), grain per row (0.703) and 100-seed weight (0.365). In path analysis study, positive direct correlation was recorded in days to male flowering (0.247), cob breadth (1.078), number of grains per cob (6.874) and 100-seed weight (0.595). Due to the crossing among the 35 maize populations, a wide range of divergence was observed in this experiment. The highest genotypes were included in cluster number V with 12 genotypes: BHM-5, PAC-60, Pacific-98, HP-222, KhaiBhutta, AS-999, Pioneer, Duranta, Kaveri 218, Chamak-07 and Golden-984. Here, the intra cluster distance was observed in cluster I (1.23), II (0.00), III (0.76), IV (2.08) and V (1.89) respectively. The highest intra cluster was recorded in cluster IV (2.08) and the lowest in cluster III (0.76)that showed that the genotypes within the intra cluster distances were closely related and inter cluster distances were recorded higher and larger than intra cluster distances.

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SOME COMMONLY USED ABBREVIATIONS

FULLNAME	ABBREVIATION
Analysisofvariance	ANOVA
Agro-ecologicalzone	AEZ
Andothers	*etal.*
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Cultivars	cv.
Co-efficientof variation	CV
Degreesof freedom	df
DegreeCelsius	îC
Environmentalvariance	$\sigma^2{}_e$
Etcetera	etc.
Food andAgricultureOrganization	FAO
Figure	Fig.
Firstgeneration	F1
Genotypicvariance	$\sigma^2{}_g$
Gram	g
Genotype	G
Geneticadvance	GA
Genotypic coefficientof variation	GCV
Heritability inbroadsense	h^2b
Kilogram	Kg
Meter	m
Mean sumofsquare	MS
MuriateofPotash	MoP
MinistryofAgriculture	MoA
Number	No.
Percent	%
Phenotypicvariance	$\sigma^2{}_p$
Percentage of coefficientofvariation	CV%
Phenotypic coefficientof variation	PCV
Randomized CompleteBlockDesign	RCBD
Replication	R
Research	Res.
Square meter	m^2
Sher-e-BanglaAgriculturalUniversity	SAU
TripleSuperPhosphate	TSP

CHAPTER I

INTRODUCTION

Maize (*Zea mays* L.) is the 3rd most significant cereal crop after wheat and rice in the world (FAO, 2016). It is also commonly known as Corn (mostly in North America) originates in the Andean region of Central America and basically first domesticated by indigenous people in southern Mexico. After domestication, maize spread quickly through North and South America, reaching the northeastern US and southern Canada prior to European colonization. Maize spread rapidly throughout Europe and from Europe, to other parts of the world after the European discovery of the Americas (Tollenaar*et al.* 1999). Taxonomically, Maize is a member of the family Poaceae (Graminae), generally recognized as the grass family. Artificial selection in Maize (from Maxican plant called Teosinte) has paved the path for advanced studies as well as a fruitful model organism for research in genetics over theyears.

Maize is one of the most prominent annual, photo-insensitive, cross pollinated cereal crops both for human and animal consumption and is grown for grain and forage utilities. It is monoecious, with staminate flowers on the terminal branched end of a tall erect stem (i.e., the tassel) and pistillate flowers on axillary shoots (i.e., ear shoots). An ear shoot consists of a shank or cob, florets with long filamentous stigmas, the silk, and enveloping spathe leaves, the husks. In the beginning of floret development, staminate florets develop on the ear shoot and pistillate florets may develop on the tassel, but they usually remain rudimentary (Bonnett, 1966). Occasionally, both staminate and pistillate florets will fully develop and become functional on the tassel (i.e., tassel seed), a phenomenon that occurs commonly on the tillers, which are elongated branches that sometimes develop from nodes lower on thestem.

Yield is a complex inherited character resulted from the interaction between the vital processes (Naushad *et al.* 2007) and associated with various contributing characters, therefore, direct selection for yield per se may not be the most efficient method for its improvement, but indirect selection for other yield related characters, which are closely associated with yield and high heritability estimates will be more effective (Mohammadia*et al.* 2003). In the year 2017/2018, the United States was the largest producer of corn with a production volume amounting to about 370.96 million metric tons. China and Brazil rounded off the top corn producing countries. Total maize production in Maize output increased the most, reaching a record in 2017, driven largely by higher production in several major exporting countries. Wheat output was high but slightly below the record set in 2016, and other coarse grain output declined in 2017 due mainly to lower barley production in Australia and lower sorghum and barley production in the United States. Global maize production is expected to grow by 161 Mt to 1.2 billion ton over the next decade, with the largest increases in China (31 Mt), followed by Brazil (24 Mt), the United States (22 Mt), the European Union (11 Mt)and Argentina (10 Mt). Increased production in Brazil will be largely driven by higher second-crop maize following soybeans. Production growth in the United States is expectedtoslowtolessthan1%p.a.overthenexttenyears,comparedto2.4% p.a. the decade before, due to slower growth in domestic demand, particularly for ethanol, and increased export competition (OECD/FAO, 2018).

Bangladesh in the year 2013-14, 2014-15 and 2015-16 was 2123572 MT, 2271998 MT and 2445578 MT, respectively (BBS, 2017). The area under maize cultivation has quickly increased to 804 thousand acres of land in FY 2014-15 from 72 thousand acres in FY 2003-04 (BBS, 2012 & 2015). So, the production of maize in Bangladesh is continuously increasing. The most limiting factor of maize research in Bangladesh is the development, improvement and maintenanceof parental/inbredlines.Ontheotherhand,theproblemofimportedhybridseedis the involvement of high price and uncontrolled quality. Moreover, the farmers cannot get the seeds timely. One important approach to improve this situation is the development of inbred lines, which can produce high yielding hybrid varieties. Before hybrid development, prospective parent (inbred line) selection is a pre-requisite.

Among the different districts in Bangladesh- Dinajpur, Chuadanga, Takurgaon, Lalmonirhat, Rajshahi, Kushtia, Rangpur and Bogra are noted to be more progressive in maize production with higher rates of growth. Both composite and hybrid maize are grown well in the loam and sandy-loam soils of the country (with three to four irrigations). Hybrid maize has a greater yield with 2.4 tons/acre (5.4 tons per ha), which is higher by one-third over composite maize (1.47 tons/acre or 3.63 tons/hectare) (BBS, 2015).

Maize (*Zea mays* L.) is an important staple crop of the world after wheat and rice. At the same time, it is a versatile crop due to its multifarious uses as feeds, food and industrial raw material. The crop serves as a source of basic raw material for a number of industries viz., starch, protein, oil, alcoholic beverages, food, sweeteners, cosmetics and biofuels (Khan and Dubey, 2015). Every part of the maize plant is useful. Green cobs of maize are used as food after cooked by roasting or boiling in water. The top green portion of the plant after harvest of the cob is fed to cattle as fodder, and the dry portion of the stem along with fibrous roots are used as fuel. The greatest advantage of maize over rice and wheat is its high bio-mass potential. Maize grain, full or broken, is used in Khichuri, gruel often mixed with pulses. Popcorn is consumed as snacks. Grains are the principal ingredients for poultry and cattle feed. Industries make use of maize for corn oil, starch, adhesives, medicines and in the manufacture of various food products like corn flakes, chips etc. People in Bangladesh consider maize as animal feed or at best a poor people's food. In other countries, however, (e.g. Indonesia, Mexico, Chile, Kenya, Central America and Zimbabwe) maize is a staple food (BBS, 2015). Maize is more nutritious than rice in terms of protein, phosphorus and carotene content. Fats and mineral contents are also higher. It is rich in Vitamin B and trace elements. Also, its price is lower than rice. The principal consumption of maize is in the form of feed for poultry although some dairy farms use maize as feed grains and its plants as green fodder for the cattle. Demand for maize in the country is growing and is expected to increase further with the establishment of new poultry, dairy and fish farms.

Maize can be produced in an extended range of conditions, from 0 to over 3800 m.a.s.l., and under precipitation levels from 200 mm to 2000 mm (Doorenbos*et al.* 1979; Hartkamp*et al.* 2001; Ortega, 1987). Though a variety of abiotic (soil, climate) and biotic (diseases, plagues) stresses affect maize, its main constraints are currently climatic factors and physical characteristics related to soil fertility (Ammani*et al.* 2013; Lone *et al.* 2009). From the agroedaphic point of view, maize can be grown all over the country. It is a fast-growing crop and grows well with the minimum temperature of 10 degreeCandthemaximum30degree C. Maize sheds pollen well and matures quickly at a temperature range from 20 degree C to 30 degree C. The average minimum and maximum temperatures of 12 degree C and 29 degree C, respectively, of Bangladesh are ideal for successful maize production. Being a short-day crop, maize can be grown throughout the year in all parts of the country.

As the world’s population increases and more people begin to include higher amounts of meat, poultry and dairy into their diets, demand for maize is expected to rise. By 2025, maize will be the developing world’s largest crop and between now and 2050 the demand for maize in the developing world is expected to be doubled (CGIAR, 2016).

A successful selection program depends not only on heritability of desirable characters but also on the information about the association among various yield component characters and their association with grain yield (Abdurakhmonov*et al*

2008; Singh *et al.* 2016). Variability is the differences between individuals in a population due to genetic composition and growing environment (Sumanth *et al.* 2017). The existence of variability is utmost role as success of any plant breeding program depends on the genetic variability and selection skill of plant breeder (Adhikari *et al.* 2018). Selection is only effective if the parent population have significant amount of variability. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provides insight information on magnitude of variability in a population and heritability shows the component of a character transmitted to future generations (Pal *et al.* 2016; Girma*et al.* 2018) Further, heritability coupled with genetic advance shows the expected genetic gain in next generation (Shukla *et al.* 2006). In addition, correlation between yield and yield attributing traits are prime important for indirect selection for those traits which have high heritability and closely associated to contributes to improve yield (Aditya & Bhartiya, 2013).

This study was conducted to elaborately understand about the genetic parameters and character associated attributes to consider the yield and its components involving 35 Maize populations to achieve following objectives:

Objectives:

1. To know the yield potentiality of different maizegenotypes.
2. To understand the nature of association of traits, direct and indirect relation between yield contributing characters of maizegenotypes.
3. To study genetic variability among the genotypes.

CHAPTER II

REVIEW OF LITERATURE

Maize is widely cultivated throughout the world and a greater weight of maize is produced each year than any other grain. It has become a staple food in many parts of the world, with the total production of maize surpassing that of wheat or rice. Due to its massive production, researchers are working diligently to improvise the genetic attributes of this crop to maximize the production. Various investigation and experimentation have been carried out throughout the world to diversify the maize potentiality. In relation to this experimentation, different relevant works are highlighted here to study the comparative aspects of maize involving yield through variability, heritability, genetic advance, correlation, path analysis and diversity studies. Therefore, important research works related to this experimentation is reviewed in this chapter under following headings:

2.1 Genetic Advance, Heritability and GeneticVariability

2.2 Correlation Coefficient and PathAnalysis

2.3 GeneticDiversity

2.1 Genetic Advance, Heritability and GeneticVariability

Ilyas *et al.* (2019); investigated two sets of maize inbred lines containing 4 inbred lines as parents viz., drought tolerant and susceptible from a diverse gene pool and crossed to produce 02 hybrids. The cross 1 comprised of a drought tolerant inbred line as VDR-51 and a susceptible inbred line 5CDR-53. The cross 2 comprised of a drought tolerant inbred line as DR3-126 and a susceptible inbred line DR-37. The trial was sown under triplicated split plot in a randomized complete block design (RCBD) under drought and rain-fed conditions. Both heritability and geneticadvanceestimateswerehigherforgrainyieldandplantheight,hence additive gene action was depicted. While, narrow sense heritability and genetic advance was lower for remaining parameters under both the environmental conditions which clearly specified that non-additive gene action was present.

Bello *et al*. (2012); used the magnitude of genetic variability, heritability and genetic gains in selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programmes. Ten open pollinated maize varieties were evaluated at the Teaching and Research farm, University of Ilorin, Nigeria, during 2005 and 2006 cropping seasons to estimate genetic variability, heritability and genetic advance of grain yield and its component characters. The effect of genotype and genotype by year interaction were significant for ear weight and grain yield, while the effect of year was highly significant ($P< 0.01$) for all the characters.

Anshuman *et al. (*2013); heritability, coefficient of variability and genetic advance values were computed on 14 characters. High to moderate estimates of GCV and PCV were recorded for anthesis silking interval, grain yield per plant, ear height, harvest index, number of grains row per cob, number of grains per row and 100-seed weight suggesting sufficient variability, thus offers scope for genetic improvement through selection. High estimates of heritability were observed for plant height, ear height and ear girth. High to moderate heritability with moderate estimates of genetic advance recorded for biological yield, grain yield per plant, plant height and ear height where careful selection may lead towards improvement for these traits. Hence, provides better opportunities for selecting plant material for these traits inmaize.

Manal *et al.* (2011); measured 13 inbred lines of corn and evaluated at two sowing dates during the 2009 growing season. The experiment was arranged in split-plot design with three replications. Results showed that, under optimal sowing, ear diameter, ear weight per plant, number of ear per plant, number of grains per plant exhibited positive and significant correlations with the genotypic and phenotypic levels of yield per plant.

Juliet *et al*. (2013); measured genetic diversity, variability, association of yield with other component traits and relative importance of direct and indirect effects of different components on yield were assessed. The genotypes studied showed a wide range of variation for all the characters. Among the traits evaluated, maximum genotypic and phenotypic coefficients of variation were observed for grain yield per plant followed by number of rows per cob and number of kernel per row. The estimates of heritability and genetic advance as per cent of mean was high for grain yield per plant, number of kernels per row and number of rows per cob. Grain yield per plant was positively and significantly correlated with cob weight, hundred kernel weight, number of kernel rows per cob and number of kernels per row. Path coefficient analysis further revealed that number of kernel rows per cob exhibited maximum positive direct effect followed by cob length. The significant association of grain yield per plant with hundred kernel weight and number of kernels per row is due to positive indirect effects through number of kernel rows per cob, days to 50% silking, plant height and coblength.

Rafiq *et al.* (2010); ten local maize inbred lines were crossed to three testers (F-107, F-131 and F-165) to develop 30 progenies. The parents, testers and crosses were evaluated in RCBD with three replications. Analysis of variability parameters revealed presence of substantial variability for all traits studied. Grain yield, ear length, ear height, 100-seed weight and ear diameter had high GCV estimates with high heritability. Genetic advance was higher for plant height, ear length, grains per row and grain yield. Genotypic correlation coefficient revealed that ear diameter, 100-grain weight, ear length, rows per ear and grains per row significantly correlated with grain yield. Path analysis revealed that highest direct effect on grain yield was exhibited by 100-grain weight followed by grains per row,kernelrowsperear,earlengthandeardiameter.Mostofthetraitsexerted their positive indirect effects through 100seed weight, kernel rows per ear and grains per row.

Hassan *et al.* (2018); evaluated 30 inbred lines of maize for ten parameters to study the genetic variability and diversity in maize inbred lines. Mean performance, variability, heritability, coefficient of variation and diversity analysis of yield and yield contributing characters (Cob height, plant height, cob length, cob diameter, number of kernel rows per cob, number of kernels per row, number of kernels per cob, 1000 kernels weight, yield per plant and pith weight) were performed. The highest weight of 1000 kernels (494.3g) was obtained from ML28, the lowest weight of 1000 kernels (213.96g) was recorded from ML21, 1000 kernels weight of phenotypic variation (82.24) was higher than thegenotypic variation (18.65), which indicates high environmental effect was supported by narrow difference between phenotypic (23.64) and genotypic (5.36) co-efficient of difference.

Hassan *et al.* (2018); estimated the heritability that allowed breeders to calculate expected progress from selection relative to germplasm sources, the type of breeding procedure used to improve the germplasm, and the amount of testing of genetic material. The objective of this study was to compare estimates of heritability and other genetic parameters for yield of maize (*Zea mays* L.) by using variances among progenies for 121 selection experiments from seven recurrent selection programs.

Saleh *et al.* (2002); experimented tropical maize hybrids, involving 10 single, four double and four three-way crosses were evaluated with their parental inbred lines and three control varieties, at University Putra Malaysia, Serdang, Malaysia, in a randomized complete block design, with three replications. The objectives were to identify hybrids superior for yield, yield components and other agronomic traits, to estimate heterosis revealed by the hybrids, and to estimate broad-sense heritability for important characters in the populations. Estimates of broad-sense heritability also varied with characters. Moderate heritability was shown for grain yield indicating a substantial amount of genetic variation in this population of hybrids. Low and negligible heritability for days to silking and 100-grain weight indicate that these traits were very much influenced by environmental factors.

