BREEDING FOR DEVELOPMENT OF WHITE HYBRID MAIZE (*Zea mays* L.)

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*This is to certify that the thesis entitled, "BREEDING FOR DEVELOPMENT OF WHITE HYBRID MAIZE (Zea mays L.)" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka in partial fulfillment of the requirements for the degree of DOCTOR OF PHILOSOPHY IN GENETICS AND PLANT BREEDING, embodies the result of a piece of bonafide research work carried out by **NASRIN JAHAN**, bearing **Registration No. 07-02613** under my supervision and guidance. No part of the thesis has been submitted anywhere for any other degree or diploma.*

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

Dated: 16/06/2019
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Dedicated

to

My Parents, Husband and Child

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ABSTRACT

The study consisted of four experiments which were conducted to characterize fifty eight inbred lines, determine the genetic variation, explore the genetic diversity, select the suitable parents their combining ability and heterosis as well as evaluate genotype-environment interaction in order to identify potential white maize hybrids during the period from November 2015 to July 2018 at Regional Agricultural Research Station (RARS), Rahmatpur, Barishal along with other four regional stations of Bangladesh Agricultural Research Institute (BARI) i.e Jashore, Jamalpur, Chattogram and Dinajpur. Eleven qualitative and ten quantitative characters were studied during morphological characterization. Based on statistical analysis of the morphological traits of the inbred lines, wide variability was found for all the characters studied and thus offered scope for selection of parental lines. Plant height, number of kernel per row, thousand grain weight and grain yield, were governed by additive genes effect, as demonstrated by high heritability and high genetic advance in percentage of mean. Days to tasseling, days to silking, ear height, ear length, ear diameter, number of kernels per row, 1000 grain weight showed significant positive correlation with grain yield both at phenotypic and genotypic levels indicating dependence of these characters on grain yield. Path coefficient analysis revealed that among the characters except silking date and plant height other characters viz., Days to tasseling, ear diameter, number of kernel per row, ear height, thousand grain weight, ear length and number of row per ear had positive direct effect on grain yield. The diversity analysis showed that the fifty-eight inbreds were clustered into seven diverged groups. On the basis of the findings of the present study the inbred lines from cluster I, IV and VII were selected as better parents (CML 330, CML 332, CML 322, CML 311, CML 331, CML 518, CML 383). The estimate of GCA effects showed that the parents P6 (CML 518), P7 (CML 383), P3 (CML 322) and P4 (CML 311) were good general combiners for improving the yield and yield contributing traits. Among all the crosses, the cross combinations CML 311×CML 331(E16), CML 331×CML 383(E20) and CML 332×CML 518(E10) were the best specific combiners for yield. The result of standard heterosis comparison with BHM 12 and BHM 13 showed that out of twenty one hybrids, only four hybrids i.e CML 322×CML 518(E14), CML 311×CML 331(E16), CML 331×CML 383(E20) and CML 332×CML 518(E10) manifested significant positive heterosis. In genetic and environmental interaction analysis the AMMI biplot analysis indicated E24 (BARI Hybrid Maize 14), E16 (CML 311×CML 331), E13 (CML 322×CML 331), E17 (CML 311×CML 518) and E14 (CML 322×CML 518) were positioned closer to the origin of the biplot which indicated their stability in performance across environments. When genotypes were compared with ideal genotypes which has both high mean yield performance and high stability across environments it was observed that E14 (CML 322×CML 518), E16 (CML 311×CML 331), E10 (CML 332×CML 518) and E20 (CML 331×CML 383) were nearest to the ideal genotypes. Considering overall performance on yield, yield contributing characters, combining ability and stability, E14 (CML 322×CML 518) and E16 (CML 311×CML 331) cross combination were found superior.

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LIST OF SOME ABBREVIATE FORM AND THEIR ELABORATIONS

Full words	Abbreviations
Agro-Ecological Zone	AEZ
Analysis of variance	ANOVA
And others / Co-workers	*et al.*
Bangladesh Agricultural Research Institute	BARI
Centimeter	cm
Coefficient of variance	CV
Critical Difference	CD
Degrees of freedom	df
First filial generation	F_1
General Combining Ability	GCA
Hectare	ha
Journal	J.
Least Significant Difference	LSD
Millimeter	mm
Murate of Potash	MoP
Nitrogen	N
Number	No.
Per hectare	ha^{-1}
Percentage	%
Randomized complete block design	RCBD
Sher-e-Bangla Agricultural University	SAU
Specific Combining Ability	SCA
Ton	t
Triple Super Phosphate	TSP

CHAPTER I
INTRODUCTION

Maize *(Zea mays* L.) is a diploid species with chromosome number of 2n = 2x = 20. In central Mexico 7000 years ago maize (*Zea mays*), also called corn, is believed to have originated from a wild grass, teosinte. Native Americans transformed maize into a better source of food (Ranum *et al*., 2014). Maize is one of the most important cross pollinated and photo-insensitive cereal crops. It is one of the most productive C_4 plant with a high rate of photosynthetic activity and it has the highest potential for carbohydrate production per unit area per day. Stem and foliage of maize plant can be used as livestock feed. Stalk, dry leave covering of cobs (husks) and shelled cobs can be used as fuel (Ahmed *et al.*, 2011). Maize contains about 72% starch, 10% protein, and 4% fat, supplying an energy density of 365 Kcal/100 g, as compared to rice and wheat, but has lower protein content (Hasan *et al*., 2018). In 2018, the United States was the largest producer with maize production volume amounting to about 370.96 million metric tons. China and Brazil rounded off the top corn producing countries (215.89 and 82 million metric tons, respectively) (Statista, 2018). About 30% of world maize production is used for direct human consumption and as an industrial input, while 70% is used as animal feed (Pavan, 2009). The global area is about 197 million ha with corresponding average annual production of over one billion metric tons (FAOSTAT, 2017). In the near future, more food will require for the increasing world's population and from maize crop maximum part of this food will come (Ali and Yan, 2012). Most of the maize grown in the United States is yellow, whereas people in Africa, Central America, and the southern United States prefer white maize. It has been estimated that in terms of cereals more than half of the increased demand in world food as a whole will be produced from maize farmers and consumers (Yan *et al*., 2011).

In Bangladesh 30 lac tons have been produced in Bangladesh occupies an area of 3.9 lac hectare (FAOSTAT, 2017). Maize is an important cereal crop in Bangladesh, which rank third only to rice and wheat in terms of cultivated area and second to rice in terms of production. With rising temperature due to global warming, traditional crops like rice and wheat are becoming less productive crops than before but it has no remarkable impact on maize production (Alam, 2008). In Bangladesh, the area of maize cultivation has been increased from 3,600 hectares in 1991-92; 9,940 hectares in 1994-95 to 38,97,12 hectares in 2016-17. Similarly, maize production have also been increased from 3,000 tons to 33,35,537 tons (BBS, 2017). The secret behind higher production in Bangladesh, most of the maize field is irrigated and farmers cultivated hybrid maize with improved production technology. Maize is planted and produced mostly in north-western and south-western districts of Bangladesh. Maize has also higher yield potentiality and versatile adaptable characteristics in terms of production seasons, different agro-climatic factors and economic benefit on investment (Mohiuddin *et al*., 2007). The net income of farmer increases from maize hybrids can be estimated by assuming that farmers replace wheat with maize (Rashid *et. al*., 2012).

Maize has potential for the highest per unit production and can be grown throughout the year. Financial returns per hactare from rabi season maize are 2-3 times more than those of wheat or boro rice (Moniruzzaman *et al.,* 2009). Farmer's produced yellow kernelled hybrid maize is used mainly for poultry and fish industries but it has not been widely used for human consumption in the country. Maize can play a vital role, along with other important cereals (rice and wheat), in meeting future needs of growing population of the country (Quayyum, 2002). With a population of 165 million people, there is a lot of scope for maize consumption. In these situations, white maize can be introduced for human consumption towards improving the food security in Bangladesh.

World production of white maize is currently estimated at around 65-70 million tons (CIMMYT, 2012), representing 12-13 percent of the annual world output of all maize. Over 90 percent of the white maize is produced in the developing countries, where it accounts for around one quarter of total maize output and just under two-fifths of the total maize area. In the developing world, a larger area is planted to white than to yellow maize in the tropical highland and sub-tropical/mid-altitude environments, and it occupies about 40 percent of the lowland tropical maize area (Dowswell *et al*., 1996). Although maize is the staple food for many countries in the world (South Africa, Brazil, Mexico, Latin American etc.) but maize production is highly dependent on poultry industry in Bangladesh, which is a major constraint for human consumption in the country. The three most common uses of white maize in U.S are food, starch and paper. White maize is used in alkaline cooking processes to produce a high-quality, light-colored flour. Approximately 80% of U.S. white maize is used in corn-based products such as tortillas, tortilla chips, corn chips, tostados and tacos and to naturally brighten starch produced from other products. White maize starch is also used in paper products.

Maize cultivation is becoming increasingly integrated by farmers into their cropping systems in Bangladesh because of higher grain yield coupled with high market demand particularly as poultry feed. Farmers usually cultivate different yellow varieties of hybrid maize in both rabi and kharif seasons with a view to achieve more economic benefit compared to rice and wheat but the area under white maize cultivation is very scanty mainly due to lack of suitable varieties, lack of farmers' knowledge on modern production technology, low market demand of white maize grain as poultry feed, lack of awareness for human consumption and lack of knowledge for preparation of maize based food items etc. Presently about 90% of produced maize grain is being used as poultry feed. The incidence of bird flu in 2008 drastically reduced the area under maize cultivation in 2009, as there was no significant demand for maize. This indicates that maize production in Bangladesh is highly dependent on poultry industry that signifies that sustainable maize production cannot be achieved without diversifying its uses, including promotion of maize for human consumption.