Zahid *et al.* (2004); broad-sense heritabilty, coefficients of variability and genetic advance values were computed for days taken to tasseling, number of days taken to silking, plant height, ear length, number of kernel rows ear-1, number of kernels row-1, 100-grain weight and grain yield plant-1. Low, medium and high estimates of broad sense heritability were found in different plant characters under study. Highest heritability estimates were found in grain yield plant-1 (0.993) and by plant height (0.990). Values of genetic advance ranged between 43.80 for grain yield plant-1 to 1.33 for number of kernel rows ear-1. Greater magnitude of broad sense heritability coupled with higher genetic advance in characters under study provided the evidence that these plant parameters were under the control of additive genetic effects. Indicating that selection should lead to a fast genetic improvement of the material

Sumathi *et al.* (2005); the genetic variability, correlations and path coefficients were studied in 47 maize inbred lines, including seven high oil strains collected from CYMMIT, Mexico for ten characters. Close resemblance between GCV and PCV was observed for all the traits indicating that selection for these characters would be much effective. Heritability estimates in general were high for all the ten characters studied. The highest heritability coupled with high genetic advance as per cent of mean was observed for plant height, total number of kernels per ear, grain yield and oil content. Genotypic correlation studies indicated that ear weight, number of rows/ear, number of kernels/row, and total number of kernels/ ear were positively associated with grain yield. Oil per cent exhibited negatively non-significant correlation with grain yield, whereas it showed positive association withnumberofrows/earonly.Pathcoefficientanalysisrevealedthatnumberof kernels per row showed high direct effect on grain yield followed by 100 seed weight, number of rows per ear and total number of kernels per plant

Ali *et al.* (2013); accessed the vigor of F1 hybrids for drought tolerance. Higher heritability and genetic advance were found for dry root weigh and total dry weight, strong genotypic correlation was found for dry root weight, dry shoot weight and total dry weight. Higher dry root and shoot weight and dry root-to shoot weight ratio was found for B-336 and Sh-139 × EV-347, B-336 × EV-347, EV-1097 × EV-340, EV-1097Q × B-316 and B-327 × EV-340.

Syed *et al.* (2000); five hundred S1 families were evaluated in the greenhouse for seedling traits in C1 recurrent selection cycle. Higher values of GCV% were toand for fresh shoot and dry root weight (28.85 and 41.95 respectively). Moderate broad-sense heritability (h2 BS) estimates were found for fresh shoot weight, dry root weight and fresh shoot length (42.45, 48.94 and 55.0 respectively). Fresh shoot weight was phenotypically, highly significantly and positively correlated with other indicated traits. Hign values of coefficients of variation, positive highly significant interrelationships, moderate broad-sense heritability (h2 BS) estimates and relative expected genetic advance (RE)g %) was also found greater for fresh shoot weight and dry root weight. It is generally concluded from the results that fresh shoot weight can be used as selection criteria while comparing S1 families at seedling stage in maize as it is easy to determine as compared to dry root weight.

Debnath (1987); estimated of genetic variability, heritability, and genetic advance for grain yield, days to silk, grain moisture, plant height and ear height in 9 maize inbreds and their 36 F (1)s over two years. The genotypes differed significantly for all characters in both years except for grain moisture in the first year. The genotypic and phenotypic coefficients of variation were highest for grain yield and lowest for days to silk. High heritability was observed in days to silk, plant height andearheight;whilethesevalueswerelowfortheresttwocharacters.High values of genetic advance were obtained for grain yield, plant height and ear height.

Rajesh *et al.* (2013); determined the various parameters of genetic variability, broad sense heritability and genetic advance estimates in newly developed 65 maize genotypes. Analysis of variance revealed that the mean sum of squares due to genotypes showed significant differences for all the 11 characters studied. High to moderate estimates of GCV and PCV were recorded for Grain yield, number of kernels per row, 100-kernel weight, ear length and plant height which represents considerable variability and offers scope for genetic improvement through selection. Grain yield, number of kernels per row, 100-kernel weight, ear length and ear height had high GCV estimates with high heritability. Moderate estimates of genetic advance with high heritability was recorded for Grain yield, number of kernels per row, 100-kernel weight, ear length, ear height and plant height which further leads to improvement of traits under selection. Thus provides better opportunities for selecting plant material for these traits in maize breeding program.

Ankit*et al.* (2017); estimated of heritability for grain yield per plant, 100 kernel weight, cob height, plant height and no. of grain rows per cob. The character grain yield per plant show moderate heritability with high genetic advance over mean. The economic trait grain yield per plant show positive significant association with the characters namely; days to 50% tasseling, days to 50% silking, days to 75% dry husk, cob height, cobs per plant, grain rows/ cob, grains per row, cob weight, 100 grain weight and grain weight percob.

Khan et al. (2019); evaluated the genotypes for yield and its associated traits is an essential step towards the development of a crop variety. Crop breeders mostly practice selection for the desired traits to identify superior genotypes. This research was conducted to assess the performance of 20 maize hybrids along with two checks at The University of Agriculture Peshawar during spring 2017 crop growingseason.Theexperimentalmaterialwasplantedinrandomizedcomplete block design with three replications. Significant differences among the hybrids were observed for plant height, ear height, days to tasseling, days to anthesis, days to silking, cob length, cob diameter, kernel rows cob-1, 100-kernel weight and grain yield. Among the hybrids, ZH1610 was observed as the earliest maturing hybrid with minimum days to tasseling (91.7), days to anthesis (93.7) and days to silking (96). Hybrid ZH169 showed maximum cob length (19.5 cm) while ZH1621 produced maximum kernel rows cob-1 (15.7). Maximum 100-kernel weight (35.0 g) was recorded for CAH153 while hybrid ZH1620 gave maximum grain yield (12412.8 kg ha-1). The present study revealed ample variation among the hybrids for yield and yield related traits. On the basis of superior performance for maturity, yield and associated traits, hybrids ZH610, ZH169, ZH1621, CAH153 and ZH1620 are recommended for commercial cultivation after multi-location trials and onward utilization in maize breedingprograms.

2.2 Correlation Coefficient and PathAnalysis

Roy *et al.* (2018); twenty-five maize genotypes were evaluated to study the genetic variability, correlations and path co-efficient analyses for yield and yield contributing characters. Analysis of variance for sixteen yield contributing traits showed highly significant variations among the genotypes. The estimates of genetic components for the yield contributing traits showed higher phenotypic coefficient of variation than genotypic co-efficient of variation indicating more environmental influence on the studied traits. Traits under study showed moderate to high heritability. The highest heritability was observed in 1000 kernel weight (79.79), seed numbers ear^{-1} exhibited the highest genetic advance (55.45) and shoot lodging (223.07) showed the highest genetic advance in percentage of mean. Thousands kernel weight exhibited the highest significant positive correlation (0.746) with yield per plant followed by husk girth (0.620) and ear length (0.432). The negative correlation with yield per plant was observed for days to anthesis, days to maturity and seed numbers per row. Path co-efficient analysisexhibited that the thousands kernel weight had a maximum positive direct effect on grain yield followed by husk girth and ear length. This experiment revealed that the selection based on thousands kernel weight, husk girth and ear length would increase grain yield for yield improvement in maize. Therefore, the research findings would be useful for the identification and selection of traits for future breeding programs of maize.

Kandel *et al.* (2018); heat stress during the flowering, pollination and grain filling periods affect maize grain yield and its attributing traits. Twenty maize inbred lines were evaluated in alpha lattice design with two replications under heat condition during spring season from February to June, 2016 at Rampur, Chitwan, Nepal. Meterological data showed maximum mean temperature (46.2–43.28°C) and minimum (30.52-30.77°C) in with relative humidity 37.05 to 49.45% inside the tunnel during in April-May which coincided with the flowering, pollination and grain filling periods. The data were analyzed statistically to study the correlation and path coefficient. The analysis of variance showed that all the lines were significantly different from each other for all traits anthesis silking interval, SPAD chlorophyll and leaf senescence, tassel blast, leaf firing, plant and ear height, leaf area index, ear per plant, cob length and diameter, number of kernel ear^{-1}, number of kernel row^{-1}, number of kernel row, silk receptivity, shelling percentage, thousand kernel weight and grain yield. Grain yield had positive and significant phenotypic correlation with silk receptivity, shelling percentage, cob length and diameter, number of kernel ear^{-1}, number of kernel row^{-1}, number of kernel row, SPAD chlorophyll, thousand kernel weight and significant and negative correlation with tassel blast, anthesis silking interval, leaf area index, leaf firing. Path analysis revealed that of thousand kernel weight, shelling percentage, number of kernel ear^{-1} and silk receptivity exerted maximum positive direct effect on grain yield. Therefore, selection of genotypes having maximum thousand kernelweight,shellingpercentage,silkreceptivityandnumberofkernelear^{-1}and shorter anthesis silking interval, no leaf firing and tassel blast is pre-requisite for attaining improvement in grain yield under heat stress condition.

Sales *et al.* (2019); aimed to analyze the cause and effect of associations between agro-morphological traits for increasing yields in maize populations cultivated. A total of 16 maize accessions of in vivo conservation works in eight different locations were evaluated, in a randomized complete block design with three replicates, totaling 48 experimental units. Genetic parameters, genotypic, phenotypic, and environmental correlation were estimated, and a path analysis was conducted. In general, accessions presented enough genetic variability, showing significant differences for all traits analyzed statistically ($P \leq 0.05$). The first cob insertion height with plant height and final plant stand variables presented heritability (h^2) higher than 80%, suggesting that superior genotypes could be determined. Highest estimates of phenotypic correlations (r_p) were found between the first cob insertion height with plant height and total number of cobs with number of cobs per plant (0.85). For estimates of genotypic correlations (r_g), the highest were between (i) the first cob insertion height and plant height; (ii) number of grains per row and number of cobs per plant; (iii) total number of cobs and final plant stand. Maize final plant stand and one thousand seed weight were observed to be traits that could be determinant in grain yieldincrease.

Abel *et al.* (2017); performed to apply and describe path analysis of perennial ryegrass seed yield components in relation to harvested seed yields. Utilising extensive yield components which included subdividing reproductive inflorescences into five size categories, path analysis was undertaken assuming a unidirectional causal- admissible relationship between seed yield components and harvested seed yield in six commercial seed production fields. Both spikelets per inflorescence and florets per spikelet had a significant ($p < .05$) direct effect on the overall seed yield; however, total path correlation coefficients showed that inflorescence size had the largest positive influence on seed yield via its indirect effects on other seed yield components.

Kumar *et al.* (2014); demonstrated the positive and significant phenotypic correlations for the grain yield in association with plant and ear height, ear length and diameter, number of seeds row per ear and 100 seeds weight except maturity traits which showed negative association with grain yield. The path analysis showed 50% tassel had highest magnitude directly effect on grain yield per plant in relation to ear height, 100 seeds weight and earcircumference.

Bekele *et al.* (2014); heritability, genetic advance and correlation was undertaken at College of Agricultural farm; Rajendranagar under rain fed condition in 2002-2003 randomized block design with three replications. It was done using twenty four hybrids with their parents (six lines and four testers) including two checks namely Mandhuri and DHM 105. The characters plant height, ear height, number of seeds per row, 100 seed weight, protein content, and grain yield per plot revealed higher values of heritability. High genetic advance coupled with heritability was observed for plant height, grain yield per plot and protein content. Thus selection based on these traits will be effective in maize breeding program. Correlation study showed negative and significant association between grain yield and oil content at genotypic level.

Basir*et al.* (2003); performed the interrelations between grain yield and its components were determined by genotypic correlation and path co-efficient analysis in eighteen maize lines/hybrids. The results indicated that grain yield was positively and significantly associated with all parameters studied. The also showed that number of kernels per row had maximum positive direct effect in grain yield. It was followed by 100-kernel weight, ear length and number of rows per ear and considered the main yield components.

Rahul *et al*. (2015); twelve maize (*Zea mays* L.) genotypes were evaluated for character association. The genotypes were significantly different for all the characters, which indicated scope for further genetic studies. High heritability along with high genetic advance was recorded for plant height, leaf length, leaf width, stem girth, number of leaves, crude protein, acid detergent fibre, dry matter yield and green fodder yield indicating the predominance of additive effects in the inheritance of these characters. The phenotypic coefficients of variation (PCV) estimates were invariably higher than their corresponding genotypic coefficient of variation (GCV) values thereby suggesting the environmental influence. High estimates of GCV and PCV were observed for plant height, leaf length, stem girth, number of cobs, number of seeds, dry matter yield and green fodder yield, suggesting that selection based on these characters would facilitate successful isolation of desirable types. Traits like plant height, leaf length, leaf width, stem girth, number of leaves per plant and dry matter yield had positive and significant correlation at genotypic as well as phenotypic level with green fodder yield and the selection based on these traits will result in improving the green fodder yield in maize.

Ram *et al*. (2013); studied the heritability, correlation and path coefficient analysis in 45 hybrids and ten parents. In pooled analysis of variability parameters revealed that the phenotypic coefficients of variation (PCV) were higher than genotypic coefficient of variation for all the characters studied indicating the role of experimental variance to the total variance. The magnitude of PCV and GCV was high for grain yield per plant followed by ear height, number of kernels per row, 100-seed weight, ear length, plant height, ear girth and number of kernel rows per ear. High heritability coupled with high genetic advance as percentage of mean was observed for ear height, grain yield per plant, plant height, number of kernels per row and ear length. In general, magnitudes of genotypic correlations were found to be higher than phenotypic correlations.

Bhiusal*et al.* (2017); estimated the extent of genetic variability and traits association in maize, fifty-five genotypes in randomized block design with three replications. 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. 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 ofmaize.

Kassa*et al.* (2019); wider range of variability observed from the mean of various quantitative traits. The genotypes that varied by cropping system depicted the presence of high level of variability. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) values were recorded for hundred grain weight (29.56 and 35.46 g), biological yield (27.22 and 31.37) and grain yield (26.60 and 31.54 q/ha), whereas the lowest GCV and PCV values were recorded for days to maturity of sole common bean genotypes. Phenotypic variance in both sole and mixed cropping systems was higher than that of genotypic variances. This implies that, considerable contribution of environmental factors to the phenotypic expression of the genotypes. High broad sense heritability as observed under both sole and intercropping systems indicated that, genetic improvement can be obtained through further selection programme. Important agronomic traits: pods per plant, seeds per pod and branches per plant had positive and significant correlation with grain yield in most cases. Path coefficient analysis at genotypic level indicated that all traits except plant height, seedsperpodandhundredgrainweightsexertedtheirpositivedirecteffecton grain yield. Hence, the current study identified the presence of wide variability between those common bean genotypes which can be used for further breeding program and selection can be made using those traits associated to yield.

2.3 GeneticDiversity

Asima*et al.* (2018); the D^2 statistics is useful tool to assess genetic diversity among genotypes. It also provides qualitative measures of association between geographical and genetic diversity based on generalized distances. In the present study hundred maize lines were subjected to D^2 analysis, which revealed the presence of substantial amount of genetic variability among them. To evaluate genetic diversity among the 100 inbred lines of maize over two years observations were recorded for six seedling root traits. ANOVA for dispersion for root traits in inbred maize lines revealed highly significant difference among all inbred lines. Inbred lines were grouped into ten clusters in year-1 analysis, twelve clusters in year-2 analysis and eight clusters in pooled over years analysis indicating the presence of genetic diversity. Maximum number of lines were accommodated in cluster-I in year-1, year-2 and in cluster-II in pooled over analysis. Maximum inter cluster distance in Y1 was recorded between cluster-X and cluster-IV. Similarly, in Y2 maximum inter cluster distance was recorded between cluster-XII and cluster-V and in pooled analysis maximum distance was recorded between cluster-VII and cluster-IV. Fresh root weight contributed maximum contribution towards divergence followed by primary root length. The pattern of distribution of lines into various clusters was random, suggesting that geographical and genetic diversity were not related. These genetically diverse inbred lines can be further used for developing superior hybrids and can also be utilized in developing synthetics andcomposites.

Immad*et al.* (2018); hierarchical clustering approach was used to group the Maize genotypes and the distance measure used was Euclidean distance. Cluster analysis using the R software grouped the 55 genotypes into distinct clusters using the

Euclidean distances between the various genotypes. All the three types of dendrograms obtained indicate single, complete, and average linkage. Single linkage group the genotypes on the basis of the similarity. It was found that when the dendrogram for single linkage was cut at a distance of 4, it revealed two distinct clusters for the 55 genotypes. It clearly classified the genotypes, with cluster one containing the individual plants and cluster two containing crosses. Level plot was also obtained which indicated at least two distinct groups with large inter clusterdistance.

Rupp *et al.* (2009); genetic structure and diversity among progenies of sweet corn using *SSRs* lociand a set of 15 progenies of *su1* genotypes that represent the diversity available to be currently used by breeding programs was analyzed in the present study. A total of 100 primers were tested, of which 77 were found to be usable in terms of high reproducibility for all sample tested and 13 were polymorphic loci. An average of 2.61 alleles per locus, were detected. The mean gene diversity of all *SSR* loci is 0.5088. The larger effective number of alleles per locus and the higher gene diversity (He>0.50) detected in 6 *SSR* loci suggest that 46% of the 13 *SSR* loci would be sufficient to the differentiation of the 15 sweet corn progenies. The global deficit of heterozygous plants was low (4.36%) for all *SSR*loci at S_5 generation. Excess of heterozygous plants occurred mainly in the 5 progenies. The FST value indicated that 65.15% of the total variance in allele frequencies at *SSRs* loci was due to genetic differences among the progenies. The higher H_o value (0.3385) was found in W46 progeny whereas the lowest value (0.00) was recorded in W06 progeny. The highest $H_e$value was 0.3368 for W28 progeny and the lowest $H_e$value (0.00) was recorded in W06 progeny. The analysis of genetic structure of *su-1* progenies of sweet corn was important for the estimation of genetic distance or similarity among the progenies and was especiallyimportanttoidentifythe*SSR* lociwithhighandlowlevels of heterozygosity, to identify the progenies at S_5 generation showing 100% of homozygous plants and progenies showing high heterozygosity.

Mahato*et al.* (2018); assessment of genetic diversity is a pre-requisite to broaden the genetic background of cultivated base of sweet corn, an endosperm mutant of field corn that alters starch biosynthesis pathway in endosperm. In the current investigation, genetic divergence among 39 inbred lines was assessed on the basis of 14 agro-morphological traits, two quality parameters and 63 microsatellite markers, selected on the basis of their association with QTLs affecting kernel quality. The cluster analysis based on unweighted pair-group method using arithmetic averages for agro-morphological and quality traits grouped the 39 inbreds into three clusters with 5, 14 and 20 genotypes, respectively. The unweighted neighbor-joining method for microsatellite markers also categorized the inbred lines into three major clusters grouping 10, 9 and 20 genotypes in cluster I, II and III, respectively. The two cluster distribution patterns showed approximately 36 percent similarity. The assay of 30 microsatellite repeats identified 82 alleles with allele size ranging from 80 to 400 bp. The major allele frequency and PIC value of the markers ranged from 0.42 to 0.79 and 0.27 to 0.63, respectively, which suggested the presence of high amount of polymorphism among the inbreds. The average heterozygosity was recorded to be 0.19 which signifies proper maintenance of inbred population. Principle co-ordinate analysis also depicted diverse nature of inbred lines and agreed well with the previously determined clustering pattern. This study has identified several inbreds, having good yield and high sugar content which will not only enhance the genetic background of sweet corn germplasm but will also lead to development of high-yielding hybrids with improvedquality.

Rafique *et al.* (2018); for the estimation of genetic diversity through cluster analysis forty most promising inbred lines were evaluated for ten different morphological traits. The field experiment was carried out under randomize complete block design (RCBD) in three replications in the field area of maize research station, Ayub Agriculture Research Institute, Faisalabad, Pakistan. According to the statistical analysis of the morphological traits of the inbred lines, wide variability exists for all the characters studied. All the genotypes were grouped into 10 clusters. The parental combinations of the most of developed promising hybrids of the research station exhibited dissimilarity range around 50%. The genotype 24 seems most diverse among all other genotypes with 60 to 80% dissimilarity. The distribution of genotypes in the study indicated that the geographical origin did not have any bearing on clusteringpattern.

Das *et al.* (2018); molecular characterization of 24 lines using 80 SSRs generated 217 alleles. Wide variation was observed for PIC (0.08–0.73), gene diversity (0.08–0.76), major allele frequency (0.33–0.96) and dissimilarity coefficient (0.37–0.77). Cluster diagram grouped the inbreds into three distinct clusters consistent with the lineage. The study identified a set of potential cross combinations to develop high yielding hybrids enriched with vitamin E, and map additional gene(s) affecting accumulation of α-tocopherol. This is the first report on biochemical- and molecular- characterization of sub-tropically adapted inbreds with *ZmVTE4*-favourable allele.

Zaffar*et al.* (2018); investigated the genetic divergence of maize (Zea mays L.) inbreds and to identify elite lines to develop potential hybrids for high altitude ecologies. Data were recorded for thirteen (13) quantitative traits viz. germination (%), root depth, shoot length, days to 50 % pollen shed, days to 50% silking, plant height, ear height, ear length, ear girth, number of kernels per row, 100 seed weight, grain yield per plant. The tested genotypes expressed significant variability with high estimates of heritability (broad sense) for all the traits revealing that these traits are amenable to genetic improvement. Grain yield per plant exhibited positive and significant correlation with plant height, ear height, ear width, number of kernels per row, number ofkernel rows and 100 seed weight at both the levels which exhibit a strong possibility for improvement of grain yield per plant by selection for these traits. Genetic divergence based on thirteen quantitative traits grouped thirty maize inbred lines into four clusters as per Mahalanobis D2 analysis employing Tocher's method which revealed wide diversity in elite genotypes owing to the involvement of diverse parental lines in the hybridization programme. Grain yield per hectare was the main factor contributing to total divergence (41.16%) which needs to be considered for highlighting clusters to be chosen for the purpose of further selection.

Vasileios *et al.* (2018); principal component and cluster analyses were used for grouping genotypes, while correlations were performed to investigate relations between all quantitative and quality characteristics. According to PCA analysis, the six newly-developed crosses, which were evaluated in different environments, showed measurable distances between the identical lines (B1×B2 (A) and B1×B2 (B)) suggesting genotype-environment interaction. Also, cluster analysis showed that some crosses, such as A1×B2 (A) and A1×B2 (B), are grouped in separate and distinct clusters indicating that dissimilar developmental environments may cause changes in quantitative traits. This may be due to the origin of the selected lines, since they were developed in different locations. Lines developed in the same location gave crosses that had similar behavior in the two locations. Also, it is clear that a kind of gene fixation is apparent from the C3 cycle in A1xA2 cross, since it is close (and similar) to the C4 cross. Crosses including A2 line showed a greater stability in bothenvironments.

Moll *et al.* (1962); expected in crosses of parents with varying degrees of genetic diversity. Other experimental findings reported in the literature indicate that crosses of unrelated inbred lines of corn show greater heterosis than crosses of related lines (4, 5, 7, 8, 9, 13). These earlier experiments involved lines derived from locally adapted material and represent a limited range of genetic differences. The question of the association of heterosis and genetic diversity over a wider range has become particularly important with increasing interest in exotic corns for breeding programs. The study to be reported here involves a wide range of varietal material to examine further thisquestion.

Ram *et al.* (2017); A 2-year study was carried out on 84 maize genotypes to assess the genetic diversity for various morphological traits and their association with yield. There was a significant variation for all the traits studied among the genotypes. Moderate value of heritability and high genetic advance over mean were found for TLB infestation, average No of cobs per plant, average no of grains per plant and area under disease progress curve. Yield was found to be highly associated with other morphological traits. Average no of grains per plant have highest direct effect on yield (r = 0.831) followed by hundred grain weight (r = 0.386). Two major clusters comprising of 43 and 41 genotypes were formed. First 3 principal components having greater than one eigenvalues contributed 76.6% of total variation. FH-3358 and PRO-65 were found suitable for Meghalaya.

Muhammad *et al.* (2017); genetic diversity in crops is essential to make improvements related to superior germplasms. Implementation of molecular markers to identify suitable genotypes speeds up the breeding progress by enhancing selection efficiency. This study was carried out to probe genetic diversity among 21 maize genotypes using 20 inter simple sequence repeat (ISSR) markers. We identified a total of 190 polymorphic bands with an average of 9.5 alleles per primer. The highest number of polymorphic bands (17) was found using ISSR marker UBC-10, whereas the lowest number of polymorphic bands (4) was found using UBC-809. The coefficient of genetic similarity rangedfrom 0.888 to 0.118%. The highest similarity was found between accessions 12 (015224) and 9 (015114), whereas the lowest similarity was found between genotypes 20 (EV-5098) and 14 R.W. Muhammad et al. 2 Genetics and Molecular Research 16 (1): gmr16019438 (015030). The polymorphism information content rangedfrom0.17to0.47.AdendrogramwasgeneratedbasedonJaccard’s distance matrix. The genotypes were found to group into two major clusters that could be further partitioned into two sub-clusters. Genotypes located within the same cluster are genetically more closely related to each other. The present study efficiently identified diverse genotypes that may be used for creating new varieties with distinct characteristics. The identified genotypes could be used as parents for future development of diverse populations.

CHAPTER III

MATERIALS AND METHODS

The experiment was executed to study the yield potentiality involving eleven characters through the genetic parameters such as genetic variability, genetic advance, heritability, correlation coefficient, path analysis, genetic diversity using 35 maize genotypes of different generations. From the beginning of the experimental work to the last data collection analysis, these all steps are presented in this chapter below under following headings:

3.1 Description of the experimentalsite

3.1.1 Experimentalperiod

The experiment was conducted during the period of Mid December 2017 to May 2018.

3.1.2 Location of theexperiment

The research work was conducted in the experimental field of Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207, during Rabi season (Mid December to May 2018).Sher-e-Bangla Nagar Thana, area 5.25 sq km, located in between 23°45' and 23°47' north latitudes and in between 90°22' and 90°23' east longitudes. Location of the experimental site is presented in Appendix 1 and 2.

3.1.3 Climaticcondition

The geographical location has a subtropical monsoon climate characterized by wide seasonal variations in rainfall, high temperatures and humidity. There are three distinct seasons in Bangladesh: a hot, humid summer from March to June; a cool, rainy monsoon season from June to October; and a cool, dry winter from October to March. In general, maximum summer temperatures range between

30°C and 40°C. April is the warmest month in most parts of the country. January is the coldest month, when the average temperature for most of the country is about 10°C. An average weather condition was enlisted for this experiment in Appendix 3.

3.1.4 Soil characteristics of the researchfield

The soils were acidic in nature, had moderate to high amounts of clay and the texture was medium (silt loam) to heavy (clay). The 2-20ƒÊm silt fraction was composed mainly of quartz, with small amounts of mica, plagioclase, K-feldspar and chlorite. Mica, kaolinite and the interstratified mineral of kaolinite and smectite were the predominant minerals in the <2 pm clay fraction. The soils of this AEZ have been developed from the Madhupur Clay and occupy a large area of 4,244 km2 (FAO. UNDP, 1988). Madhupur Tract or Red Soil Tract is a forest based land. The area is also known for the production of mango, banana, pomelo and pineapple. But deforestation in the last few decades has made a great loss to the environment which will not be recovered in future (Rahman *et al.* 2010). The optimum soil pH is 6.6 – 7.3 (SRDI,2001).

3.2 Description of theExperiment

3.2.1 Planting materialsused

35 Maize genotypes were used to execute the experiment in 360msq of land in three replications during 2017-2018(Rabi season) cropping season. The germination percentage of the genotypes were satisfactory, uniformed with 94-96% respectively. The genotypes were used presented in Table 1.

Table 1. Name and source of the genotypes used in the experimental study

Serial Number	Genotypic code	Genotypes	Source of collection
1.	G1	BHM-13	BARI
2.	G2	BHM-12	BARI
3.	G3	BHM-14	BARI
4.	G4	BHM-5(F1)	BARI
5.	G5	BHM-5(F3)	BARI
6.	G6	BHM-6(F1)	BARI
7.	G7	BHM-6(F3))	BARI
8.	G8	BHM-7	BARI
9.	G9	PAC-399	Lal Teer
10.	G10	PAC-984	Lal Teer
11.	G11	PAC-60	Lal Teer
12.	G12	Pacific	Petrocem Co.
13.	G13	Pacific-98	Petrocem Co.
14.	G14	HP-222	Petrocem Co.
15.	G15	Dekalb-30B07	Agrovet limited
16.	G16	Dekalb Super Gold	Agrovet limited
17.	G17	Dekalb Super	Agrovet limited
18.	G18	KhaiBhutta	BARI
19.	G19	Krishibid-102	Krishibid group
20.	G20	Shuvra	BARI

Table 1. Name and source of the genotypes used in the experimental study (Continued)

Serial Number	Genotypic code	Genotypes	Sourceof collection
21.	G21	AS-999(F1)	ACI
22.	G22	AS-999(F3)	ACI
23.	G23	Uttaran	Lal Teer
24.	G24	Misty	BARI
25.	G25	NK-40	Lal Teer
26.	G26	Bio Seed	BARI
27.	G27	Pioneer	Petrocem Co.
28.	G28	PAC-559	Lal Teer
29.	G29	Duranta	Ispahani
30.	G30	Cornell	Ispahani
31.	G31	Kaveri(218)	Ispahani
32.	G32	Kohinor-1820	Lal Teer
33.	G33	Kohinor	LalTeer
34.	G34	Chamak-07	Supreme Seed Co.
35.	G35	Golden-984	Supreme Seed Co.

3.2.2 Experimental Design andLayout

The experiment was designed and laid out in Randomized Complete Block Design (RCBD) with 3 replications. The supplied experimental land was 360msq in total. The field was divided into 3 blocks and the individual block size was 3m × 30m. Spacing was maintained 60cm × 20cm, row to row distance was 60cm, line to line distance was 20cm, block to block distance was 1m. The Genotypes were distributed randomly without biasness.

3.3 Growing ofcrops

3.3.1 Preparation of the mainland

The investigation field was first opened with power tiller and was exposed to the sun for a week for growing 35 maize genotypes. The field was prepared through ploughing, cross ploughing and laddering for proper tillage condition. Harrow, spade, hammer, rope and other instruments were used for preparing the land. Weeds, stubbles were removed; larger clods were broken into small particles to ensure exact growing condition. The plot was partitioned into three unit blocks according to the experimental design. Recommended doses of manures and fertilizers were used and mixed thoroughly. Proper irrigation and drainage channels were maintained around each block. Each unit block was designed keeping 5 cm height from the drains. After the completion of plot preparation, seed were sowing in properarrangement.

3.3.2 Application of manures andfertilizers

Green manure and decomposed organic matter were used at the rate of 6 ton/ha before final land preparation. For land preparation chemical fertilizers were applied such as Urea (14kg), TSP (8kg), MOP (6kg), Gypsum (6kg), Zinc Sulphate (1kg) and Boric Acid(1kg) in 360 ^{2}of the experimental land. The rest amount of Urea was applied 25 days after the first installment. The manure and fertilizer doses were enlisted in Table2.

3.3.3 Planting of seeds in thefield

The 35 maize genotypes were planted in lines each having a line to line distance 20 cm and row to row distance 60 cm under direct planting in well prepared plot on 20 December2017.

3.3.4 Aftercare

After the emergence of seedlings, different intercultural operations as well as protective activities were applied for proper growth and development of the plant.

3.3.4.1 Netting

To protect the crop from insect, birds and pest attack; the area was covered with net.

Table 2. Dose and method of manures and fertilizers application at the field

***For 360$n^2$of experimental land**

Name of the Manures andFertilizers	Actual Dose/ha (For Rabi Season)	First Application Basal Dose/ha	Second Application After 25 Days Dose/ha	Third Application After 45 Days Dose/ha
Cow-dung	4-6 tons	1 ton	-	-
Urea	172-312 kg	14kg	7kg	-
TSP	168-216 kg	8kg	-	-
MP	96-144 kg	6 kg	-	-
Gypsum	144-168 kg	6 kg	-	-
Zinc Sulphate	10-15 kg	1kg	-	-
Boric Acid	5-7 kg	1 kg	-	-

3.3.4.2 Thinning and gap filling

First thinning was done after 10 days of crop emergence on 30 December 2017 and second thinning was also done after 10 days of first thinning to maintain proper growth. Gap filling was not applied because the crop emergence was about 100%.