White maize is a type of grain that is grown throughout the world, though it is known as "white corn" in some areas of the world. Endosperm colour in maize is controlled by a single gene. The production of carotenoid pigments in the endosperm due to the presence of a single (dominant) Y allele and results in yellow seeds. When two recessive y alleles are present, carotenoids are not produced and the endosperm becomes white and the result is white maize seed. When comparing nutritive value of white maize with yellow maize it was found that vitamins viz. thiamine, riboflavin, niacin, calcium (Ca) and iron (Fe) provided more by white maize than yellow maize. (Muzhingi *et al.*, 2011). From 100 gm maize grain, protein contents are 9.28% and 8.12% from white and yellow maize, respectively. White maize also has a medium glycemic index which help in reducing the obesity. In Bangladesh for food preparation, only some of the rural people make flat bread with mixing the flour of maize with wheat (1:2 ratio) but hundreds of maize based food items/recipes are available worldwide, and some of which can be introduced in Bangladesh for increasing the consumption of maize particularly by the rural poor people. A good number of local food items (porota, luchi, ruti, khichuri, khoi, moa, naru, khir, payesh, pitha, roasted cob etc.) can also be prepared from maize, which can also be popularized through awareness building of the farm households. Findings indicate that maize grain can supply more energy compared to wheat or rice that can be the best option for improving the family nutrition of rural households particularly for the poor people. However, in making food items, people generally do prefer white maize based food items compared to yellow maize. Therefore, white maize should be extended through introducing modern varieties of white maize along with component technologies for increasing production and human consumption.

Till to date BARI has succeeded to develop fifteen hybrid maize and seven composite/open pollinated (OP) varieties along with their production technologies. All the BARI maize hybrids are yellow kernelled except three varieties BHM 12, BHM 13 and BHM 14. Among the BARI developed maize varieties (hybrid/OP), Shuvra is the only open pollinated variety of white maize. Besides, the Plant Breeding Division of BARI has developed some advanced lines of white maize. The Non-government Organization ‘Bangladesh Rural Advancement Committee (BRAC)’ has also developed a single cross hybrid variety of white maize (cv. Uttara 3). Therefore, more promising varieties/lines (OP/hybrid) of white maize need to be developed for on priority basis for increasing its cultivation area and production.

The choice of germplasm is an essential and crucial step in any plant breeding program, whether for the development of varieties or to produce hybrids, and can determine the success or failure of the selection process. The presence of genetic divergence among accessions of germplasm is essential; however, if the germplasm employed in the cross also present high values for the traits of interest satisfactory results are obtained. Evaluation of genetic diversity within the available germplasm is important to know the source of gene for particular traits (Tomooka, 1991). Precise information about the extent of genetic divergence on characters used for discrimination among the population is crucial in any crop improvement program, because selection of plants based on genetic divergence has become successful in several crops (Dubey *et al.,* 2006). The understanding of genetic variability present in a given crop species for the traits under improvement is imperative for the success of any plant breeding program (Sankar *et al.*, 2006).

Combining ability analysis is of special importance in cross pollinated crops like maize as it provides information for identifying the potential inbred parents that can be used for producing hybrids and synthetic maize varieties (Vasal, 1998). Mainly two factors per se behaviour of a line itself and the behaviour of line in hybrid combination affect the commercial production of hybrids. Through the estimation of general combining ability (GCA) and specific combining ability (SCA) effects the behaviour of a line in hybrid combination is assessed. Diallel analysis which involves the crossing of all lines in all possible combinations is an efficient method for the study of combining ability and also the gene action of the characters under study. Among the tested lines the best combinations with general combining ability of individual lines and specific combining ability between the lines are helpful to get more desirable recombinants which enables for further improvement of the crop.

For genetic improvement of different traits, utilization of heterosis are fundamental tools for enhancing productivity in the form of filial one hybrid (Garcia *et al.,* 2009). Heterosis increases yield potential and improves adaptations to stress in maize; however, the underlying mechanism of heterosis and combining ability remains elusive (Ararus *et al.*, 2010). Heterosis, expressed in crosses between individuals from different populations, depends on the presence of genes with non-additive effects in controlling desirable characteristics and the genetic divergence between them. Phenomenon of heterosis has been exploited extensively in crop breeding, leading to significant increase in yield. The amount of heterosis expressed in a F_1 hybrid is mainly influenced by the genetic diversity (Moll *et al.,* 1965).

Stability refers to the ability of genotypes to be consistent, both with high or low yield levels in varying environment and adaptability refers to adjustment of an organism to its environment which implies that a genotype may produces high yield in specific environment and poor yield in another environment.. Hybrid adaptability across diverse environments is usually tested by its interaction with different environments. Genotype is considered to be more adapted or stable if it has a high mean yield and low fluctuated in yielding ability across diverse environments. Crop breeders have been striving to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of different environmental conditions. The combined effect of the environment and the genotype which interact with one another determines the phenotype of an organism. Thus, when selection is done based only on mean of yields genotype × environment interaction limits the effectiveness of selection (Dehganpour and Moghadam, 1999). With the help of multi environment testing the potential of genotypes and stability of their performance can be judged (Mahajan and Khehra, 1992). The effect of G x E becomes more apparent when conducting multi-location and multi-years trials to estimate and predict yield based on limited experimental data; to determine yield stability; the pattern of response of genotypes across environments and to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years at new sites (Crossa, 1990). Stability analysis helps to identify genotypes which are adaptable for wide and specific environments and divides large geographical area into subareas.

Considering the present status of maize cultivars and the scope of development of hybrid maize, the present research was planned with the following objectives:

i) To determine the genetic variation of important morphological, yield and yield contributing characters among the inbred lines,
ii) To screen out the suitable parents which are likely to provide better recombinant during hybridizations,
iii) To study the combining ability of parents and crosses for yield and its component,
iv) To estimate the magnitude of heterosis for important characteristics,
v) To study the performances of tested hybrids under different agro-ecological zones.

CHAPTER II
REVIEW OF LITERATURE

Related works on maize for genetic variability and diversity, heterosis, combining ability, stability and their relationship related to present study are reviewed below.

2.1 Genetic variability, heritability and genetic advance

Possibility of achieving improvement in any crop plants depends mainly on the magnitude of genetic variability. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and phenotypic components. Since, the phenotypic expression of a complex character like yield is a combination of genotype, environment and their interaction, it is necessary to partition overall variability into heritable and non-heritable components with the help of appropriate statistical techniques. Knowledge of genetic variability, heritability and genetic advance is helpful for quick improvement, through appropriate breeding methodologies by selecting suitable genotypes.

Heritability is the proportion of total genotypic variance to total phenotypic variance. High heritability estimates were reported for hundred grain weight by (Debnath and Sarkar, 1981) in maize.

Liao *et al.* (1987) studied five maize inbreds and they reported highest broad sense heritability for ear diameter and hundred grain weight.

Gouesnard *et al.* (1989) showed high heritability for the traits plant height and ear height, while moderate to high heritability values observed for number of rows per ear (23.5%).

Heritability was estimated by (Reddy and Agarwal, 1992) in ten set of inbred lines of maize for various agronomic characters. They reported that days to 50 percent silking, plant height and ear height had high heritability values indicating these traits had good potential for improvement through an intra-population technique.

Thirty-eight inbred lines of maize were evaluated by Mani and Bisht (1996) and observed significant variation for all the characters.

Tusuz and Balabandi (1997) observed the highest heritability in the broad sense for days to 50 percent silking (93%) and it was the lowest for the traits plant height (12%), ear height (31%) and yield (6%).

Singh *et al.* (1998) concluded that plant height, ear height, ear length, grain yield per plant and grain yield per plot recorded high to moderate estimates of heritability in both seasons.

Tiwari and Verma (1999) studied twenty eight genotypes of maize and reported that heritability estimates were invariably moderate to high for all the traits. High heritability along with high genetic advance was observed for grain yield and baby corn yield. Hence, these two traits were considered the most suitable for further improvement through selection.

Singha and Prodhan (2000) reported high heritability estimates along with high expected genetic advance for grain yield, ear height, ear length and total soluble solids. The yield attributing characters *viz.*, days to 50 percent silking, ear length, ear height, number of kernel rows per ear, hundred grain weight, protein content, oil content and grain yield had high heritability whereas days to 50 percent tasseling recorded moderately high heritability coupled with low GCA indicating the predominance of non-additive gene action and hence improvement of such traits is possible through heterosis breeding program.

Gupta and Salgotra (2004) studied variability and reported the high phenotypic (PCV) and genetic (GCV) coefficients of variation accompanied by high genetic advance (GA) for straw yield and ear height.

Turi *et al*. (2007) estimated the magnitude of genetic variability for yield and yield components in maize genotypes under agro climatic conditions of Peshawar valley. Significant variability was observed for ear length, number of row per ear, fresh ear weight, grain moisture content, 300 grains weight and grain yield. Among the tested genotypes Sarhad white had the maximum ear length (16cm) while PESV-3-1 and EV-2 x Pahari had the least ear length (11cm). Azam and EV-2 x Pehari had the maximum number of grain rows per ear (16cm), while in Jalal and FRW-4 x EV-3 (13cm) gave the minimum grain rows per ear was recorded. Data recorded for fresh ear weight showed that genotype FRW-4 X EV-3 (Late) had the maximum fresh ear weight (14.30kg) while the minimum fresh ear weight (4.4kg) was recorded for EV-2.

An experiment was conducted at department of genetics and plant breeding, Allahabad school of agriculture, Sam Higginbottom institute of agriculture technology and sciences, deemed university by Vashistha *et al*. (2013).They observed that the mean sum of squares due to genotypes showed significant differences for all the characters except for number of ears per plant. Broad sense heritability, coefficients of variability and genetic advance values were computed for fourteen 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 row per ear, number of kernel per row and hundred seed weight.