3.3.4.3 Irrigation

Irrigation played an important part in crop growth and development. Irrigation was provided repeatedly at pre-flowering and milking stage after 10th, 20th, 30th, 40th, 50thand 60thdays (Days after Transplanting) accordingly.

3.3.4.4 Weeding

Weeding was done to keep the field free from any unwanted plants other than the desired one. It also helped to provide aeration of soil, to conserve the soil moisture, for better growth anddevelopment.

3.3.4.5 Plantprotection

Chloropyriphose was applied after 45-50 days against sucking pest as jassid and aphids.

3.4 Harvesting, threshing andcleaning

In this experiment was executed using 35 maize genotypes. Therefore, the maturity level was different at different times. The crops were harvested after the husk cover dried; turned yellowish completely. The grains became strong and yellow; moisture percentage was lower; cobs of five randomly selected plants of each line were separatelyharvested.

3.5 Datacollection

3.5.1 Days to maleflowering

Data were recorded during the time of male flowering of 35 maize genotypes.

3.5.2 Days to femaleflowering

Data were recorded during the time of female flowering of 35 maize genotypes.

3.5.3 Days tomaturity

Data were recorded during the different time of maturity of 35 maize genotypes.

3.5.4 Plantheight

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

3.5.5 Cob length

Cob length was measured in millimeter from the bottom to the tip of the cob with the help of a meter scale.

3.5.6 Cob breadth

Cob length was measured in millimeter from the three position of cob with the help of slidecalipers.

3.5.7 Number of rows percob

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

1- Veryfew
2- Few
3- Medium
4- Many
5- Verymany

3.5.8 Number of seeds per row

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

3.5.9 Number of seeds per cob

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

3.5.10 Weight of 100-grain(g)

Weight of 100- grains from the composite sample of ears of five randomly selected plants in each plot wastaken.

3.5.11 Total yield per plant(kg)

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

3.6 Statisticalanalysis

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

3.7 Estimation of the different types ofvariability

By applying following formulae genotypic and phenotypic coefficient of variation and heritability were estimated as described below:

3.7.1 Estimation of genotypic and phenotypicvariance

Genotyping and phenotypic variances were estimated according to the formula given by Johnson et al., (1955). The genotypic variance (^{2}) was calculated by subtracting error mean square (EMS) from the genotypic mean square (GMS) and dividing it by the number of replication (r) as per following formula-

Genotypic variance, σ_g^2

Genotypic variance,$\sigma_g^2 = \frac{GMS-EMS}{r}$

Where,

GMS= Genotypic mean square

EMS= Error mean square

r = Number of Replication\

Phenotypic variance, ^{2}=σ^2+ EMS

Where,

^{2}=Phenotypic variance

σ^2= Genotypic variance

EMS = Error mean square

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

Genotypic and phenotypic co-efficient of variations were estimated according to Burton (1952) and Singh and Chaudhary (1985):

Genotypic co-efficient of variation, GCV= $\frac{\sqrt{^{2}}}{\bar{}} \times 100$

Where,

^{2} = Genotypic variance

$\bar{}$ =Populationmean

Phenotypic co-efficient of variations,PCV= $\frac{\sqrt{^{2}}}{\bar{}} \times 100$

Where,

^{2}= Phenotypic variance

$\bar{}$ =Populationmean

3.7.3 Estimation ofheritability

Heritability in broad sense (h2b) was estimated according to the formula suggested by Johnson et al. (1955) and Hanson et al. (1956):

Heritability, $^{2}=\frac{^{2}}{^{2}} \times 100$

Where,

^{2}= Genotypic variance,

^{2}= Phenotypic variance

3.7.4 Estimation of geneticadvance

Estimation of genetic advance was done following formula given by Johnson *et al*. (1955) and Allard (1960):

Genetic advance, GA = $^{2} \times \quad \times$

Where,

^{2}= Heritability

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

= Phenotypic standard deviation

3.7.5 Estimation of genetic advance inpercentage

Genetic advance in percent of mean was calculated by the formula of Comstock and Robinson (1952) as follows:

Genetic advance in percentage of mean, GA (%) = $\frac{}{\bar{}} \times 100$

Where,

GA = Genetic advance

$\bar{}$ = Population mean

3.8 Estimation of correlationcoefficient

The correlation coefficient (r) between two variables such as X and Y can be estimated using following formula (Singh and Chaudhary, 1985):

$$= \frac{\sum \quad {}_{2} - \frac{\sum \quad \sum}{} \quad {}_{2}}{\sqrt{}\{\sum \quad {}^{2} - \frac{(\sum \quad)}{}\}\{\sum \quad {}^{2} - \frac{(\sum \quad)}{}}$$

Where,

$\sum \qquad - \frac{\sum \quad \sum}{}$ = Sum of products of X and Y

$\{\sum \quad {}^{2} - \frac{(\sum \quad)^{2}}{}\}$ = Sum of squares of X

$\{\sum \quad {}^{2} - \frac{(\sum \quad)^{2}}{}\}$ = Sum of squares of Y

3.9 Path co-efficientanalysis

Path co-efficient analysis was developed by Dewey and Lu (1959) and also quoted in Singh and Chaudhary (1985) by applying simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect independent variables on the dependent variables.

In order to estimate direct and indirect effect of the correlated characters viz; ${}_{1}$, ${}_{2}$, ${}_{3}$; yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as followed:

$${}_{1}= \quad {}_{1}+ \quad {}_{2} \quad {}_{1} \quad {}_{2}+ \quad {}_{3} \quad {}_{1} \quad {}_{3}$$

$${}_{2} = \quad {}_{1} \quad {}_{1} \quad {}_{2}+ \quad {}_{2}+ \quad {}_{3} \quad {}_{2} \quad {}_{3}$$

$${}_{2}= \quad {}_{1} \quad {}_{1} \quad {}_{3}+ \quad {}_{2} \quad {}_{2} \quad {}_{3}+ \quad {}_{3}$$

Where,

r = simple correlation coefficient and

P= path coefficient (unknown).

P in the above equations may be conveniently solved by arranging them in matrix form and total correlation is partitioned as follows:

$_1$ = The direct effect of $_1$ on y

$_1$ $_1$ $_2$= The indirect effect of $_1$ via $_2$ on y

$_1$ $_1$ $_3$ = The indirect effect of $_1$ via $_3$ on y

Residual effect was calculated after the estimation of direct and indirect effect of the characters studied. The following formula was used to calculate the residual effect:

^{2}RY=1-

$\sum$ .riy Where,

^{2}RY=(^{2});andhenceresidualeffect,R=(^{2})$^{1/2}$

= Direct effect of the character on yield

Riy = Correlation of the character with yield

3.10 Multivariateanalysis

The selected characters were conducted under multivariate analysis methods; principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA), cluster analysis and ^{2}analysis through GENSTATE 4.2 program.

3.10.1 Principal component analysis(PCA)

Principal component analysis is one of the multivariate techniques and dimension-reduction tool that can be used to reduce a large set of variables to a small set that still contains most of the information in the large set. It can be used to know the inter-relationships among several characters and can interpret through 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 coordinate analysis(PCO)

Principal coordinate analysis is equivalent to PCA, but it is used to calculate inter-unit distances. with the use of all dimensions of p, it gives the minimum distances between each pair of n points similarity matrix (Digby *et al.* 1989). Inter distances between genotypes were estimated 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. That provides two-dimensional plots that helped in separating different populations involved.

3.10.4 Clusteranalysis

Genotypes were involved into groups, based on 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 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 Analysis for average intra and inter clusterdistance

The inter-class cluster show the distance between data point with cluster center, meanwhile intra-class cluster show the distance between the data point of one cluster with the other data point with another cluster. Intra cluster distances of average computation for each cluster was estimated through ^{2}values within the numbers of a cluster obtained from the PCO after the clusters are formed. By applying formula $\sum \frac{{}^{2}}{\quad}$

Where,

$\sum$ ^{2}= The sum of distances between all possible combinations (^{2}values represent the distance within cluster)

n = The genotypes included in a cluster

To calculate the inter cluster distance between the cluster point one by one and the distance between them. The cluster diagram was drawn using the values between and within the clusters distances which presents a momentary idea of the pattern of diversity among the genotypes included in acluster.

3.11 Analysis of Genetic Divergence (statistical analysis)

Genetic divergence among the 35 genotypes investigated were assessed by applying Mahalanobis' ^{2}statistics and its auxillary analysis. Multivariate analysis was done utilisingMahalanobis D2 statistic (Mahalanobis, 1936).

Mahalanobis' ^{2}statistics

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

‘∧’= ——= ————————————————

+

Now,‘∧’(stat)=-mlog ∧ =-{ $-($ $+$ $+1)/2$}log ∧

Where,

m = $-($ $+$ $+1)/2$

n = number of variables or characters

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

n = df for error + varieties

e = 2.7183

Data were analyzed to find out the genetic divergence employed the ^{2}statistics by Rao (1952).

^{2}ij = $\sum($ $-$ $)^{2}$

Where,

^{2}ij = 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

Plate 1. Photographs showing experimental field preparation

CHAPTER IV

RESULTS AND DISCUSSION

This chapter represents the constructive presentation and valued discussion on the experiment that carried out with 35 Maize genotypes. The genetic parameters and character association in relation to the yield and its component attributes were computed, statistically analysed and systematically obtained the results. Therefore, the outcomes are discussed below with narration under the following headings:

4.1 Analysis ofVariance

4.2 Genetic Variability, Heritability, GeneticAdvance

4.3 CorrelationAnalysis

4.4 Path Analysis(coefficient)

4.5 Genetic DiversityAnalysis

4.1 Analysis ofVariance

Analysis of variance was carried out to partition the variances into its components. The results of the analysis revealed highly significant differences among the mean values for all traits i.e. days to male flowering, days to female flowering, days to maturity, plant height, cob length, cob breadth, number of rows per cob, number of seeds per row, 100-seed weight and yield per plant (Table 3 and 4).

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

Characters	Mean sum of square		
	Replication (r-1) = 2	**Genotype (g-1) = 34**	**Error (r-1)(g-1) = 68**
Days to male flowering	0.64	10.82**	1.66
Days to female flowering	54.60	12.47**	1.87
Days to maturity	10.24	4.85**	2.36
Plant height (cm)	371.14	872.33**	153.34
Cob length (cm)	13.24	4.28**	1.16
Cob breadth (cm)	7.98	4.28**	0.72
No. of rows per cob	0.17	9.92**	0.55
No. of seeds per row	276.69	74.10**	9.13
Number of seeds per cob	57812.62	27896.88**	3713.39
100-seed weight (g)	2.14	23.77**	4.11
Yield per plant (g)	1742.81	834.80**	131.28

**: Denote Significant at 1% levelofprobability *: Denote Significant at 5% level of probability

Table 4. Range, mean, CV (%) and standard deviation of 35 maize genotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Days to male flowering	61.00	68.00	64.98	1.98	1.29	0.49
Days to female flowering	56.33	66.67	61.31	2.23	1.37	0.52
Days to maturity	127.00	130.67	128.82	1.19	1.53	0.58
Plant height (cm)	205.16	258.97	238.72	5.19	12.38	4.68
Cob length (cm)	14.83	18.87	16.96	6.36	1.08	0.41
Cob breadth (cm)	12.57	17.30	15.30	5.55	0.85	0.32
No. of rows per cob	12.57	22.38	14.11	5.25	0.74	0.28
No. of seeds per row	24.52	46.96	36.37	8.31	3.02	1.14
No. of seeds per cob	350.44	798.95	513.58	11.87	60.94	23.03
100-seed weight (g)	27.33	39.67	31.81	6.37	2.03	0.77
Yield per plant (g)	51.89	117.51	81.77	14.01	11.46	4.33

CV (%) = coefficient of variation, SD = standard deviation and SE = standard error

4.2 Genetic Variability, Heritability and GeneticAdvance

Prominent variation and significant differences in genetic variability, heritability and genetic advance are depicted in Figure 1 and Figure 2. Also a cooperative study has been carried out and presented in Table 4 as well as in Table 5. The mean performances of the 35 Maize genotypes with various growth characters and yield components are shown in Appendix5.

4.2.1 Days to maleflowering

The Maximum days to male flowering was estimated in G30 (68.0) and the minimum in G8 (61.0) (Table 4 and Appendix 6). Mean performance and coefficient of variation was recorded 64.98 and 1.98% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 4.71, 3.05 and 1.66 (Table 5). Phenotypic coefficient of variance (3.34) was higher than genotypic coefficient of variance (2.69) and environmental coefficient of variance (1.98) (Table 5). Heritability was recorded 64.82 and genetic advance was 2.9 at 5% level of significance. Days to male flowering was positively and significantly correlated with the other traits (days to female flowering, days to maturity, plant height, cob breadth, row per cob, seed per row, seed per cob, 100 seed weight and yield per plant). Similar findings were observed in Zahid *et al.* (2004) investigation that broad-sense heritabilty, coefficients of variability and genetic advance values were computed for low, medium and higher in relation to days taken to tasseling, number of days taken to silking.

4.2.2 Days to femaleflowering

The Maximum cob length was estimated in G5 (66.67) and the minimum in G29 (56.33) (Table 4 and Appendix5). Mean performance and coefficient of variation was recorded 61.31 and 2.23% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 5.41, 3.53 and

1.87 (Table 5). Phenotypic coefficient of variance (3.79) was higher than genotypic coefficient of variance (3.06) and environmental coefficient of variance (2.23) (Table 5). Heritability was recorded 65.33 and genetic advance was estimated at 3.13 at 5% level of significance. Days to female flowering was positively and significantly correlated with the other traits (days to male flowering, days to maturity, plant height, cob length, cob breadth, row per cob, seed per row, seed per cob, 100 seed weight and yield perplant).

4.2.3 Days tomaturity

The Maximum cob length was estimated in G15 (130.67) and the minimum in G17 (127.0) (Table 4 and Appendix 6). Mean performance and coefficient of variation was recorded 128.82 and 1.19% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 2.52, 0.16 and 2.36 (Table 5). Phenotypic coefficient of variance (1.23) was not higher than genotypic coefficient of variance (6.32) and environmental coefficient of variance (7.19) (Table 5). Heritability was recorded 46.53 and genetic advance was estimated at 2.21 at 5% level of significance. Days to maturity was positively and significantly correlated with the other traits (days to male flowering, days to female flowering, days to maturity, plant height, cob breadth, row per cob, seed per row, seed per cob, 100 seed weight and yield perplant).

Plate 2. Photographs showing growing stages of various genotypes of maize

4.2.4 Plantheight

Height is one of the most heritable and easily measured traits in maize (Jason et al., 2014). Here, considerable differences were observed in terms of mean sum square performance among the genotypes (Table 3 and 4). Plant height ranged from 205.16(G6) to 258.97(G9); mean performance and coefficient of variation were estimated 238.72 and 5.17% respectively (Table 4 and Appendix 5). The phenotypic and genotypic variability observed and presented in Figure 1 andTable 5. The phenotypic variability (around 9) was recorded higher in terms of genotypic variability (around 7). Bello *et al.* (2012); Anshuman *et al.* (2013), Hassan *et al.* (2018); Zahid *et al.* (2004) reported highest heritability estimates were found in grain yield plant-1 (0.993) and by plant height (0.990). Similar findings also recorded in Alvi*et al.* (2003) experimentation.

4.2.5 Cob Length

The maximum cob length was estimated in G22 (18.87 cm) and the minimum in G5 (14.90 cm) (Table 4 and Table 6). Mean performance and coefficient of variation was recorded 16.96 and 6.36% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 2.20, 1.04 and 1.16 (Table 5). Phenotypic coefficient of variance (8.76) was higher than genotypic coefficient of variance (6.02) and environmental coefficient of variance (6.36) (Table 5). Heritability was estimated 47.18 and genetic advance was recorded 1.44 at 5% level of significance. Cob length was positively and significantly correlated with the other traits (days to male flowering, days to female flowering, days to maturity, plant height, cob breadth, row per cob, seed per row, seed per cob, 100 seed weight and yield per plant). Anshuman *et al.* (2013); Juliet *et al.* (2013) estimated higher heritability and genetic advance. The greater heritability means lower environmentaleffects.

4.2.6 Cob Breadth

The maximum cob breadth was estimated in G15 (17.30cm) and the minimum in G20 (12.57cm) (Table 4 and Appendix 5). Mean performance and coefficient of variation was recorded 15.30 and 5.55% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 1.91, 1.19 and 0.72 (Table 5). Phenotypic coefficient of variance (9.03) was higher than genotypic coefficient of variance (7.12) and environmental coefficient of variance (5.55) (Table 5). Heritability was estimated 62.26 and genetic advance was recorded 1.77 at 5% level of significance. Cob breadth was positively and significantly correlated with the other traits (days to male flowering, days to female flowering, days to maturity, plant height, cob breadth, row per cob, seeds per row, 100 seed weight and yield per plant). Rafiq *et al.* (2010); Hassan *et al.* (2018) observed high heritability and genetic advance to contribute in yield characters.

4.2.7 Number of rows percob

The genotypes that were used in the experiment showed significant differences as well as variation for various number of seed row per cob (Table 4 and Table 6). The maximum number of seed row per cob was estimated in G12 (22.38cm) and the minimum in G24 (12.57cm) (Table 4 and Appendix 5). Mean performance and coefficient of variation was recorded 14.11 and 5.25% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 3.67, 3.12 and 0.55 (Table 5). Phenotypic coefficient of variance (13.58) was higher than genotypic coefficient of variance (12.53) and environmental coefficient of variance (5.25) (Table 5). Heritability for this trait was impressively higher (85.08%) with compared lower genetic advance (3.36 at 5% level of significance) that reflecting a positive relation and suitable selection for this character) (Table 5 and Figure 3). Juliet *et al.* (2013) showed similar findings for the genotypes studied a wide range of variation for all the characters.

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

Parameters	±^{2}p	±^{2}g	±^{2} e	PCV	GCV	ECV	h^{2}	GA (5%)	GA s(% mean)
Days to male flowering	4.71	3.05	1.66	3.34	2.69	1.98	64.82	2.90	4.46
Days to female flowering	5.41	3.53	1.87	3.79	3.06	2.23	65.33	3.13	5.10
Days to maturity	2.52	0.16	2.36	1.23	6.32	7.19	46.53	2.21	6.17
Plant height (cm)	393.00	239.66	153.34	8.30	6.48	5.19	60.98	24.90	10.43
Cob length (cm)	2.20	1.04	1.16	8.76	6.02	6.36	47.18	1.44	8.51
Cob breadth (cm)	1.91	1.19	0.72	9.03	7.12	5.55	62.26	1.77	11.58
No. of rows per cob	3.67	3.12	0.55	13.58	12.53	5.25	85.08	3.36	23.80
No. of seeds per row	30.79	21.66	9.13	15.26	12.80	8.31	70.34	8.04	22.11
Number of seeds per cob	11774.55	8061.16	3713.39	21.13	17.48	11.87	68.46	153.04	29.80
100-seed weight (g)	10.66	6.56	4.11	10.27	8.05	6.37	61.50	4.14	13.00
Yield per plant (g)	365.79	234.50	131.28	23.39	18.73	14.01	64.11	25.26	30.89

σ^{2}p : Phenotypic variance
σ^{2}g : Genotypic variance
σ^{2} e : Environmental variance

PCV : Phenotypic coefficient of variation
GCV : Genotypic coefficient of variation
ECV : Environmental coefficient of variation

h^{2} :Heritability
GA(5%) : Genetic advance(5%)
GA (% mean) : Genetic advance (% mean)

4.2.8 Number of seeds perrow

The genotypes that were used in the experiment showed significant differences as well as variation for various number of seed per row (Table 5 and Table 6). Themaximum number of seed row per cob was estimated in G28 (46.96) and the minimum in G3 (24.52) (Table 4 and Appendix 5). Mean performance and coefficient of variation was recorded 36.37 and 8.31% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 30.79, 21.66 and 9.13 (Table 5). Phenotypic coefficient of variance (15.26) was higher than genotypic coefficient of variance (12.80) and environmental coefficient of variance (8.31) (Table 5). Heritability for this trait was impressively higher (70.34%) with compared lower genetic advance (8.04 at 5% level of significance) that reflecting a positive relation and suitable selection for this character) (Table 5 and Figure 2). In the findings of Rafiq *et al.* (2010) and Hassan *et al.* (2018) recorded higher genetic advancefor plant height, ear length, grains per row and grain yield.

4.2.9 Number of seeds per cob

The genotypes that were used in the experiment showed significant differences as well as variation for various number of seeds per cob (Table 4 and Appendix 5). The maximum number of seed row per cob was estimated in G12 (798.95) and the minimum in G17 (350.44) (Table 4 and Appendix 5). Mean performance and coefficient of variation was recorded 513.58 and 11.87% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 11774.55, 8061.16 and 3713.39 (Table 5). Phenotypic coefficient of variance (21.13) was higher than genotypic coefficient of variance (17.48) and environmental coefficient of variance (11.87) (Table 5). Heritability for this trait was impressively higher (%) with compared lower genetic advance (153.04 at 5%

Plate 3. Photographs showing cob formation, male flower (tassel) and female flower (silk) stages of various genotypes

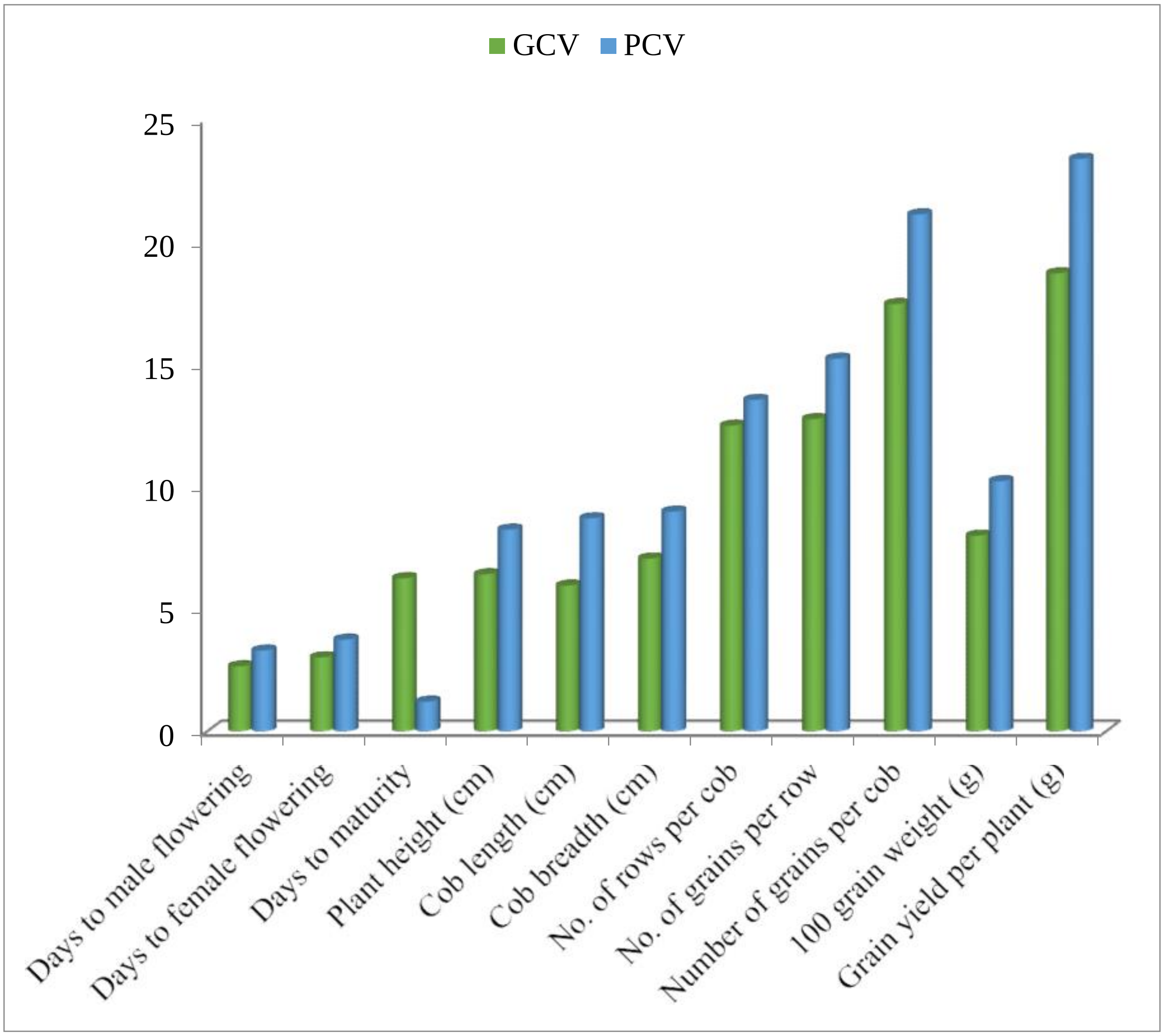

Fig 1. Genotypic and phenotypic variability in maize

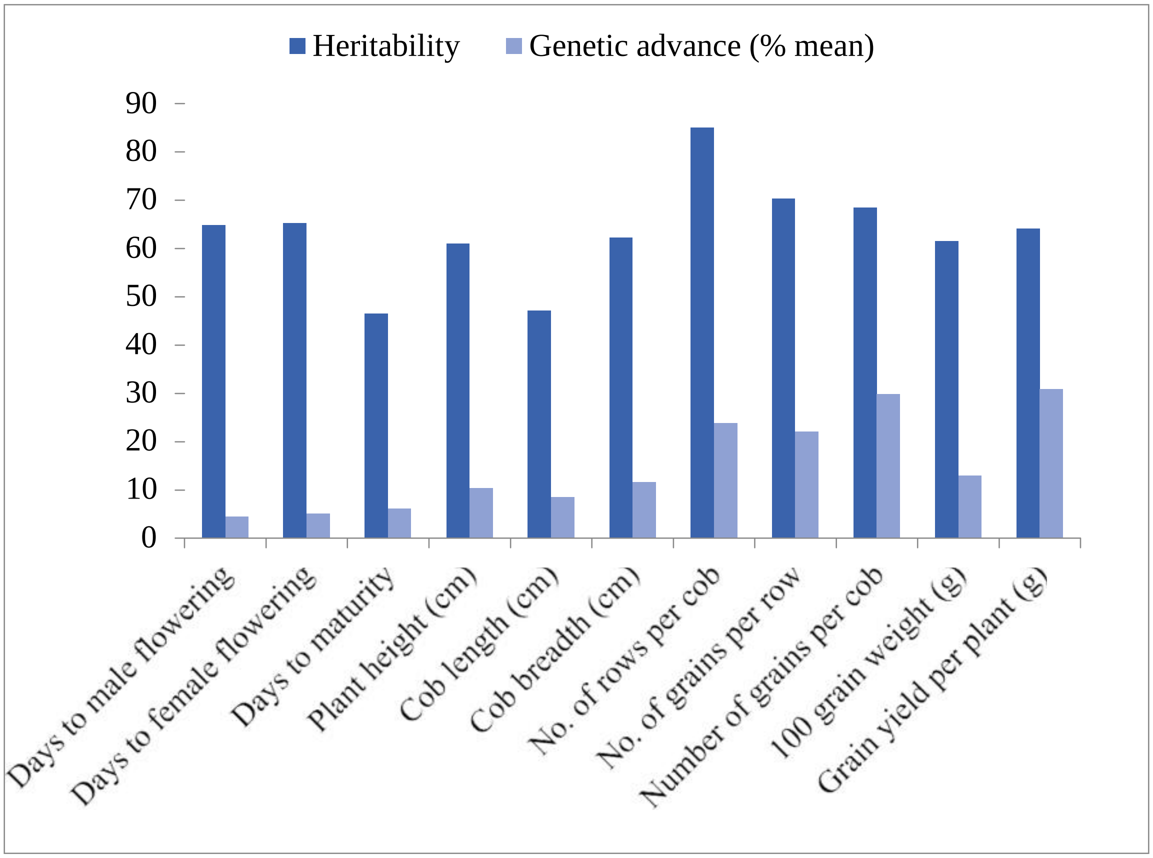

Fig 2. Heritability and genetic advance as percent over mean in maize

level of significance) that reflecting a positive relation and suitable selection for this character (Table 5 and Figure 2).

4.2.10 100-seedweight

The genotypes that were used in the experiment showed significant differences as well as variation for 100 seed weight. The maximum number of seed row per cob was estimated in G29 (39.67) and the minimum in G1 (27.33) (Table 4and Appendix 5). Mean performance and coefficient of variation was recorded 31.81 and 6.37% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 10.66, 6.56 and 4.11 (Table 5). Phenotypic coefficient of variance (10.27) was higher than genotypic coefficient of variance (8.05) and environmental coefficient of variance (6.37) (Table 5). Heritability for this trait was impressively higher (61.50%) with compared lower genetic advance (4.14 at 5% level of significance) that reflect a positive relation and suitable selection for this character) (Table 5 and Figure 2). In the findings of Rajesh *et al.* (2013), high to moderate estimates of GCV and PCV were recorded for Grain yield, number of kernels per row, 100-kernel weight, ear length and plant height which represents considerable variability and offers scope for genetic improvement throughselection.

4.2.11 Total yield perplant

The genotypes that were used in the experiment showed significant differences as well as variation for total yield per plant (gm) (Table 4 and Appendix 5). The maximum number of seed row per cob was estimated in G12 (117.51) and the minimum in G17 (51.89) (Table 4 and Appendix 5). Mean performance and coefficient of variation was recorded 81.77 and 14.01% respectively (Table 4). The phenotypic, genotypic as well as environmental variances for this character were estimated 365.79, 234.50 and 131.28 (Table 5). Phenotypic coefficient of variance(23.39)washigherthangenotypiccoefficientofvariance(18.73)and environmental coefficient of variance (14.01) (Table 5). Heritability for this trait was impressively higher (64.11) with compared lower genetic advance (25.26 at 5% level of significance) that reflecting a positive relation and suitable selection for this character) (Table 5 and Figure 2). Hassan *et al.* (2018), Khan et al. (2019) and Debnath (1987) reported High values of genetic advance were obtained for grain yield.

4.3 Correlationanalysis

This investigation on yield and its component attributes as well as their inter relationship with direct and indirect contribution has profound importance in terms of future breeding programs.

Yield is the ultimate result that is the combination of several components characters and environmental effects. Understanding the interaction of component characters among themselves with environmental factors plays crucial role in the implementation of plant breeding program. Analysis study on correlation factor provide information on the nature and extend of the characters association, between two pairs of metric characters. By considering this it would be possible to identify the genetic upgradation in one character by the selection of the other pair. Thus, this knowledge about character association will positively enhance the possible identification for higher yielding genotypes for future studies in breeding sector. The genotypic and phenotypic correlations between the pairs of character attributes are presented in Table 6 and 7. From the table, it can be depicted that the genotypic correlation coefficients among the different pairs of yield and its component contributing characters are mostly higher than the phenotypic correlation coefficient for different genotype of maize. The results are discussed below with the followingattributes:

4.3.1 Days to maleflowering

It showed highly positive significant correlation with plant height and negative significant correlation with days to female flowering at both genotypic and phenotypic level (Table 6). Non-significant positive correlation was observed with days to maturity, cob length, seed per row, and 100-seed weight at both genotypic and phenotypic level (Table 6). Non-significant negative correlation was observed with cob breadth and grain yield per plant. Rajesh *et al.* (2013) showed positive significant association with the characters namely; days to 50% tasseling, days to 50% silking.

4.3.2 Days to femaleflowering

It showed highly negative and significant correlation with plant height, cob length, cob breadth, and 100-seed weight (Table 6 and Figure 3). Unfortunately, positive and significant correlation was not observed in the Table 6.

4.3.3 Days tomaturity

It showed highly positive and significant correlation with cob breadth, row per cob, seed per row, seed per cob, and grain yield per plant (Table 6) at genotypic level. Negative non-significant correlation was observed with 100-seed weight (Table 6 and Figure 3). Khan *et al.* (2019) reported similar resultfindings.

4.3.4 Plantheight

Plant height showed significant positive correlation with cob length, cob breadth, 100 gm seed weight at both the genotypic and phenotypic correlation coefficient (Table 6). It showed non-significant negative correlation with number of row per cob, number of seed per row, number of seed per cob and non-significant positive correlation with total seed yield (Table 6 and Figure 3). Kumar *et al.* (2014) was observed similar report demonstrated the positive and significant phenotypic correlations for the grain yield in association with plant and ear height

4.3.5 Cob length

Cob length showed significant positive correlation with cob breadth, 100 gm seed weight, total seed weight at both the genotypic and phenotypic correlation coefficient (Table 6). It showed non-significant positive correlation with number of rows per cob, number of seed per row, number of seed per cob (Table 6). Number of seeds per row and number of seed per cob showed positively significant correlation in terms of genotypic correlation coefficient (Table 6 and figure 3). In this case, significant negative association was not found for any level of significance (Table 6). Basir*et al.* (2003) estimated positive correlation to cob length contributing in yieldfactor.