Kumar *et al.* (2014) evaluated newly developed eighty six maize genotypes to determine the various parameters of genetic variability, broad sense heritability and genetic advance at Maize Research Centre, Agricultural Research Institute, Rajendranagar, Hyderabad. Analysis of variance revealed that the mean sum of squares due to genotypes showed significant differences for all the characters studied. High heritability accompanied with high to moderate genotypic and phenotypic coefficient of variation and genetic advance were exhibited for the traits yield per plant, plant height, ear height, number of kernels per row, 100-kernel weight which indicates that most likely the heritability is due to additive gene effects and selection may be effective in early generations for these traits. Whereas high to moderate heritability along with low estimates of genetic advance were observed for days to 50 per cent tasseling, days to 50 percent silking, days to maturity, shelling percentage, ear length, ear diameter and number of kernel rows per ear.

Twenty two maize hybrids were evaluated by Begum *et al.* (2016) to find out their variability of grain yield and its component characters. Significant differences were found among the genotypes for the characters studied. Ear length and grain yield (t/ha) had moderate genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The heritability was high for all the characters. The characters viz. plant height, ear height and thousand grain weight, showed high heritability along with high genetic advance.

Patil *et al.* (2016) stated that grain yield per plant exhibited highest genetic advance which was followed by plant height and ear height. They also observed that grain yield per plant showed the highest heritability (98.00%) followed by plant height, number of kernels per row and hundred grain weight.

Huda *et al*. (2016) carried out an experiment to assess the genetic variability for twenty five maize genotypes. They recorded the highest grain yield per plant (272.21g) in BARI Hybrid Maize 6 and the lowest grain yield per plant (180.40 g) was found from the genotype of NZ-003. Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the yield contributing traits.

Sravanti *et al*. (2017) used forty two maize genotypes as a experimental material to study the heritability and genetic advance for yield and its contributing traits. The analysis of variance revealed the presence of significant variability among the maize genotypes under study. Among all the studied characters, ear eight exhibited the highest PCV (27.52) and GCV (26.42), whereas the lowest PCV (3.45) and GCV (3.07) were recorded for days to maturity. Ear height and grain yield per plant expressed high heritability coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling these traits.

2.2 Correlation studies

Grain yield in any crop depends on many component characters which influence yield either singly or jointly and either directly or indirectly through other related characters. Selection for yield on the basis of *per se* performance alone may not be effective but when component characters associated with yield selection become more effective which is biometrically determined by correlation coefficient and path analysis. The correlation between the characters may exist due to various reasons such as pleiotropy, genetic linkage and association of loci or presence of block of loci governing variability for different characters on the same chromosomes.

The inter relationship of quantitative characters with yield determine the efficiency of detection in breeding program. It merely indicates the intensity of association. Phenotypic correlation reflects the observed relationship, while genotypic correlation underline the true relationship among characters. Selection procedures could be varied depending on the relative contribution of each. An understanding of the nature and extent of association of the component characters with grain yield and amongst themselves is an essential pre-requisite for formulating best breeding program.

Bhole and Patil (1984) concluded that the genotypic correlations were relatively higher than phenotypic ones, indicating a strong inherent association of the characters under study with a probable influence of environment on their expression. They observed that plant height had highly significant genotypic correlation with ear length. Further, highly significant and positive genotypic correlations were also noticed for ear length and dry weight of ears with grain yield in maize.

Saha and Mukherjee (1985) observed that grain yield per plant was significantly correlated with grains per ear and 100-grain weight. Sharma and Kumar (1987), also reported that grain yield per plant was positively associated with plant height, number of internodes, leaf area and plant height.

Singh *et al.* (1991) noticed that grain yield per plant had significant positive correlations with plant height and ear weight in F_1 and F_2 generations under alkaline soil and with leaf area in both the generations under normal soil. Debnath and Khan (1991), revealed that days to silking, plant height, number of kernels per row and 1000-grain weight had strong positive contributions to grain yield.

Saha and Mukherjee (1993) reported positive significant correlations between grain yield per plant with 100 grain weight, ear length, ear diameter, number of grain rows per ear and number of grains per row. The ear diameter and number of kernel per row had higher direct and indirect effects on grain yield.

Mahajan *et al.* (1995) concluded that the grain yield was only correlated with the ear length. Among the yield contributing characters ear length and diameter, number of kernels per row and grain weight contributed directly or indirectly towards grain yield in maize.

According to Satyanarayana and Saikumar (1996) grain yield was positively correlated with kernel rows per ear, ear length, ear circumference and 100 grain weight.

Kumar and Kumar (1997) determined that in general, values of genotypic correlations were slightly higher than the corresponding phenotypic values. Significant positive correlations were reported for plant height, days to 50 per cent maturity, ear length and ear height with yield per plant in maize.

Khakim *et al.* (1998) noticed that grain yield was positively correlated with plant and ear height, leaf area, ear number, ear length, row number, grain number per row and per ear, grain weight per ear, ear weight and 1000-grain weight.

Rather *et al.* (1999) in a study showed that days to 50 percent silking was positively correlated with ear height and grain yield but plant height had no association with grain yield.

Kumar and Kumar (2000) concluded that the grain yield and oil content were contrasting selection criteria. Selection based on plant height, ear weight, number of kernel rows per ear and number of kernels per ear was desirable for grain yield. However, for improved oil content, late maturing and dwarf plant types with lower number of kernel rows and kernels per ear in addition to lower 100 grain weight were desirable. Hence, a balanced selection of high yielding hybrids with moderate oil content need to be emphasized while breeding for both grain yield and oil content.

Umakanth and Khan (2001), observed that grain yield per plot showed significant and positive correlations with eardiameter, ear length, plant height and 100-seed weight. Path analysis revealed that plant height followed by number of kernels per row, 100-seed weight, ear length and ear diameter showed the maximum positive direct genotypic effects as well as indirect contribution through other characters on grain yield.

Choudhary and Chaudary (2002) showed that days to tasseling and grain weight showed no association with other traits at phenotypic level. Plant height was significantly correlated with ear length, grain yield per plant and grain yield per plot in the negative direction. Ear length had significant and positive correlations with grain yield per plant.

Jun *et al.* (2003) showed that maize yield was closely related to ear length, 100 grain weight, ear width and kernel numbers per row. Yield was also related to plant height, ear height, stem diameter and leaf area index.

Hossain *et al.* (2004) found that yield was positively correlated with plant height, ear height, ear length, ear diameter and negatively correlated with days to 50 percent tasseling and days to 50 percent silking. The genetic correlation coefficients were higher than the phenotypic correlation coefficients.

Sumathi *et al.* (2005) in genotypic correlation studies indicated that grain weight, number of rows per ear, number of kernels per row, and total number of kernels per ear were positively associated with grain yield. Oil per cent exhibited negatively non-significant correlation with grain yield, whereas it showed positive association with number of rows per ear only. Path coefficient analysis revealed that number of kernels per row showed high direct effect on grain yield followed by hundred grain weight, number of rows per ear and total number of kernels per plant.

Yield was positively and significantly correlated with plant height, ear height, ear length, dry weight of ears per plant, number of kernels per row, hundred grain weight and ear diameter. On the contrary, days to 50 percent tasseling, days to 50 percent silking and days to maturity are negatively correlated with grain yield. The genetic correlation coefficients were higher than phenotypic correlation coefficients (Sadek *et al*., 2006).

Singh *et al.* (2006) reported significant positive correlations for grain yield with days to 75 per cent husk, plant height, ear height and number of ears.

Sofi and Rather (2007) reported that the genotypic correlation coefficient revealed that ear diameter, 100-seed weight, ear length, number of kernel rows per ear and number of kernels per row showed the greatest correlation with grain yield. Path analysis indicated that hundred seed weight had the greatest direct effect on grain yield, followed by number of kernels per row, number of kernel rows per ear, ear length and ear diameter.

Brar *et al.* (2008) reported that plant height, ear height, ear length, ear diameter and number of ears per plot had significant positive genotypic and phenotypic correlations with yield per plot.

Akbar *et al.* (2008) noticed that plant height had highly significant genotypic and phenotypic association with ear height and days to 50 per cent tasseling with days to 50 per cent silking. All traits had significant genotypic association but not significant phenotypic association with grain yield.

In a study of association analysis in maize by Shinde *et al.* (2009) revealed that high positive correlation of grain yield were found with ear weight, ear length, plant height, total dry matter, 1000-grain weight, leaf area per plant and shelling percentage.

Rafiq *et al.* (2010) carried out an experiment to to determine the various parameters of genetic variability and nature of interrelationships among traits affecting maize grain yield and genotypic correlation coefficient revealed that ear diameter, hundred grain weight, ear length, number of rows per ear and number of kernel per row significantly correlated with grain yield.

Fifteen elite yellow maize inbred lines were evaluated by Ogunniyan and Olakojo (2014) and their study revealed that days to anthesis and silking, plant height and number of leaf per plant were positively correlated. Grain yield was positively correlated with ASI (Anthesis Silk Interval), plant and ear heights, number of leaf per plant and leaf area.

The grain yield per plant showed highly significant positive correlation with ear diameter, number of kernels per row, ear length and plant height when genetic divergence in forty genotypes (38 inbreds and 2 hybrids) of maize were evaluated to study association between different characters by Patil *et al.*(2016).

According to Begum *et al.* (2016) ear length, ear diameter and kernel per row had highly significant positive correlation with grain yield. However, the deviations between genotypic and phenotypic correlation and magnitude of environmental correlation suggested considerable influence of growing environment in expressing almost all the characters.

2.3 Path coefficient studies

Knowledge of interrelationship between yield and its components is obvious for efficient selection of desirable plant type. Assuming yield is a contribution of several characters which are correlated among themselves and to the yield, path coefficient analysis was developed (Wright, 1921; Dewey and Lu, 1959). Unlike the correlation coefficient which measures the extent of relationship, path coefficient measures, the magnitude of direct and indirect contribution of a component character to a complex character and it has been defined as a standardized regression coefficient which splits the correlation coefficient into direct and indirect effects and thus enable the breeders to judge best about the important component characters during selection.