4.3.6 Cob breadth

Cob breadth showed significant positive correlation *w*ith the genotypic and phenotypic correlation coefficient (Table 8). It showed non-significant negative correlation with number of rows per cob, number of seed per row, number of seed per cob and non-significant positive correlation with total seed yield (Table 6).

4.3.7 Number of seed row percob

Number of seed row per cob showed positive and significant correlation with days to female flowering, number of seed per row, seed per cob and 100-seed weight (Table 6). Positive non-significant correlation was observed with cob length, cob breadth (Table 6). Non-significant negative correlation was observed with days to male flowering and plant height. Zaffar*et al.* (2018) showed similar experimental report on positive and significant correlation to seed row per cob.

Table 6. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of Maize

		DMF	DFF	DM	PH (cm)	CL (cm)	CB (cm)	RPC	GPR	GPC	100GW (g)
DFF	G	-0.431**									
	P	-0.293**									
DM	G	0.120	-0.216*								
	P	0.013	-0.084								
PH (cm)	G	0.226*	-0.664**	-0.093							
	P	0.145	-0.454**	0.175							
CL (cm)	G	0.092	-0.542**	0.047	0.774**						
	P	0.042	-0.376**	0.076	0.634**						
CB (cm)	G	-0.029	-0.448**	0.314**	0.741**	0.956**					
	P	-0.043	-0.370**	0.124	0.565**	0.877**					
RPC	G	-0.265**	0.022	0.393**	-0.082	0.057	0.124				
	P	-0.223*	0.010	0.107	-0.125	0.043	0.093				
GPR	G	0.094	-0.004	0.245*	0.012	0.206*	0.114	-0.020			
	P	0.059	-0.003	0.097	-0.014	0.153	0.070	0.049			
GPC	G	-0.133	0.003	0.432**	-0.034	0.205*	0.195*	0.698**	0.703**		
	P	-0.105	0.008	0.127	-0.084	0.142	0.117	0.689**	0.751**		
100GW (g)	G	0.125	-0.519**	-0.303**	0.323**	0.369**	0.159	-0.154	0.068	-0.062	
	P	0.097	-0.274**	-0.035	0.210*	0.249*	0.163	-0.125	0.103	-0.002	
GYP (g)	G	-0.077	-0.211*	0.228*	0.124	0.365**	0.265**	0.577**	0.688**	0.905**	0.365**
	P	-0.054	-0.110	0.084	0.018	0.241*	0.187	0.560**	0.724**	0.896**	0.433**

** = Significantat1%. * = Significant at5%.

4.3.8 Number of seed perrow

Number of seeds per row showed positive and significant correlation with days to days to maturity and cob length at genotypic level (Table 6). Non-significant positive correlation was observed with days to male flowering and cob breadth both genotypic and phenotypic level (Table 6).

4.3.9 Number of seeds per cob

Number of seeds per cob showed positive and significant correlation with days to maturity, cob length, cob breadth, row per cob and seed per row (Table 6). Non-significant positive correlation was estimated with days to female flowering at both genotypic and phenotypic level (Table 6). Non-significant negative correlation was observed with days to male flowering at both phenotypic and genotypic level (Table 6).

4.3.10 100- seedweight

Significant positive correlation was observed with, plant height, cob length, number of seed per row and total yield per plant at both phenotypic and genotypic level of significance (Table 6). Days to male flowering, cob breadth showed non-significant positive correlation at both genotypic and phenotypic level (Table 6). Non -significant negative correlation was observed with days to female flowering, days to maturity and number of seed row per cob at level (Table 6). Total grain yield showed absolute positive significant correlation 100-seed weight (Table 6). Sofi and Rather (2007) reported similar findings that correlated with grain yield and 100-seed weight.

Dekalb-30B07(G-15)Pacific (G-12)DekalbSuper (G-17)

Plate 4. Photographs Showing different types of cob of maize genotypes

Misty (G-24)Kohinor (G-33)AS-999 (G-22)

Plate 4. Photographs Showing different types of cob of maize genotypes(Continued)

Cornell (G-30) BHM-06 (G-6) PAC-559 (G-28)

Plate 4. Photographs Showing different types of cob of maize genotypes (Continued)

4.4 Path analysis(coefficient)

The path coefficient analysis was first developed by Wright (19210 and demonstrated by Dewey and Lu (1959) in order to create the positioning of correlation coefficients into direct and indirect contribution of various characters of the yield. The correlation indicate the association pattern of components traits with yield; representing overall influence of a particular trait on yield whereas path coefficient analysis provides cause and effect relationships of the component traits. Path coefficients are standardized versions of linear regression coefficient analysis. It measures the direct influence of one variable upon other. It is a great deal for the breeders to know the cause and effect relations, direct and indirect relationships among the traits for further genetic improvement and research. The direct and indirect effects of path coefficient analysis are presented in Table9.

4.4.1 Directeffects

Four out of ten characters showed positive direct effect on grain yield per plant. The characters that represents direct effect were days to male flowering (0.247), cob breadth (1.078), number of seeds per cob (6.874). and 100-seed weight (0.595). On the other hand, negative direct effects were observed in days to female flowering (-0.031), days to maturity (-0.272), plant height (-0.156), cob length (-1.119), number of seed row per cob (-4.121) and number of seeds per row (-4.111). Therefore, path coefficient analysis for grain yield per plant showed direct relationship with days to male flowering, cob breadth, number of seeds per cob and 100-seed weight (Table 7). In this case, selection for any of these independent traits leads to improving the genotypes for the grain yield per plant in breedingprograms.

4.4.2 Indirecteffects

Days to male flowering had positive indirect effect with days to female flowering (0.0130, number of seed row per cob (1.092) and 100-seed weight (0.0740. However, it had negative indirect effect through days to maturity (-0.033), plant height (-0.035), cob length (-0.103), cob breadth (-0.031), number of seeds per row (-0.385) and number of seeds per cob (-0.917) (Table 7). Days to female flowering had positive indirect effect on days to maturity (0.059), plant height (0.103), cob length (0.607), number of seeds per row (0.016) and number of seeds per cob (0.023). On the other hand, it showed negative indirect effect through days to male flowering (-0.107), cob breadth (-0.483), number of rows per cob (-0.090) and 100-seed weight (-0.309) (Table 7). Days to maturity had positive indirect effect with days to male flowering (0.030), days to female flowering (0.007), plant height (0.014), cob breadth (0.339) and number of seeds per cob (2.970). At the same time, it showed negative indirect effect through cob length (-0.052), number of rows per cob (-1.620), number of seeds per row (-1.007) and 100-seed weight (-0.180) (Table 7). Plant height had impressive positive indirect effect with days to male flowering (0.056), days to female flowering (0.020), days to maturity (0.025), cob breadth (0.799), number of seed rows per cob (0.336) and 100-seed weight (0.192). Whereas, it showed negative indirect effect through cob length (-0.866), number of seeds per row (-0.048) and number of seeds per cob (-0.235) (Table 7). Cob length showed positive indirect effect with days to male flowering (0.023), days to female flowering (0.017), cob breadth (1.031), number of seeds per cob (1.412) and 100-seed weight (0.219). On the other hand, it had negative indirect effect with days to maturity (-0.013), plant height (-0.121), number of rows per cob (-0.236) and number of seeds per row (-0.847) (Table 7). Cob breadth had positive indirect effect with days to female flowering (0.014), number of seeds per cob (1.337) and 100-seed weight (0.095); whereas, days to male flowering (-0007), days to maturity (-0.086), plant height (-0.115), cob length (-1.070), number of seed rows per cob (-0.511) and number of seeds per row (-0.470) had negative indirect effect (Table 7). Number of seed rows per cob had positive indirect effect withplant

Table 7. Partitioning correlation coefficient into direct (bold) and indirect effect

Characters	Days to male flowering	Days to female flowering	Days to maturity	Plant height (cm)	Cob length (cm)	Cob breadth (cm)	No. ofrows per cob	No.of grains per row	Number of grains per cob	100 grain weight (g)	Genotypic correlation with yield
Days to male flowering	**0.247**	0.013	-0.033	-0.035	-0.103	-0.031	1.092	-0.385	-0.917	0.074	-0.077
Days to female flowering	-0.107	**-0.031**	0.059	0.103	0.607	-0.483	-0.090	0.016	0.023	-0.309	-0.211*
Days to maturity	0.030	0.007	**-0.272**	0.014	-0.052	0.339	-1.620	-1.007	2.970	-0.180	0.228*
Plant height (cm)	0.056	0.020	0.025	**-0.156**	-0.866	0.799	0.336	-0.048	-0.235	0.192	0.124
Cob length (cm)	0.023	0.017	-0.013	-0.121	**-1.119**	1.031	-0.236	-0.847	1.412	0.219	0.365**
Cob breadth (cm)	-0.007	0.014	-0.086	-0.115	-1.070	**1.078**	-0.511	-0.470	1.337	0.095	0.265**
No. of rows per cob	-0.065	-0.001	-0.107	0.013	-0.064	0.134	**-4.121**	0.081	4.799	-0.092	0.577**
No. of grains per row	0.023	0.000	-0.067	-0.002	-0.231	0.123	0.081	**-4.111**	4.830	0.040	0.688**
No. of grains per cob	-0.033	0.000	-0.118	0.005	-0.230	0.210	-2.877	-2.889	**6.874**	-0.037	0.905**
100 grain weight (g)	0.031	0.016	0.082	-0.050	-0.412	0.171	0.635	-0.279	-0.424	**0.595**	0.365**

Residual effect: 0.016

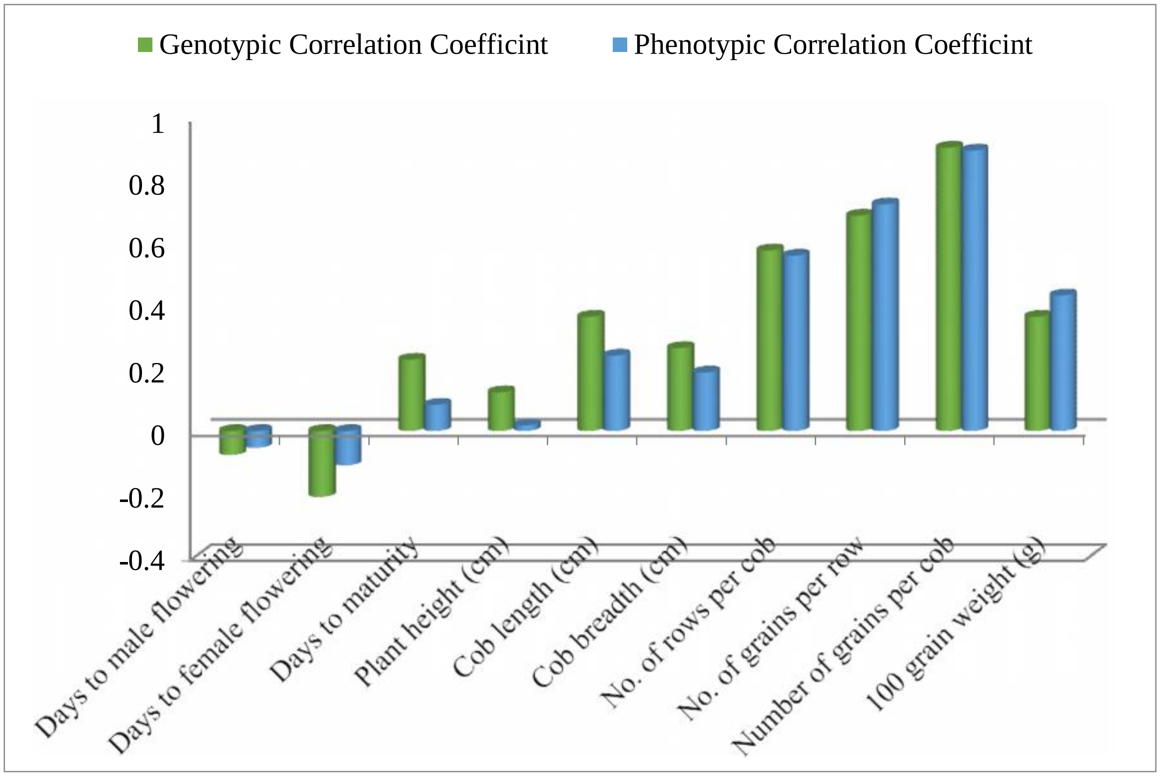

Fig 3. Graphical representation of genotypic and phenotypic correlation of yield contribution traits with yield

height (0.013), cob breadth (0.134), number of seeds per row (0.081) and number of seeds per cob (4.799). However, it showed negative indirect effect on days to male flowering (-0.065), days to female flowering (-0.001), days to maturity (-0.107), cob length (-0.064) and 100-seed weight (-0.092) (Table 7). In case of number of seeds per row had positive indirect effect with days to male flowering (0.023), cob breadth (0.123), number of seed rows per cob (0.081), number of seeds per cob (4.830) and 100-seed weight (0.040). In contrast, it had negative indirect effect with days to maturity (-0.067), plant height (-0.002), cob length (-0.231) and no effect with days to female flowering (0.000) (Table 7). Number of seeds per cob showed positive indirect effect with plant height (0.005), cob breadth (0.210) and no effect with days to female flowering (0.000). On the other hand, it represented negative indirect effect with days to male flowering (-0.033), days to maturity (-0.118), cob length (-0.230), number of rows per cob (-2.877), number of seeds per row (-2.889) and 100-seed weight (-0.037) (Table 7). 100-seed weight had positive indirect effect with days to male maturity (0.031), days to female flowering (0.016), days to maturity (0.082), cob breadth (0.171) and number of rows per cob (0.635). However, it showed negative indirect effect with plant height (-0.050), cob length (-0.412), number of seeds per row (-0.279) and number of seeds per cob (-0.424) (Table7).

4.5 Geneticdiversity

Genetic diversity serves as a way for populations to adapt to changing environments. Thus, genetic diversity plays in important role in improvement of new breeding program through selection and introduction with diversified crop characters. The capability of the population to adapt to the changing environment will depend on the presence of the necessary genetic diversity (Pullin, 2002). The success of hybridization depends upon the selection of suitable parental genotypes and performance of their cross combinations.

4.5.1 Non-hierarchicalclustering

In this non-hierarchical clustering, 35 maize genotypes were used and grouped with the application of covariance matrix into five different clusters. The highest 35% genotypes were included in cluster number V (12; G4, G5, G11, G13, G14, G18, G21, G27, G29, G31, G34, G35); 30% genotypes in cluster number IV (11; G1, G2, G6, G7, G15, G16, G19, G23, G24, G25, G30), 20% genotypes in cluster number I (7; G8, G9, G10, G20, G22, G28, G32) and11% genotypes in cluster number III (4; G3, G17, G26,G33); the lowest 3% genotypes were included in cluster number II (1; G12). The composition of clusters with different genotypes is presented in Table 8.

4.5.2 Principal component analysis(PCA)

Here, principal component axes were estimated according to the Eigen values, percent variation and cumulative percent variation. The results showed the first principal axis for days to male flowering greatly accounted for the variation among the genotypes representing 31.51% of the total variation among the genotypes (Table9)

The first seven characters of the principal component axes with eigen values was accumulated around 96.70% of the total variation among the eleven characters. The rest four characters were contributed around 3.3% of the total variation (Table 9). According to the principal component analysis, the principal component axis showed two-dimensional scatter diagram using 35 maize genotypes. The scatter diagram is represented in Figure4.

Table8. Distribution of 35 genotypes of maize in different clusters (Mahalanobis' generalized distance D^2)

Cluster no.	Accession No.	No. of populations
I	G8, G9, G10, G20, G22, G28, G32	7
II	G12	1
III	G3, G17, G26, G33	4
IV	G1, G2, G6, G7, G15, G16, G19, G23, G24, G25, G30	11
V	G4, G5, G11, G13, G14, G18, G21, G27, G29, G31, G34, G35	12
Total		35

Table 9. Eigen values and yield percent contribution of 11 characters of 35 genotypes

Principle component axes	Eigen values	Percent variation	Cumulative % of Percent variation
I	3.466	31.51	31.51
II	2.666	24.24	55.75
III	1.359	12.35	68.1
IV	1.098	9.99	78.09
V	0.908	8.25	86.34
VI	0.746	6.78	93.12
VII	0.394	3.58	96.7
VIII	0.298	2.71	99.41
IX	0.060	0.55	99.96
X	0.003	0.03	99.99
XI	0.001	0.01	100

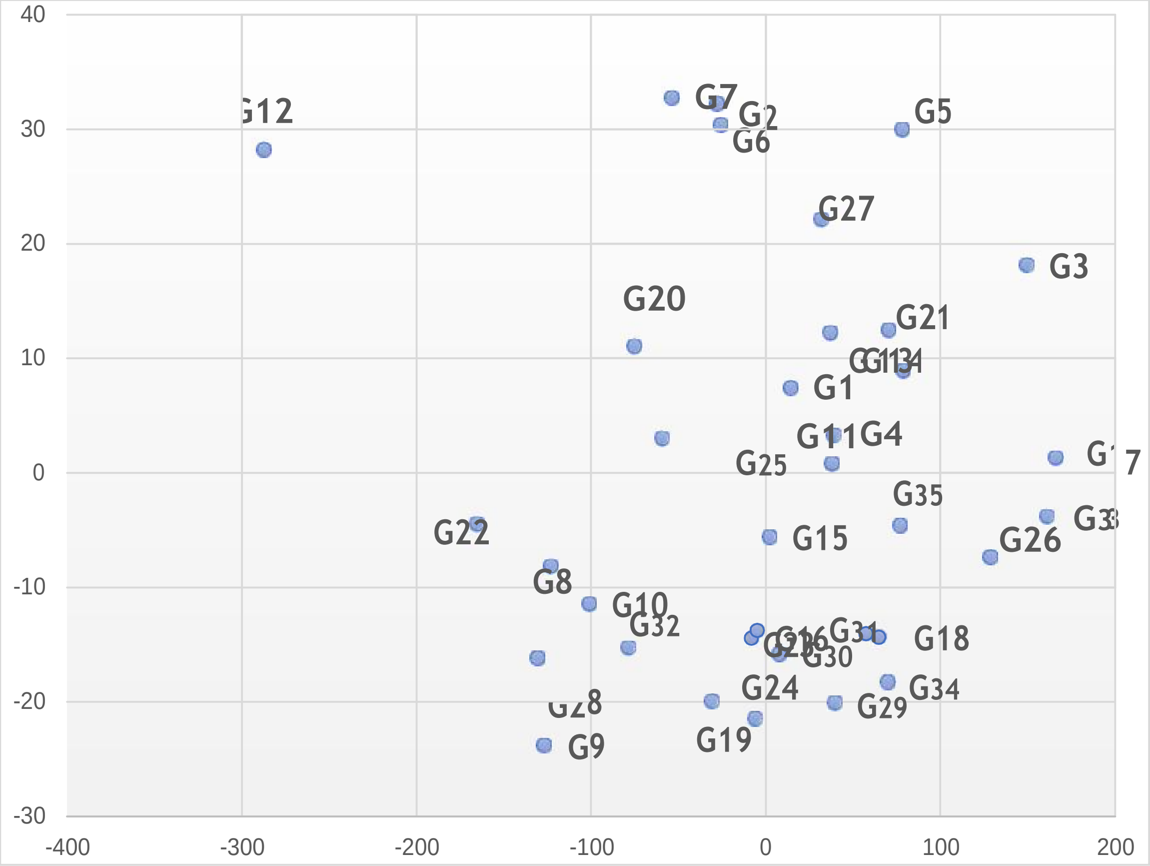

Fig 4. Scattered diagram of 35 maize genotypes

4.5.3 Inter and Intra clusterDistance

Through canonical variate analysis inter and intra cluster distance was analyzed and presented in Table 11 and nearest and farthest cluster distance are presented in Table 12. The maximum value for the cluster distance D2 were recorded in cluster III (18.740) followed by cluster II (15.470, 13.032). The intra and inter cluster distances (D2) values clearly showed in Table 11. The farthest cluster distance was recorded in cluster III that means it represented the highest diversified genotypes than other clusters. The nearest cluster distance was recorded in cluster IV and cluster V with 3.441 values which denoted the less diversified genotypes (Table12).

Here, the intra cluster distance was observed in cluster I (1.23), II (0.00), III (0.76), IV (2.08) and V (1.89) respectively. The highest intra cluster was recorded in cluster IV (2.08) and lowest in cluster III (0.76) that showed that the genotypes within the intra cluster distances were closely related and inter cluster distances were recorded higher and larger than intra cluster distances that indicated the genotypes had wider genetic diversity among the genotypes in different groups (Table 11 and12).

4.5.4 Clusterdiagram

The cluster diagram showed the distribution of the 35 maize genotypes grouped into five sections. The positioning nature of the genotypes were remarkably diversified among the genotypes (Figure 5).

4.5.5 Cluster mean analysis

The cluster mean analysis was estimated using 35 maize genotypes grouped into five cluster with eleven characters involvement (Table 10). Here, within the clusters compared the considerable differences among the clusters for all the character studied. The maximum cluster mean value for days to male flowering was observed in cluster III (65.5) and the minimum was in cluster II (62.0). In case of days to female flowering, the maximum mean value was observed in cluster II (63.3) and the minimum was recorded in cluster IV (60.9). Days to maturity showed highest in cluster II (129.7) and lowest value in cluster III (128.3). The maximum mean value for plant height was observed in cluster I (247.4) and the minimum was recorded in cluster II (209.4). Cob length showed the highest value in cluster I (17.6) and the lowest value in cluster II (15.8). Cob breadth was observed the highest value in cluster I (15.9); whereas the lowest was observed in cluster II (14.4). The maximum mean value for number of rows per cob was estimated in cluster II (22.4) and the minimum was estimated in cluster V (13.4). Number of seeds per row showed the highest mean value in cluster I (41.6) and the lowest value in cluster III (27.1). The maximum value for number of seeds per cob was observed in cluster II (799.0) and the minimum was in cluster III (364.5). The maximum value for 100-seed weight was calculated in cluster III and IV (32.3); however, the minimum was calculated in cluster II (28.7). Total yield per plant shoed the highest in cluster II (117.5) and the lowest value in cluster III (58.9).

Table 10. Cluster mean values of 11 different characters of 35 genotypes

Characters	I	II	III	IV	V
Days to male flowering	65.4	62.0	65.5	65.2	64.6
Days to female flowering	61.0	63.3	61.7	60.9	61.6
Days to maturity	128.9	129.7	128.3	128.8	128.9
Plant height (cm)	247.4	209.4	238.1	236.9	238.0
Cob length (cm)	17.6	15.8	16.8	17.1	16.7
Cob breadth (cm)	15.9	14.4	15.1	15.3	15.1
No. of rows per cob	15.1	22.4	13.5	13.7	13.4
No. of grains per row	41.6	35.5	27.1	38.8	34.2
Number of grains per cob	626.7	799.0	364.5	530.7	457.8
100 grain weight (g)	31.8	28.7	32.3	32.3	31.4
Grain yield per plant (g)	100.0	117.5	58.9	86.0	71.9

Table 11. Intra (Bold) and inter cluster distances (D^2) for 35 genotypes

Cluster	I	II	III	IV	V
I	**1.23**	9.779	11.689	4.526	7.662
II		**0.00**	18.740	13.032	15.470
III			**0.76**	7.633	4.388
IV				**2.08**	3.441
V					1.89

Table 12.The Nearest and the farthest cluster distances

Cluster	Nearest cluster distance	Farthest cluster distance
I	IV (4.526)	III (11.689)
II	I (9.779)	III (18.740)
III	V (4.388)	II (18.740)
IV	V (3.441)	II (13.032)
V	IV (3.441)	II (15.470)

4.5.6 Contribution of characters towards divergence of thegenotypes

Relative contribution of characters towards divergence of the genotypes was observed and presented in Table 13. The character involved in highabsolute magnitude for vector 1; considered to be responsible for primary differentiation and the character involved in high absolute magnitude in vector 2 was considered to be responsible for secondary differentiation. If the same character was obtained equal magnitude for the both vectors than the character was considered responsible for primary at the same time secondarydifferentiation.

In vector 1, days to male flowering (0.1387), plant height (0.0249), cob breadth (0.0439), number of seed rows per cob (0.4963), number of seeds per row (0.2522), number of seeds per cob (0.0083) and seed yield per plant (0.1354) had positive value responsible for the genetic divergence in this axis. On the other hand, days to female flowering (-0.0793), days to maturity (-0.0196), cob length (-0.5781), 100-seed weight (-0.4010) had negative value towards the divergence of thegenotypes

In vector 2, days to female flowering (0.1317), cob length (0.3700), number of rows per cob (1.0200), number of seeds per cob (0.7554) and 100-seed weight (0.7554) was observed positive divergence value; whereas, days to male flowering (-0.0764), days to maturity (-0.0754), plant height (-0.0064), cob breadth (-0.3695), number of seed per row (-0.0446) and seed yield per plant (-0.3057) was observed negative value for the divergence of the genotypes.

Number of rows per cob and number of seeds per cob both had positive value; thus, these two characters are important towards the divergence of the genotypes investigated (Table 13).

Table 13. Relative contributions of the ten characters of 35 varieties to the total divergence

Characters	Principal Component	
	Vector-1	Vector-2
Days to male flowering	0.1387	-0.0764
Days to female flowering	-0.0793	0.1317
Days to maturity	-0.0196	-0.0754
Plant height (cm)	0.0249	-0.0064
Cob length (cm)	-0.5781	0.3700
Cob breadth (cm)	0.0439	-0.3695
No. of rows per cob	0.4963	1.0200
No. of grains per row	0.2522	-0.0446
Number of grains per cob	0.0083	0.0378
100 grain weight (g)	-0.4010	0.7554
Grain yield per plant (g)	0.1354	-0.3057

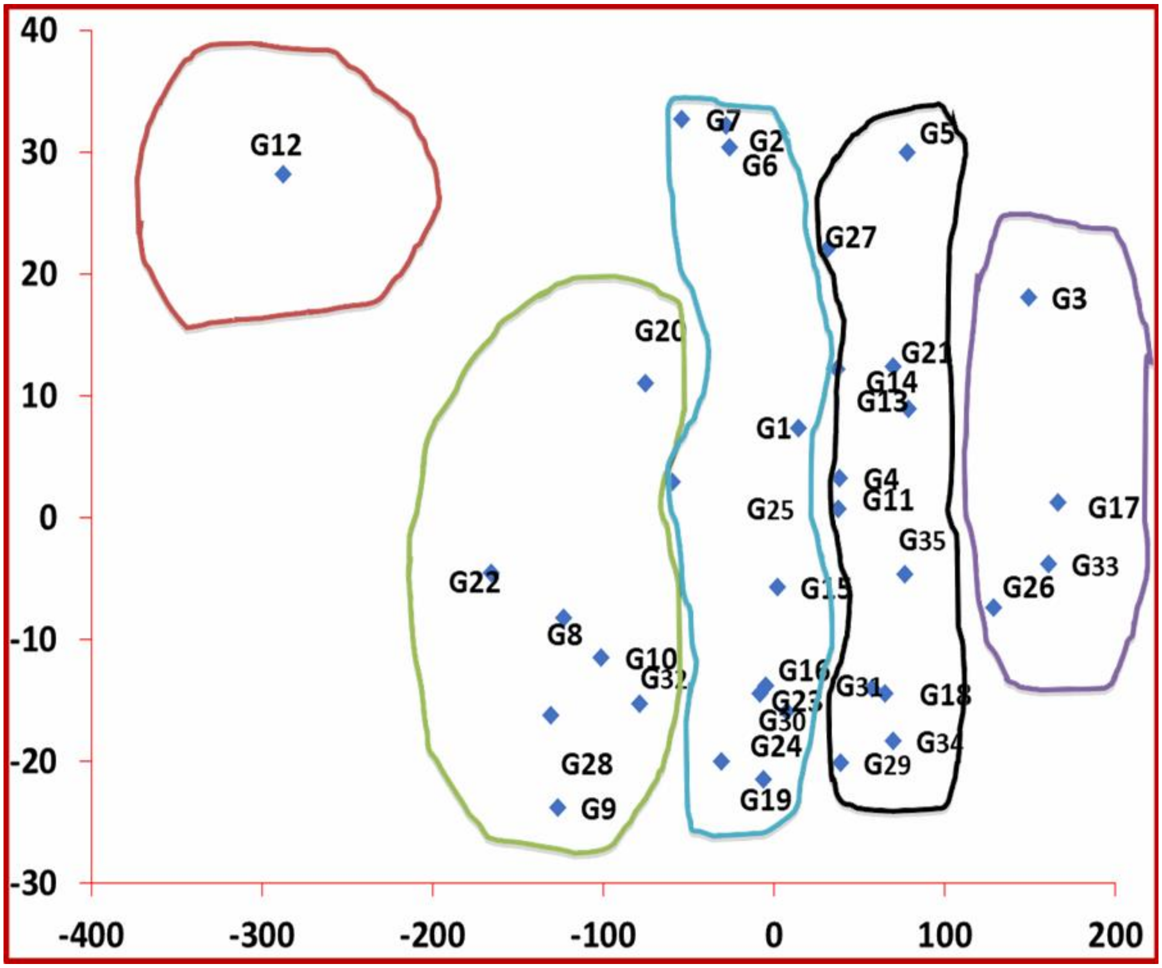

Fig 5. Cluster diagram of Maize genotypes of based on their principal component scores

CHAPTER V

SUMMARY AND CONCLUSION

The research investigation was conducted in the experimental area inSher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka during the Rabi season from 20thDecember 2017 to 10thMay 2018. The main research concern was to study genetic parameters and character association of yield and its component attributes in maize. In order to justify the following character association with yield 35 maize genotypes were used in this research program as experimental materials. The experiment was laid out in Randomized Block Design (RCBD) with three replications. Genetic variability, genetic advance, heritability, path analysis, correlation co-efficient analysis and genetic diversity was estimated using those 35 maize genotypes to determine the positive and significant relation of yield and its componentattributes.

Among the eleven component characters showed highly significant difference through analysis of variance. The maximum days to male flowering was estimated in genotype Cornell (68.0) and the minimum in genotype BHM-7 (61.0). The maximum days to female flowering was estimated in genotypeBHM-5 (66.67) and the minimum was in genotype Duranta (56.33). The maximum days to maturity was estimated in genotype Dekalb-30B07 (130.67); while the minimum in genotype Dekalb Super (127.00). Plant height ranged from the lowest 205.16(BHM-6) to the highest 258.97(PAC-399). The maximum cob length was estimated in genotype AS-999 (18.87 cm) and the minimum was in BHM-5 (14.90 cm). The maximum cob breadth was estimated in genotype Dekalb-30B07 (17.30cm) and the minimum in genotype Shuvra (12.57cm). The maximum number of seed row per cob was estimated in genotype Pacific (22.38cm) and the minimum in genotypeMisty (12.57cm). The maximum number of seed row per cob was estimated in genotype PAC-559 (46.96) and the minimum in genotype BHM-14 (24.52). The maximum number of seed row per cob was estimated in genotype Pacific (798.95) and the minimum in genotype Dekalb Super (350.44). The maximum number of 100-seed weight was estimated in genotype Duranta (39.67) and the minimum in genotype BHM-13 (27.33). The maximum grain yield was estimated in genotype Pacific-98 (117.51) and the minimum in genotype Dekalb Super (51.89).

Characters that are involved in this experiment such as days to male flowering, days to female flowering, days to maturity, plant height, cob length, cob breadth, number of rows per cob, number of grains per row, number of grains per cob, 100-seed weight and yield per plant showed higher heritability than genetic advance; at the same time phenotypic variability was also higher than genotypic variability. The maximum phenotypic variability was observed in number of grains per cob and the lowest in days to male flowering comparatively (Figure 1). The maximum heritability was observed in number of rows per cob 85.08 and the lowest in days to maturity 46.53. High heritability accompanied with high to moderate GCV and genetic advance indicates the most likely the heritability is due to additive gene effects. Among the eleven characters that were used in this investigation phenotypic coefficient of variation was comparatively higher than the genotypic coefficient of variation; whereas the highest phenotypic coefficient of variation was recorded in number of grains per cob (21.13) and the lowest in days to maturity(1.23).