Kang *et al.* (1983); reported relatively a large and positive direct effect of ear weight on grain yield at both the phenotypic and genotypic levels. The direct effect of plant height on grain yield was also reported to be positive and highly desirable.

In a study involving twenty four genotypes of popcorn, Sharma and Kumar (1987) observed that grain yield of maize was directly influenced by number of grains per row, plant height, ear diameter and 100-grain weight. Further, among the positive traits influencing the yield, the role of number of grains per row was prominent.

The path coefficient studies by Devi (1990) also indicated the maximum direct effect of 100 grain weight and total number of kernels per ear on grain yield.

Singh *et al.* (1995) studied thirty six diverse maize genotypes and concluded that there was a highly significant positive correlation between yield and number of kernel per row. Path analysis indicated that kernel per row, days to maturity and number of rows per ear had high direct effects on yield.

Singh *et al.* (1999) indicated that the highest positive direct effect on yield was exhibited by kernel rows per ear, followed by plant height and ear diameter.

Vaezi *et al.* (2000) showed that 300 kernel weight and kernel depth had the highest positive effect on grain yield whereas ear diameter had a negative indirect effect on grain yield through some traits. Geetha and Jayaraman (2000) observed number of kernels per row exerted a maximum direct effect on grain yield.

Devi *et al.* (2001) reported that the plant height, days to 75 per cent silking, and maturity, ear length, number of kernel rows per ear, number of kernels per row and 100 grain weight positively influenced the yield directly and also indirectly through several yield components.

Cheng *et al.* (2002) showed that importance of eight yield components to grain yield and suggested that more attention should be paid to ear length, ear diameter and kernel percentage.

Venugopal *et al.* (2003) reported that plant height, ear height, ear length, ear diameter, 100 grain weight and number of kernels per row were positively associated with grain yield. Although the character number of kernel rows per ear had a direct positive contribution towards grain yield, it had indirect negative influence through ear length, 100-grain weight and number of kernels per row. Days to 50 percent tasseling, days to 50 percent silking had exhibited negative influence both directly and indirectly.

Plant height, days to silking, ear length and ear height showed significant positive correlation with total grain yield. Path coefficient analysis revealed that early silking, plant height, ear length, ear height and lesser ear diameter directly contributed to increased ear yield (Viola *et al.*, 2003).

Srivas and Singh (2004) observed that characters such as plant height, days to 50 per cent silking, stem girth, leaf length, leaf width and number of leaves per plant had positive direct effect on dry fodder yield at phenotypic levels.

Shelake *et al.* (2005) path analysis revealed high magnitude of direct effects for all characters at the genotypic level. The number of days to 50 per cent tasseling, number of days to 50 per cent silking and harvest index showed higher genotypic direct effect. Biological yield per plant had the highest negative genotypic direct effect on grain yield

Kumar *et al.* (2006) in a study revealed that days to 50% tasselling, anthesis silking interval (ASI), ear height and 100-seed weight had the highest direct effect on grain yield. Days to 50% silking which exhibited negative direct effect on grain yield, however, influenced the yield indirectly through days to 50% tasselling.

Jiang *et al.* (2007) showed that kernels per plant was arranged for the top position among the many agronomic traits that contributed to the yield enhancement of a single plant and was followed by kernels per row, 1000-kernel weight and leaf orientation value.

Path analysis revealed that 100 seed weight exerted the maximum positive direct effect followed by plant height and number of leaves above ear on grain yield. Positive indirect effect on yield was through plant height, ear height, number of leaves above ear, chlorophyll content at 50% silking, flag leaf area, ear length, ear diameter and 100-seed weight (Saidaiah *et al.*, 2008). Akbar *et al.* (2008) showed that all traits exerted positive direct effect on grain yield per plant except days to 50 per cent silking.

Shinde *et al.* (2009) reported that path analysis revealed the highest positive or indirect effects of ear weight followed by plant height and shelling percentage on grain yield.

Rafiq *et al.* (2010) studied thirty hybrid of maize which was developed when ten local maize inbred lines were crossed to three testers (F-107, F-131 and F-165) at Maize Research Station, Ayub Agricultural Research Institute, Faisalabad, Pakistan during 2007-08 to determine the various parameters of genetic variability and nature of interrelationships among traits affecting maize grain yield. Path analysis revealed that highest direct effect on grain yield was exhibited by 100 grain weight followed by grains per row, kernel rows per ear, ear length and ear diameter. Most of the traits exerted their positive indirect effects through 100 seed weight, kernel rows per ear and grains per row.

Munawar *et al*. (2013) conducted a experiment with seven hybrids of maize and Path coefficient analysis revealed that number of grains per row had the maximum direct effect on yield followed by stem diameter, cob girth and cob height. Plant height, cob position, cob length, number of rows per cob and grain weight had direct negative effects on grain yield which indicated that improvement of these traits is essential before selecting them for high grain yield.

Teodaro *et al.* (2014) studied path analysis of two genetic classes of maize and showed that number of grain per row and weight of hundred grains are directly correlated to yield are indirectly influenced through the effect of ear length and ear diameter.

Twenty two maize hybrids were evaluated by Begum *et al.* (2016) and Path coefficient analysis revealed that plant height (0.659), ear length (0.934) and kernel rows per ear (0.715) had highly significant positive direct effect on grain yield suggesting their importance during selection.

Path analysis were undertaken in seventeen maize (*Zea mays* L.) genotypes by Sarmabarua e*t al*. (2017) for grain yield and yield contributing traits and revealed that days to 50 percent silking (1.918) had shown the highest positive direct effect on grain yield followed by days to 50 percent pollen shedding (1.779), days to 75 percent dry husk (0.840), plant height (0.753) and number of kernels per row (0.600) indicating these characters can be strategically used to improve grain yield of maize.

2.4 Genetic diversity

One of the potent techniques of assessing genetic divergence is the D^2 statistic which was proposed by Mahalanobis in 1936.This technique is useful tool for quantifying the degree of divergence between biological population at genotypic level and in assessing relative contribution of different components to the total divergence both intra and inter cluster level (Murty and Arunachalam, 1966; Ram and Panwar, 1970 and Sachan and Sharma,

1971) thus helps in the selection of genetically divergent parents for exploitation in hybridization programmes. The D^2 technique has been used in assessing the variability present in crops like maize, jowar, bajra, wheat, linseed, cotton, tobacco, alfalfa and *brassicas* (Moll and Stuber, 1974).

The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce high heterotic effects (Ghaderi *et al*., 1979). Manifestation of heterosis usually depends on the genetic divergence of the two parental varieties (Saxena *et al.,* 1988). The quantification of genetic diversity through biometrica1 procedure made it possible to choose genetically diverse parents. In maize, qualitative and quantitative traits have been used to establish core collection and to study phenotypic diversity (Alika *et al.,* 1993). Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from the same variety (Vasal, 1998).

Singh and Chaudhari (2001) evaluated fifty five inbred lines for genetic divergence and grouped into five clusters. Among these cluster II had the maximum number of 16 inbreds followed by clusters IV and clusters V with 11 and 10 inbreds, respectively. The highest inter cluster distance was observed between clusters I and IV indicating wider diversity between them**.**

Khumkar and Singh (2002) grouped the inbred lines into six clusters. The maximum intra-cluster distance was recorded for cluster IV, where as the maximum inter cluster distance was observed between cluster III and V. Among the characters evaluated plant height, 100 kernel weight and number of kernel per row had the greatest contribution towards genetic divergence.

On the basis of D^2 analysis, the genotypes were grouped into 16 clusters by Singh *et al.* (2003). Cluster I comprised the maximum number of genotypes (18) whereas, cluster XIII to XVI comprised a single genotype in each indicating there was wide range of variations among the genotypes. Clustering pattern indicating that genetic diversity was due to genetic distance.

Datta and Mukherjee (2004) carried out an experiment with 32 inbred lines to determine the genetic divergence through multivariate analysis. They opined that grouping based on D^2 could be relied upon only when the characters of major importance like yield and maturity are taken into consideration. For selecting parents for hybrids, greater importance should be given to cluster mean of which the individual inbreds are members or on inter cluster distances of that particular cluster with other or the individual performance of the constituents. They also suggested that selection for the improvement of the yield potential, important yield components like ear weight and ear length should considerable contribution towards divergence of different inbred lines. Yield components and days to 50 percent silking are of major importance for the improvement of productivity therefore, major emphasis will be laid on these characters only.

An experiment was conducted by Singh *et al.* (2005) to study the genetic divergence of 23 maize genotype using D^2 analysis .The genotypes fell into six clusters. The cluster means were higher for 50 percent tasseling, 50 percent silking, plant height, ear height, ear length, number of grain per row and 100 grain weight in cluster IV; for ear diameter, days to maturity and number of rows per ear in cluster II ; and for grain yield per plant in cluster III followed by cluster II. Genotypes belonging to these clusters offer a good scope for improvement through selection and hybridization.

More *et al*. (2006) studied forty-five diverse genotypes of forage maize for genetic diversity and identify the suitable genotypes for hybridization programmes based on clustering pattern. The genotypes were grouped into 7 clusters using Mahalanobis D2 statistics. Cluster II was the largest with 25 genotypes followed by cluster III with 11 genotypes and cluster I with 5 genotypes. The clusters IV, V, VI and VII were mono genotypic. The maximum inter-cluster distance was observed between clusters I and VI followed by distance between clusters I and IV and clusters I and V. Clusters V and VI exhibited the minimum inter-cluster distance.

Ivy *et al.* (2007) observed genetic divergence of twenty-five genotypes of maize using D^2 and principal component analysis. The genotypes under study fell into five clusters. Wider genetic diversity among the genotypes of different groups was suggested due to the inter-cluster distances were higher than intra cluster distances. The intra-cluster value was the maximum in cluster V and the minimum in cluster I. The inter cluster D^2 values showed the maximum distance between cluster II and III followed by the distance between II and I. The cluster means were higher for days to maturity, plant height and ear height in cluster II; grain yield per plant was higher in cluster IV. The maximum contribution of kernel weight and days to maturity towards genetic diversity was reported by (Ahmed, 2007).

Hoque (2008) used thirty-eight maize inbreds and reported that grain weight and grain yield contributed the maximum towards diversity offers good scope for the improvement of yield through selection of parents.

Amiruzzaman (2010) studied with forty-two inbred lines and grouped them into eight clusters with the assumption that those within the same clusters have smaller D^2 value among themselves, than those belonging to other clusters. The distribution pattern indicated that the maximum 9 inbred lines were included in cluster III followed by 8 in cluster VII and 6 each in cluster VI and II. The remainders have been distributed in four clusters: 5 in cluster I, 3 each in cluster V and VIII and the least number 2 in cluster IV. The clustering pattern of the inbred lines under this study did not necessarily follow their geographical distribution. This means it was fairly at random. The inbred lines coming from the same population have gone to different clusters.

Kadir (2010) showed that genetic diversity with twenty QPM inbreds for sixteen characters and estimated the contribution of each trait towards the expression of genetic divergence measured by D^2 values. It was revealed from his study that, the highest contributor was ear height followed by days to silking, percent tryptophan content, ear length, ear diameter and 100- grain weight.

Azad *et al*. (2012) evaluated thirty yellow inbred lines of normal maize for thirteen parameters to study the genetic divergence using multivariate analysis. They grouped thirty inbreds into six distinct clusters. The genotypes within the same cluster were closely related because the intra-cluster distances in all the six clusters were more or less low. The highest inter-cluster distance was observed between cluster I and cluster IV and the lowest between the cluster II and III. The cluster V had the highest (9) and cluster IV contained the lowest (1) number of genotypes. Cluster VI showed the highest mean values for kernel yield and all the yield contributing traits except days to 50 percent tasseling and 50 percent silking. For ear height and ear length Cluster II had the lowest mean values. Days to maturity and ear diameter showed the maximum contribution towards total divergence among different characters. Based on medium to high inter-cluster distances, six inbred lines viz. ML06, ML10, ML14, MK19, ML25 and ML26 were selected for hybridization program.

Seventy nine inbred lines and three checks were evaluated and observations were recorded for thirteen quantitative traits by (Kage *et al*., 2013). Analysis of variance revealed that highly significant difference among all inbred lines. Inbred lines were grouped into fourteen clusters, indicating the presence of genetic diversity. The cluster I is having highest number of genotypes (67). The maximum inter cluster distance was observed between clusters II and XII (22.41) and the highest intra cluster distance was in cluster XII (5.46) and also wide range of variation was observed in cluster mean performance for the characters studied.

Khan *et al*. (2013) observed genetic divergence in seventeen CIMMYT Maize inbred lines including one check based on some morphological traits and grain yield using Mahalanobis D^2-statistics. The genotypes were grouped into four clusters. The cluster II contained the highest number of lines (6), while the cluster I contained only single genotype. The maximum inter-cluster distance was noticed between the cluster I and IV and the minimum between cluster I and II. The highest intra-cluster distance was observed in the cluster IV and lowest in cluster I. The genotypes in the cluster III showed better performances having shorter growth duration, short stature, shortest ear height, better shelling percentage and reasonable yielding ability.

Azam *et al.* (2013) evaluated forty nine CIMMYT, India Maize inbred lines based on some morphological traits and grain yield. Genetic divergences of inbred lines of maize were estimated using D^2 and principal component analysis. The genotypes under study fell into five clusters. The maximum intra cluster value was observed in cluster IV and minimum in cluster V. The inter cluster D^2 values revealed that the maximum distance among the cluster. The highest inter cluster distance was observed between cluster II & I and the lowest inter cluster distance was illustrated in cluster III & I. The cluster means were higher for days to 50 percent tasseling, days to 50 percent sillking, plant height, ear height, ear length, number of rows per ear, number of grains per row in cluster IV; ear diameter and grain yield per plant was found higher in cluster II. It is expected that crossing of inbred lines belonging high to medium D^2 values tend to produce high heterosis for yield.

Amiruzzaman *et al.* (2014) evaluated twenty five yellow inbred lines of normal maize for eleven parameters to study the genetic divergence using Mahalonabiss D^2 and Rao's canonical variate analysis. The twenty five inbreds fell into five distinct clusters. The highest inter-cluster distance was observed between cluster I and VI and the lowest between the cluster II and III. The cluster IV and V each contained the highest number of genotypes. Cluster V showed the highest mean values for kernel yield and all the yield contributing traits except 1000-kernel weight and cluster II had the lowest mean values for plant and ear height and maturity characters. Days to silking, ear length, number of kernels/row, 1000-kernel weight and kernel yield showed the maximum contribution towards total divergence among different characters.

Akhi *et al.* (2017) characterized sixty exotic inbred lines of maize from CIMMYT for a few morphological attributes and grain yield. The inbred lines of the existing investigation were grouped into five distinct non-overlapping clusters based on D^2 analysis. Cluster II exhibited the highest mean values for ear length and ear diameter, cluster V for number of grain /ear and total grain weight. The lowest mean value for plant height & ear height were found in cluster II and cluster IV for days to pollen shedding and days to silking. Days to silking, plant height, ear length (cm), number of rows per ear, number of grains per ear showed the maximum contribution towards total divergence among different characters. The inbred lines were characterized for their morphological traits and kernel yield to achieve more heterotic partners to get higher heterosis.

Shazia *et al*. (2017) assessed genetic diversity in forty seven maize inbred lines based on morphological traits. D^2 analysis was performed and clustering was done using Tocher's

Method. All the inbreds were grouped into 7 clusters. Cluster number IV contained highest number (29) of inbreds and cluster III and VI contained the lowest number (2) of inbreds. Cluster II and V, V and VI, VI and VII showed maximum distance between them suggesting higher probability of heterotic hybrids if selection of parents is done from these pairs of groups. Days to tasselling, and days to maturity showed the highest contribution to total divergence. This study gave an insight into the variability pattern of the inbred lines which will be helpful in their further utilization.

For the estimation of genetic diversity through cluster analysis forty most promising inbred lines were evaluated by Rafique *et al.* (2018) for ten different morphological traits. The field experiment was carried out under randomized 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 distribution of genotypes in the study indicated that the geographical origin did not have any bearing on clustering pattern.

2.5 Combining ability

Combining ability is an important aspect of hybrid breeding program. The term was first introduced by Sprague and Tatum (1942). Rojas and Sprague (1952) stated that the value of an inbred line in the commercial production of hybrid maize is determined by two factors, the characteristic of the line itself with respect to yielding ability, pollen shedding, disease resistance, etc. and the behavior of the line in hybrid combinations. The concept of GCA and SCA has become increasingly important to plant breeders because of the widespread use of hybrid cultivars in many crops (Wilson *et al.*, 1978). Over the years, the combining ability concept has become increasingly important not only in maize but in other crops as well. Combining ability studies provide information on the genetic mechanisms controlling the inheritance of quantitative traits and enable the breeders to select suitable parents for further improvement or use in hybrid breeding for commercial purposes. The inbred line's performance and their combining ability for yield and traits contributing to yield influence the development of high yielding and widely adapted hybrids of maize. General combining ability refers to the average performance of the genotype in a series of hybrid combinations and is a measure of additive gene action whereas, specific combining ability is the performance of a parent in a specific cross in relation to general combining ability. General combining ability (GCA) is associated with additive genetic effects, while SCA is related to non-additive (dominance, epistatic and genotype x environment interaction) effects. The effects of general combining abilities (GCA) and specific combining abilities (SCA) are important indicators of potential value for inbred lines in hybrid combinations.

The evaluation of crosses among inbred lines is an important step towards the development of hybrid varieties in maize. This process ideally should be through the evaluation of all possible crosses (diallel crosses), where the merits of each inbred line can be determined. A Diallel analysis provides good information on the genetic identity of genotypes especially on dominance-recessive relations and some other genetic interactions.

Genova (1984) reported predominant role of non-additive gene effects in the inheritance of grain yield, ear diameter and 1000-kemel weight in 9 x 9 diallel analyses. Debnath and Sarkar (1988) reported equal importance of both additive and non-additive components for number of kernel rows per ear and number of kernel per row, whereas Debnath (1989) also observed nearly equal importance of both additive and non-additive gene effects for ear length, kernel rows per ear and kernels per row.

Results of Crossa *et al.* (1990) suggested that both additive and non-additive effects are important in controlling the expression of grain yield and days to silking; however, non-additive effects are more important in controlling grain yield than in determining days to silking in CIMMYT's tropical late yellow maize germplasm.

Beck *et al*. (1990) observed the importance of additive genetic effects in controlling expression of yield in CIMMYT's subtropical and temperate early-maturity maize germplasm and concluded that general combining ability was significant for plant height, ear height, days to silking and yield, while specific combining ability was significant for ear height, days to silking and yield. Similar results were also reported in CIMMYT's tropical early and intermediate-maturity germplasm (Vasal *et al*., 1992a).

Positive SCA indicate that lines are in opposite heterotic groups, while negative SCA effects indicate that lines are in the same heterotic group (Vasal *et al.,* 1992).

Pal and Prodhan (1994) reported higher magnitude of SCA component in comparison to GCA component for grain yield, oil content, number of grains per row, number of rows per ear, and ear length indicating the importance of non-additive gene effects in controlling these traits. On the contrary, Alika (1994) found predominance of additive gene action for ear length, number of kernels per row and days to silking.

Satyanarayana *et al*. (1995) stated that both additive and non-additive gene effects were important for days to 50 per cent tasseling and yield. Mohammed (1995) observed that genetic variances for ear length and number of ears per plant were mainly additive, while plant height, ear weight, grain weight per ear, hundred grain weight and yield were non-additive.