Here, the total yield showed positive and significant genotypic and phenotypic correlation coefficient with other concerning characters specially days to maturity, plant height, cob length, number of grains per cob and 100-seed weight. Days to male flowering, cob breadth, number of grains per cob and 100-seed weight revealed positive direct effects on yield per plant. On the other side days to female flowering, days to maturity, plant height, cob length, number of rows per cob and number of grains per row showed negative direct effects on yield per plant.

To investigate the genetic diversity different analysis had been performed to find out the suitable relation among the genotypes. Principal component analysis, cluster mean analysis, canonical variate analysis and D^2 statistics had been performed to observe the genetical divergence and that was showed in the Tables and Figures. Cluster mean values of 11 different characters of 35 genotypes were grouped into five categories; among them the highest 35% genotypes were included in cluster number V with 12 genotypes: BHM-5, PAC-60, Pacific-98, HP-222, KhaiBhutta, AS-999, Pioneer, Duranta, Kaveri 218, Chamak-07 and Golden-984; (12; G4, G5, G11, G13, G14, G18, G21, G27, G29, G31, G34, G35) and the lowest were 3% genotypes were included in cluster number II (1; Pacific G12).Between inter and intra cluster mean values, inter cluster distances were recorded higher than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups involved. The maximum value for the cluster distance D2 were recorded in cluster III (18.740) followed by cluster II (15.470, 13.032). The farthest cluster distance was recorded in cluster III that means it represented the highest diversified genotypes than other clusters. The nearest cluster distance was recorded in cluster IV and cluster V with 3.441 values which denoted the less diversified genotypes. In this case, days to male flowering, number of rows per cob, number of seeds per cob and 100-seed weight contributed towards cluster mean performance; the maximum in cluster numberV.

From this experimental study, the eleven characters such as days to male flowering, days to female flowering, days to maturity, plant height, cob length, cob breadth, number of rows per cob, number of grains per row, number of grains per cob and 100-seed weight had positive and significant combination and relation in total yield effect per plant. At the same time, among the 35 maize genotypes some (PAC-60, Pacific-98, HP-222, KhaiBhutta, AS-999, Pioneer,Duranta, Kaveri 218, Chamak-07 and Golden-984)showed diversified genotypic representation for the understanding of excellent selection and preservation in future experimentation as well as breeding (hybridization) program.

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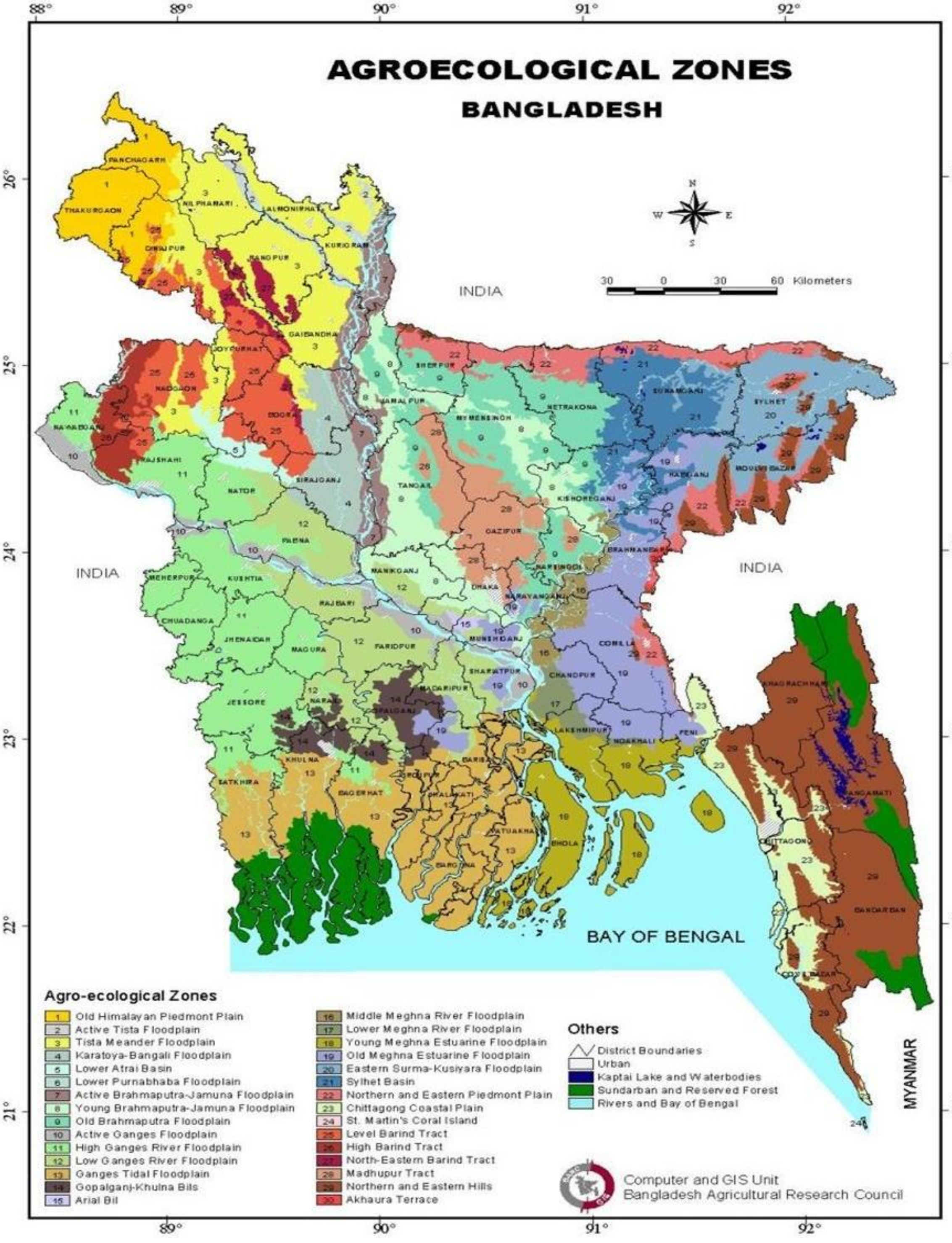
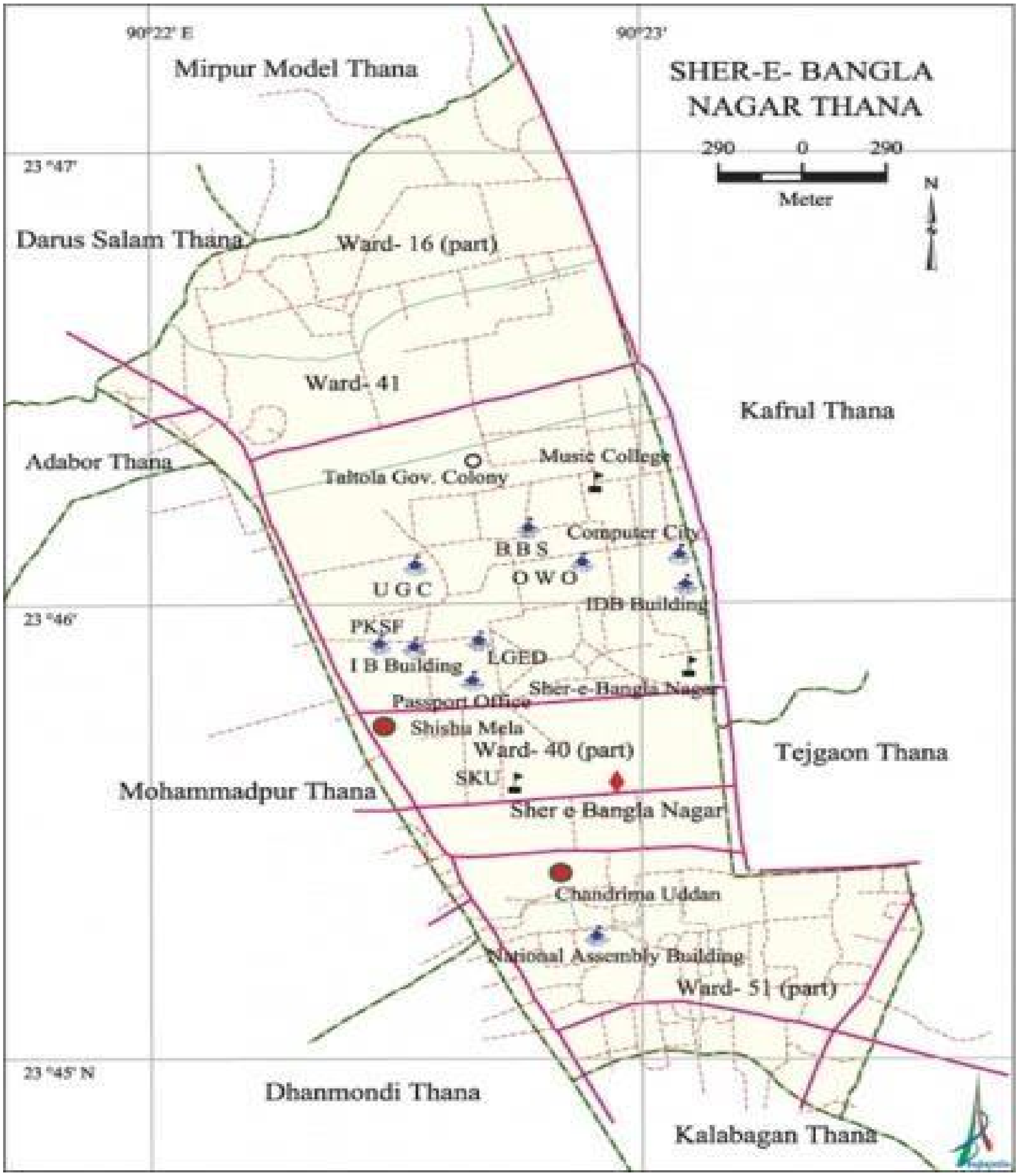
APPENDICES

Appendix 1. The map of the experimental site (Bangladesh)



Appendix 2. The map of Sher-e-Bangla Nagar, Dhaka, Bangladesh



Appendix 3. Monthly average air temperatures, relative humidity and total rainfall during the experimentation

Month (2018)	***Air Temperature(C)**		***Relative Humidity (%)**	***Rainfall(mm)**
	Maximum	**Minimum**		
December (2017)	29	13	79	-
January	27	7	72	-
February	34	13	66	-
March	35	15	63	15
April	36	19	68	90
May	36	21	80	250

*Monthly Average of air temperature, relative humidity, rainfall percentage

Source: Bangladesh Meteorological Department, Agargaon, Dhaka-1207 and Weather Climate Online

Appendix 4. Characteristics of the soil of the experimental area

A Morphological characteristics of the experimental area

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

B. Physical and chemical properties of the soil of experimental area

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

Source: Soil Resources Development Institute, Farmgate, Dhaka

Appendix 5. Mean performance of different characters of 35 Maize genotypes

Genotypes	Days to male flowering	Days to female flowering	Days to maturity	Plant height (cm)	Cob length (cm)	Cob breadth (cm)	No. of rows per cob	No. of seed per row	Number of seeds per cob	100-seed weight (g)	Yieldper plant (g)
G1	67.33	61.33	128.67	232.87	17.51	15.24	13.68	36.47	500.93	27.33	70.95
G2	65.00	62.33	128.33	205.92	16.34	14.11	12.71	42.56	540.99	31.55	85.26
G3	66.33	63.00	128.33	222.09	16.47	14.41	14.98	24.52	366.55	31.67	58.00
G4	66.00	65.00	129.67	236.82	16.68	15.05	13.23	35.91	476.09	29.92	71.35
G5	63.00	66.67	127.67	210.58	14.90	13.33	12.60	34.71	437.32	29.38	64.01
G6	62.00	62.67	127.33	205.16	14.83	13.10	14.32	37.43	536.26	37.70	101.90
G7	66.33	62.67	127.67	206.56	16.10	14.64	14.00	40.36	567.80	28.85	81.38
G8	61.00	62.00	129.33	245.75	16.86	15.31	15.39	41.07	635.11	32.34	102.57
G9	66.00	60.00	127.33	258.97	18.87	17.18	15.26	41.76	636.83	36.39	116.28
G10	63.67	60.67	128.00	250.71	17.72	16.41	14.85	41.31	614.78	29.08	89.70
G11	62.67	62.33	128.67	239.44	17.04	15.98	15.34	31.10	477.21	29.41	70.41
G12	62.00	63.33	129.67	209.42	15.82	14.38	22.38	35.53	798.95	28.66	117.51
G13	65.00	63.33	130.67	227.04	16.55	15.47	12.99	36.80	477.29	31.19	74.43
G14	62.00	62.67	129.67	231.16	16.01	14.73	12.70	34.41	436.31	30.48	66.46
G15	64.00	57.33	130.67	244.10	18.49	17.30	13.40	38.43	511.70	31.71	80.97
G16	67.00	58.33	130.00	252.62	17.08	15.94	14.45	36.09	521.23	32.90	85.59
G17	65.00	61.33	127.00	239.84	16.67	15.38	12.78	27.39	350.44	29.49	51.89
G18	66.00	61.00	127.67	254.06	17.77	16.12	12.78	35.23	449.81	31.30	70.46
G19	65.33	60.67	127.67	257.83	17.42	14.85	14.14	38.40	543.72	33.68	91.70
G20	68.00	61.33	129.33	228.92	15.03	12.57	13.40	44.19	589.63	27.66	81.57
G21	66.00	60.67	128.67	227.54	14.85	14.35	12.76	34.87	444.87	29.96	66.81
G22	66.33	60.33	130.00	241.15	18.68	17.28	17.12	39.45	676.89	32.56	109.67
G23	63.67	63.00	128.33	253.42	18.01	16.52	13.67	37.91	518.96	30.34	78.48
G24	65.67	62.00	130.00	258.74	17.48	15.14	12.57	41.42	518.41	35.72	92.63

Appendix 5. Continued.

Genotypes	Days to male flowering	Days to female flowering	Days to maturity	Plant height (cm)	Cob length (cm)	Cob breadth (cm)	No. ofrows per cob	No. of seeds per row	Number of seeds per cob	100-seed weight (g)	Yield per plant (g)
G25	63.00	61.67	129.67	235.75	16.84	15.27	14.65	38.95	572.87	30.54	88.01
G26	63.33	62.00	129.00	246.59	18.79	17.14	12.90	29.94	386.27	34.33	66.25
G27	65.67	61.67	129.00	215.68	16.03	14.25	12.64	38.17	481.39	34.59	81.62
G28	66.00	62.33	129.00	253.17	18.54	16.62	13.64	46.96	642.03	32.91	105.85
G29	66.33	56.33	128.33	255.92	18.80	15.82	13.69	34.50	472.32	39.67	93.45
G30	68.00	57.67	128.67	252.94	17.57	15.80	12.91	39.07	504.67	35.24	89.65
G31	66.00	59.67	130.33	254.21	16.58	15.30	15.05	30.27	457.63	30.34	68.98
G32	66.67	60.00	129.00	253.40	17.33	16.04	16.03	36.75	591.61	31.89	94.21
G33	67.33	60.33	128.67	243.75	15.11	13.56	13.28	26.73	354.70	33.79	59.54
G34	62.00	60.00	128.00	258.62	18.09	16.26	14.13	31.47	445.48	30.07	67.20
G35	64.67	60.33	128.67	244.63	16.57	14.72	13.38	32.75	438.18	30.64	67.34

Appendix 6. PCA score

	PCA 1	PCA 2
1	14.11	7.35
2	-28.11	32.17
3	149.09	18.08
4	38.63	3.24
5	77.84	29.94
6	-25.85	30.33
7	-53.91	32.68
8	-123.32	-8.18
9	-127.03	-23.84
10	-101.21	-11.50
11	37.83	0.76
12	-287.59	28.15
13	36.84	12.20
14	78.66	8.90
15	1.95	-5.65
16	-8.01	-14.45
17	166.02	1.25
18	64.90	-14.38
19	-31.18	-19.98
20	-75.40	11.03
21	70.11	12.41
22	-165.66	-4.51
23	-4.72	-13.77
24	-6.43	-21.49
25	-59.63	2.96
26	128.39	-7.41
27	31.54	22.10
28	-130.78	-16.21
29	39.16	-20.12
30	7.63	-15.87
31	57.57	-14.06
32	-78.85	-15.31
33	160.70	-3.85
34	69.83	-18.32
35	76.86	-4.65