In an experiment on maize conducted by Ling *et al*. (1996) reported that grain yield per plant exhibited epistasis. Additive gene action appeared to be more important for ear thickness and kernel rows per ear. Inheritance of ear length, hundred grain weight and grain yield per plant was controlled by dominant and epistatic effects. For ear thickness, recessive genes had positive effects and dominant genes had negative effects and for other characters the gene effects were vice versa.

Preciado *et al*. (1997) observed that general combining ability and specific combining ability were significant for yield, days to silking and grain filling period.

Mathur *et al*. (1998) reported that there was a significant GCA variance for days to silking, ear length, ear diameter and number of rows per ear, number of grains per row and grain yield per plant. The SCA variance was significant for ear length. Singh and Singh (1998) indicated that GCA was more important for ear length and number of kernels per row and SCA was more important for grain yield per plant, ear diameter, number of kernels per ear, 100-grain weight, days to silking, plant height and ear height. Joshi *et al*. (1998); found that there was preponderance of non-additive gene action in the expression of yield per plant, protein and starch content, while for oil content and hundred grain weight there was preponderance of additive gene action. However, Roy *et al.* (1998); observed involved of high x high, high x low, high x average and low x average general combiners for high yield in the same crop in their study.

Konak *et al*. (1999) showed that higher SCA variances were noted for grain yield, 1000-grain weight, ear height, ear length and earliness. Higher GCA variances were noted for plant height and number of rows per ear. Kumar *et al*. (1999) found that for grain yield and yield component characters non-additive gene action was predominant. Soliman and Sadek (1999) concluded the higher positive and significant GCA effects for grain yield. Talleci and Kochaksaraci (1999), observed significant GCA effects for plant height, number of grain rows per ear, number of grains per row, ear weight, hundred grain weight and grain yield per plant.

Geetha and Jayaraman (2000), revealed that additive and dominance components were significant for plant height, ear height, days to silking, days to tasseling, ear length and yield per plant. Positive relationship between SCA effect of grain yield and yield contributory characters were reported by Ivy and Howlader (2000).

An experiment was conducted by Akanda (2001) where 7x7 diallel crosses were evaluated and found that GCA variance was highly significant for grain yield, ear length, ear breath and number of kernel/row. It indicated that the expressions of these characters were controlled by additive gene effects. Significant GCA and SCA variance for days to silk, number of row/ear and 1000 kernel weight suggested additive and non-additive gene actions in expression of these characters. However, higher magnitude of GCA variance than corresponding SCA variance indicated predominance of additive gene action. He also showed that CML 329 and CML 323 was good general combiner for grain yield. The hybrid CML 325 x CML 329 showed significant SCA effect produced the highest grain yield. He also suggested that *per se* performance and SCA effect should be considered simultaneously in selecting the promising hybrids.

Vacaro *et al.* (2002) reported that mean square for GCA effects was greater than that for SCA effects for the traits like plant height, point of insertion of the first ear, number of ears per plant, number of grains per ear, root and stalk lodging and grain yield indicating the performance of additive gene effects.

Hussain *et al.* (2003) found non additive gene effects for number of kernels per ear in maize.

Alexander and Bindiganavile (2004) studied early maturity maize varieties across seven South African countries and they found good GCA effects for grain yield.. Singh (2004), reported that highly significant GCA effect for hundred kernel weight and ear length and significantly negative SCA effects for days to silking and maturity. They also found non-additive gene action of grain yield.

According to Katna *et al.* (2005) both the GCA and SCA effects were significant for leaf area per plant, plant height, ear height, ear length, ear circumference, kernel rows per ear, kernels per row, hundred seed weight and grain yield per plant. They also reported preponderance of additive gene effects was important in the expression of all the above traits.

Both additive and non-additive gene effects are important in maize were reported by Rokadia and Kaushik (2005). The presence of marked additive and non-additive gene effects indicated the need for exploiting both fixable and non fixable components of genetic variance for increasing productivity in maize.

Uddin *et al.* (2006) reported significant SCA effects involving of all the three possible combinations between parents of high x high, high x low and low x low general combiners for kernel yield in maize.

Importance of both additive and non-additive genetic variance was reported by Verma and Narayan (2008) on QPM maize in l0xl0 half diallel fashion across environments. They also reported the predominant role of non-additive component controlling all the studied characters.

Combining ability effects for grain yield and some important agronomic characters of maize in a 7x7 diallel analysis excluding reciprocals were estimated by Ahmed *et al.* (2008). They found that variances due to both general combining ability (GCA) and specific combining ability (SCA) were highly significant for all the characters indicated the presence of additive as well as non-additive gene effects for controlling the traits. However, relative magnitude of these variances indicated that additive gene effects were more prominent for all the characters studied except grain yield/plant.

Uddin *et al.* (2008) observed GCA and SCA variance for yield per plant number of kernels per row and 100-kernels weight were significant, which indicated importance of additive as type of gene action for these characters. The ratio of SCA and GCA variances were high for the all character studied that revealed the preponderance of non additive type of gene action. The lines IPB 911-16, IPB 911-12, IPB 911-2, IPB 911-18 and IPB 911-47 showed significant positive GCA effect and simultaneously possessed high mean value indicating that the *per se* performance of the parents could prove as an useful index for combining ability. The crosses exhibited significant SCA effects involved high x high, high x low, low x high, average x low and low x low general combining parents.

Ten F_1 hybrids derived from 5 X 5 diallel cross were evaluated for grain yield and its contributing characters through combining ability analysis in maize (Alam *et al.*, 2008). Significant general and specific combining ability variances were observed for all the characters except ear height. Almost equal role of additive and non-additive gene actions was observed for days to maturity. Additive genetic variance was preponderant for grains per ear and 1000-grain weight and non-additive gene action was involved in plant height, ear height, days to silking and days to maturity.

Kadir (2010) in his study observed that specific combining ability (SCA) variances were non-significant for ear length and ear diameter suggests that these two traits were predominantly controlled by additive type of gene action. The mean squares showed that the non-additive effects (SCA) were more important than additive effects (GCA) for plant height, ear height, days to pollen shedding, days to silking, number of kernnel per row, 100-seed weight, percent poor husk cover and grain yield per plant.

Four maize inbred lines Zheng 58, Chang 7-2, PH4CV and PH6WC were crossed with four maize inbred lines C4-4-43, C6-5-10, C34-4-20 and C50-5-4 to obtain 16 cross combinations according to incomplete diallel design (Zhijun *et al*., 2012). The obtained sixteen combinations and their parents were sown in field plots in Hohhot, Nei Menggu, China in 2011 to analyze the combining ability of six major characters (plant height, ear diameter, ear length, hundred kernel weight, kernels per ear and kernel weight per ear). It was found that the inbred line C6-5-10 had significantly positive general combining ability effects for the above six characters except for plant height. The combinations derived from C6-5-10 gave high kernel yield, ideal plant type and desirable plant height, and so C6-5-10 might be used as a good parent. Its two combinations with desirable plant type, C50-5-14 x Chang 7-2 and C6-5-10xZheng 58, showed high-yielding potential, and therefore had a tendency to improve a good variety.

An experiment was conducted by Elmyhum (2013) where six inbred lines were crossed with two testers (CML144 and CML159) to produce twelve F_1 hybrids. Twelve F_1 hybrids and two standard checks viz., BHQP542 and a normal maize hybrid, Jibat, were evaluated in 2010/2011 at Ambo Agricultural Research Centre. Genetic differences were observed from mean squares of treatments for all traits except days to maturity, ear diameter, number of kernel rows per ear, protein content (%) and oil content (%).

Combining ability was studied for grain yield, days to tasseling, days to silking, plant height and ear height in a diallel cross involving seven elite maize inbred lines by Amiruzzaman *et al.* (2013) and reported that variance due to GCA and SCA were highly significant for the characters studied, indicating both additive and non-additive type of gene action were important for controlling the traits. Predominance of non-additive gene action was observed for all the traits. Plant and ear height showing desirable significant negative GCA effects and simultaneously possessed desirable high mean values, indicating that per se performance of the parents could prove as an useful index for combining ability. Additive × additive, additive × dominance and dominance × dominance gene interactions were involved in deriving good specific cross for yield.

An experiment was conducted to study the combining ability in newly derived lines at Agricultural Research Station, Arabhavi, UAS, Dharwad by Kage *et al.* (2013). The results revealed that among ten female lines, L2 was the best general combiner for plant height, ear height, ear length, hundred grain weight, grain yield per hectare and fodder yield per hectare. Whereas, among thirty crosses, L8 x T3 is the best specific combination for plant height, ear height and grain yield per hectare.

Haydar and Paul (2014) made a study to combining ability of yield and yield components by crossing six diverse maize inbred lines in a half diallel mating design. GCA to SCA ratios were less than one for plant height, ear diameter, ear length and number of kernels row per ear indicating a preponderance of additive over non additive gene action. The crosses $P_1 \times P_2$, $P_3 \times P_5$ and $P_5 \times P_6$ were exhibited significant and positive SCA effects for yield and ear diameter, number of row per ear and number of grains per ear of yield contributing characters. The parents P_1 (IL_4), P_3 (IL_{18}) and P_5 (IL_{23}) were good general combiner for grain yield and yield attributing characters.

Ahmed *et al*. (2014) carried out an experiment to determine the general combining ability (GCA) of the parents and specific combining ability (SCA) of the crosses in a 8×8 diallel cross of white grain quality protein maize (QPM). Significant mean sum of squares due to GCA and SCA were observed for all the characters studied. Higher magnitude of SCA variance than GCA variance clearly indicated the predominance of non-additive gene action for all the traits. The parental lines P_4, P_7 and P_6 were found to be the best general combiner for yield components and these parents could be used as donor parents in hybridization to improve traits like days to tasseling, days to silking, plant height, ear height, ear length, ear diameter, grains per ear and 1000 grain weight by accumulation of favorable genes.

Amin *et al*. (2014) observed significant general and specific combining ability variances for all the characters studied. They found that additive genetic variance was preponderant in plant height, ear height, ear length, ear diameter, and kernel weight and non-additive gene action was involved in days to silking, number of kernels per ear and kernel yield. The good combining parents for different traits could be used in hybridization to improve yield and other desirable traits as donor parents for the accumulation of favorable genes**.**

Ram *et al*. (2015) estimated the general Combining Ability (GCA), specific Combining Ability (SCA) and heterosis of F_1 crosses. Analysis of Variance revealed significant differences among genotypes, parents and crosses for all the traits. The interaction of Line × Tester was highly significant for all the traits. Both, non-additive and additive types of gene action were observed to influence the expression of traits among the crosses. Among the lines, CM 141, V335 and V351 were promising as observed to be the superior general combiner. Cross CM 141 × CML 161 was among the best cross as the cross recorded positive and significant SCA effect, high heterosis and high per se performance for grain yield and other important traits.

An experiment was conducted by Niyonzima *et al*. (2015) at Zonal Agricultural Research Station, V.C. Farm, Mandya, University of Agricultural Sciences, Bangalore, Karnataka state during rabi 2010. The analysis of variance indicated the presence of significant variability among the genotypes for almost all the quantitative traits studied. Combining ability analysis showed the predominant role of non-additive gene action for inheritance of all the characters studied. The lines MAI31, MAI28, and MAI35 were best general combiners exhibiting high GCA effects in a desirable direction for three traits each.

Hoque *et al*. (2016) was carried out a study in 6x6 diallel crosses for combining ability analysis for grain yield, maturity and growth parameters in maize. Variances due to GCA were much higher in magnitude than SCA indicated additive gene effects were much more important for all characters except ear length, thousand grain weight and ear height. The Parent P_5 was the best general combiner for yield and most of the yield contributing characters. The Parent P_1 & P_2 were the best general combiner for both dwarf and earliness. The crosses which showed significant SCA effects for yield were involving average x average, average x low and low x low general combining parents.

Talukder *et al.* (2016) studied combining ability in a 7×7 half diallel cross in maize for grain yield and yield contributing characters. Significant general and specific combining ability variances were observed for all the characters studied. The significant estimates of GCA and SCA variances suggested the importance of both additive and non-additive gene actions for the expression studied traits. In these studies, variances due to SCA were higher than GCA for all characters, which revealed the predominance of non-additive gene action (dominance and epistasis) for controlling these traits. Parents P_1 and P_4 were excellent general combiner for days to tasseling and silking while parents P_1 and P_5 for early maturity. Parent P_4 for short height; parents P_4 and P_7 for higher thousand kernel weight. The parents P_4 and P_6 having good combining abilities for yield.

Forty five F_1s generated by 10 × 10 half diallel were evaluated by Dhoot *et al.* (2017). The ratio of GCA/ SCA variance revealed that there was preponderance of additive gene action in the expression of yield and yield contributing characters viz,. ear length, number of grain rows per ear, hundred grain weight, grain yield per plant, harvest index under study. Parent P1 (Number of grain rows per ear), P6 and P7 were good general combiners for another yield and yield attributing characters. Hybrid P1 x P5 showed the highest positive significant SCA effects (48.60) along good per se performance (151.67 g per plant) and positive significant economic heterosis (26.39 %) for grain yield per plant. This hybrid also exhibited positive significant SCA effects for hundred grain weight and harvest index.

An investigation was carried out by Purushottam and Shanthakumar (2017) to assess the combining ability in maize genotypes using a diallel mating design (without reciprocal crosses) using six homozygous lines namely, DMIT 121, DMIT 123, DMIT 124, DMIT 125, DMIT 113 and DMIT 118. Analysis revealed the presence of higher magnitude of SCA variance than GCA variance indicating predominance of non-additive gene action for all the ear traits. Crosses having one of their parent with good general combiner for all the traits having H x L or L x H GCA status showing dominance and epistatic interactions.

Karim *et al*. (2018) made a study to isolate superior inbred lines and better combining parents for suitable hybrids and to determine percent of heterosis using standard commercial checks in a 7 × 7 diallel analysis excluding reciprocals over five environments. The mean sum of square obtained from combined analysis of variance showed the presence of genetic variability among the crosses, environment and crosses ×

environment interaction for all of the characters under study. The variances for general combining ability (GCA) and specific combining ability (SCA) of variance were found significant for all the characters. However, relative magnitude of variances indicated that additive gene effects were more prominent for all the characters studied. GCA and SCA effects both showed significant interaction with environment for all the traits.

2.6 Heterosis

Heterosis has also been recognised as one of the major landmarks in crop improvement. Crosses between parents of presumably different origins gave greater heterosis than crosses between parents that were presumably more closely related (Allard, 1960). Positive correlation between heterosis in a cross with the genetic distance of the parents has been widely reported (Paterniani and Lonnquist, 1963; Moll *et al*., 1965). Heterosis has been exploited profitably in many cross-pollinated crops by crossing highly selected inbred lines. Mian, 1985; reported higher levels of heterosis with increased divergence within a certain range, which declined in extremely divergent crosses. The extent of heterotic response of the F_1 hybrids largely depends on the breeding value and genetic diversity of the parents included in crosses, and on the environmental conditions under which hybrids are grown (Hallauer and Miranda, 1988).

The commercial usefulness of a hybrid would primarily depend on its performance in comparison to the best commercial variety of the concerned crop species. In many cases, the superior parent of the hybrid may be inferior to the best commercial variety. In such cases, it will be desirable to estimate heterosis in relation to the best commercial variety of the crop. Such an estimate is of commercial or direct practical value in plant breeding and termed as economic, standard or useful heterosis.

Presence of hybrid vigour in maize was reported by many workers (Debnath, 1989 and Crossa *et al.,* 1990). High parent heterosis (9.6%) for grain yield among crosses was observed in CIMMYT's tropical early and intermediate maturity maize (Beck *et al*.,1990).

Beck *et al.* (1991) reported low estimate of high-parent heterosis (16% in U.S. and 9.9% in Mexican environment) in CIMMYT's subtropical and temperate intermediate maturity maize germplasm, although in subtropical early maturity germplasm moderate levels of heterosis (13%) was noticed by Vasal *et al.* (1992).

Nagda *et al*. (1995) studied twenty F_1 hybrids and reported that fifty crosses exhibited significant positive heterosis for grain yield over best check and revealed significant negative heterosis for days to silking, plant height and ear height in all crosses except one cross.

Ling *et al*. (1996) confirmed that mean heterotic effect was the highest for grain yield per plant followed by grain weight and ear thickness. Saha and Mukherjee (1996), reported that there was significant positive heterosis for grains per ear and the crosses with the highest heterosis for hundred grain weight and grain yield per plant had high negative heterosis for percentage grain conversion.

Ling *et al.* (1999) noted that the hundred grain weight of all hybrids was greater than the female parents. But heterosis of mid parental value differed according to the relative grain weight of parents. Kumar *et al*. (1999) observed heterosis over better parent for grain yield which were ranged from 26.31 to 37.30%. Stojokovic *et al*. (1999) reported that the partial or complete dominance of dominant alleles with additive effects were the main contributors to yield heterosis in maize.

Netaji *et al.* (2000) observed significant and positive heterosis and heterobeltiosis for grain yield in more than twenty hybrids and expression of heterobeltiosis was most evident for grain yield per plot, followed by test weight, ear length, ear height, plant height and number of seed rows per ear.

Shahwani *et al.* (2001) noticed positive and significant heterosis in seventeen hybrids, while 11 hybrids showed heterobeltiosis for ears per plant.

Saleh *et al.* (2002) reported high estimates of heterosis for grain yield, ear weight, grain weight per ear, moderate estimates for plant and ear height, shelling percentage, ear diameter, number of kernel rows per ear, number of kernels per ear row and grain weight.

Galad (2003) observed significant positive and negative standard heterosis for number of rows per year .Standard heterosis for thousand kernel weight varied from -40.1 to 24.35%. For ears per plant standard heterosis varying from -12.15 to 42.99% was recoreded. Nine crosses exhibited positive and significant heterosis over BHQPY-545. This indicated more prolificacy of the test cross over the standard check. Betran *et al*. (2003); reported that Mid Parent Heterosis and Better Parent Heterosis of 157% and 126%, respectively in tropical maize. Singh (2003), reported highly significant negative heterobeltiosis and standard heterosis for early silking.

A line x tester analysis was undertaken by Kaushik et al. (2004) using twenty four early maturity maize inbred lines of white grain color with three testers at three locations for yield and yield attributes maturity and quality traits. They observed thirty out of seventy two crosses exhibited strandard heterosis for grain yield per plant. They also noticed that one cross showed significant and commercially acceptable standard heterosis for grain yield per plant (17.24%).

Uddin *et al.* (2006) made crosses among seven inbred lines in a diallel fashion and showed the range of heterobeltiosis expressed by different crosses was from 8.23 to 25.78 per cent and -0.22 to -8.31 per cent, respectively, for grain yield and days to silking and ten crosses out of 21 showed significant positive heterosis. They also found significant negative heterosis for days to tassel, days to silk, plant height and ear height. The better performing four crosses (P1 × P7, P6 × P7, P1 × P4 and P4 × P5) can be utilized for developing high yielding hybrid varieties as well as for exploiting hybrid vigor.

Maize population derived from crosses among eight inbred lines in a diallel mating system were investigated for heterosis and combining ability of selected inbred lines for yield and yield components by Gissa *et al*. (2007). The crosses and parents were evaluated in a randomised complete block design with three replications at Bako Research Center, Ethiopia. They observed that values for mean mid-parent heterosis (MPH) ranged from 2.9% for days to maturity to 89.2% for grain yield and high-parent heterosis from 0.65% for ear diameter to 64% for grain yield. All crosses exhibited positive MPH for ear and plant height, ear length, kernels per row and grain yield.

Ahmed *et al.* (2008) in their study observed that all the crosses showed significant positive heterobeltiosis for grain yield per plant. The range of heterobeltiosis expressed by different crosses was from 42.97 to 163.24 % and -3.76 t -11.92 %, respectively, for grain yield and days to silking.

Uddin *et al.* (2008) conducted a line x tester analysis in maize involving twelve lines and three testers for grain yield and its components to determine the heterosis. Standard heterosis ranged from - 28.29 to 28.41%; -12.29 to 24.38%; -1.11 to 24.44%; -14.75 to 6.67%; -17.24 to 11.26% and -10.94 to 20.83% for grain yield per plant, number of grains per row, number of rows per ear, ear length, ear diameter and hundred kernel weight, respectively. Alam *et al.* (2008); showed significant negative heterosis for days to maturity.

Abdel-Monaem *et al.* (2009) showed positive significant heterosis values as average percentage from mid-parents were 153.96, 182.66 and 479.29% for ear diameter, ear length and grain yield per plant, respectively. On the other hand highest values of heterotic effects over higher parent were 136.61, 144.66 and 325.57% for ear diameter, ear length and grain yield per plant, respectively.

Amiruzzaman (2010) in his study with QPM hybrids showed that for kernel yield out of 21 F_1S, four crosses (PI x P2, PI x P7, P2 x P4 and P3 x Ps) expressed significant positive heterosis over the QPM check BHM 5. The maximum significant positive heterosis 6.35% over the check was recorded by PI x P7 followed by 6.10% in PI x P2, 4.15% in P2 x P4 and 3.15% in P3 x Ps.for this trait. He also observed that, in normal maize hybrids three crosses viz., QI x Q7. Q2 x Q3, and Q4 x Q6 expressed significant positive heterosis for yield coupled with other yield components like ear length, ear diameter, number of kernels per ear and thousand kernel weight over the commercial check variety Pacific11. The other desirable crosses were Q6 x Q7 and QI x Q2 showed significant positive heterosis for kernel yield and yield components like length of ear, ear diameter and kernel weight.

Kadir (2010) in his study with QPM hybrids found that most of the crosses showed significant high positive heterosis over standard check variety and better parent for grain yield/plant. It was evident that CML-162 x CML-191 had the highest heterosis followed by CML-164 x CML-191, CML-191 x CML-162, CML-162 x CML-170 over standard check variety and better parent while, moderate to high heterosis was observed from CML-188 x CML-162, CML-191 x CML-164 and CML-170 x CML-193.

Iqbal *et al*. (2011) examined single cross hybrids including four local checks to test the combining ability and magnitude of heterosis among elite maize inbred lines.They observed that hybrids exhibited heterosis in grain yield varying from 19-40% over the best check.

Heterosis estimates for most of the hybrids had positive mid parents (MP %) and better parents (BP %) heterosis value for the yield and its component by Abuali *et al*. (2012). The ranges of heterotic responses observed in this study were on to130.92 % and 125.28%, observed in this study.

Amiruzzaman *et al.* (2013) studied heterosis for grain yield, days to tasseling, days to silking, plant height and ear height in a diallel cross involving seven elite maize in-bred lines. Standard heterosis for grain yield ranged from -17.60 to 9.71%. For other traits, desirable heterosis varied from -0.10 to -4.42%; -0.03 to -4.20%; -2.44 to -42.11% and -1.33 to -21.87% for days to tasseling, days to silking, plant height and ear height, respectively.

Shushay (2014) reported significant standard heterosis of crosses over the commercial checks for traits such as grain yield, plant height, ear height, ear length, ear diameter, number of kernel rows per ear, number of kernel per row, thousand kernel weight and number of ears per plant. Grain yield of the crosses over the standard checks ranged from -32.16 to 13.02%.

Ten maize inbreds were crossed as lines to eight testers (Quality Protein Maize donors) in Line X Tester mating design to generate eighty F_1 crosses by Ram *et al*. (2015). Standard heterosis for grain yield ranged from -56.45 to 53.31 %. Based on combining ability and hybrid vigour, the lines V335 and V351 figured to be potential lines which to be converted in to QPM lines to develop local QPM hybrids. The QPM donor CML 141 based on its GCA, SCA and heterosis estimates seems to be most promising donor for conversion program.

Mahmood *et al*. (2016) conducted an experiment where five inbred parents were crossed in a diallel fashion excluding reciprocals and fifteen genotypes including 10 hybrid combinations and 5 parents were tested to estimate combining ability and heterosis in maize hybrid combinations for ear traits, plant height and leaf area. Statistical analysis revealed significant difference for kernel rows ear-1 ($P \leq 0.05$), and highly significant difference ($P \leq 0.01$) for days to silking, plant height, leaf area, kernels row-1, 1000-kernel weight and grain yield. Hybrid P3×P5 and P3×P4 was marked as suitable for breeding early maturing hybrids due to negative heterosis values. High heterosis for plant height was recorded for P2×P3 with significant SCA effects. The highest thousand kernel weight was obtained for the hybrid P2×P3 with highly significant heterosis and SCA.

Kumar and Babu (2016) carried out an investigation to assess the combibing ability and heterosis for nine characters viz., days to 50% tasseling, days to 50% silking, days to maturity, plant height, cob length, kernel rows per cob, hundred seed weight, protein content and grain yield per plant in twenty-nine genotypes. The cross combination DHK-12-2141 × DHK-12-2047 recorded significant magnitudes of all three types of heterosis in desirable direction for kernel rows per cob while the same cross registered significant relative heterosis and heterobeltiosis for plant height, cob length, hundred seed weight and grain yield per plant.

2.7 Stability

For quantitative traits like yield the relative performance of different genotypes often varies from one environment to another. Thus, genotype x environment interaction does exist when phenotypic response made by a change in environment is not the same for all genotypes (Comstock and Moll, 1963). A commercial variety must have stable performance and broad adaptation over a range of environments in addition to high yield potential. But its evaluation becomes complicated due to genetic heterogeneity, a complex biological basis, and genotype x environment interactions (Austin and Lee, 1988).

The crop production is the function of genotype, environment and their interaction (GEI). A significant G x E interaction for a quantitative trait such as seed yield can seriously limit the efforts on selecting superior genotypes for improved cultivar development (Kang and Gorman, 1989). Significant GEI results in changing behavior of the genotypes across different environments or changes in the relative ranking of the genotypes (Crossa, 1990). The potential of genotypes and stability of their performance can be judged by multi environment testing (Mahajan and Khera, 1992). Thus, genotype x environment interaction limits the effectiveness of selection when selection is done based only on mean yields. It is more practical to develop and release varieties which are adapted to more than a single environment and can be successfully grown over a range of environments.

Momotaz *et al.* (1992) studied a stability analysis with eight maize genotypes for grain yield in five different locations. A highly significant environment and genotype x environment suggested that considerable interaction of genotypes with environments. The bi and S^2di values revealed that Ferke (1) 8326 and Delhi 8468 may be suitable for cultivation in favourable environment while the check variety Barnali for unfavorable environment.

Satyanarayana and Kumar (1995) reported significant variation for eight promising genotypes of maize and G x E interaction for grain as well as fodder yields.

Gharde and Deshmuka (1996) evaluated fourteen genotypes of maize including eight hybrids and six composites for stability under eight artificially created environments. The result showed that G × E interaction was significant for all the characters under study. Singh *et al.* (1996); analysed ten genotypes of maize under six environments for their stability. The results revealed that genotype × environment interaction was significant for all the traits except ear girth, rows per ear, seeds per row and hundred seed weight, but the linear component of G × E interaction was significant for all of the traits except seeds per row.

Xuejun (1997) analyzed eleven maize hybrids for yield stability in seven Chinese provinces. Zhongdan had the highest average yield and good stability.

Choukan (1999) studied nine medium maturity maize hybrids under ten locations for three years and observed hybrids *viz*., (B73 × K1264) × M017/11-1, (K1264/1 × L17/12-1) × M017/11-1, K1259/3 × B73 and (K2509 × B73 × M017 were classified as stable hybrids. Alvarez and Ruiz (1999) reported the significant environments, genotypes and G x E interaction effects in maize.

An experiment was conducted in Assam, India, to study the phenotypic stability of twenty one maize genotypes used as baby corn over four environments for yield (yield per plot) and yield attributing characters (days to 50% tasselling, plant height, ear height, ear length, ear girth, number of ears per plant, stem girth and number of kernel rows per ear) by Sharma and Saikia (2000). The mean squares due to the genotype x environment (GE) interaction were significant for all the characters except stem girth. For all the characters except stem girth, both linear and nonlinear components were significant, while for the stem girth only nonlinear component contributed towards GE interaction variance. GANGA-11, FH-3104, CHH-72 and HKH-1075, with average stability for high ear yield, were the best genotypes.

Choukan (2000) studied ten maize single cross hybrids by for their stability in grain yield, thousand kernel weight, kernel numbers per row and rows number per ear using regression coefficient (bi), deviation from regression (S^2di), stability variance, coefficient of variation (CV) and simultaneous selection method for grain yield and stability indices at 14 locations in Iran for 2 years. According to the results, using all stability indices, hybrids No. 6 (KL17/2-5 x MO17) and No. 10 (KSC704) were determined as stable hybrids. Grain yield showed positive and highly significant correlation with 1000 kernel weight (r=0.45**), kernel depth (r=0.40**) and kernel numbers per row (r=0.64**).

Seven early maturing open pollinated (OP) and five yellow hybrid maize varieties were evaluated by Ogunbodede *et al*. (2001) at twenty two locations representing the different agroecologies of Nigeria. Significant location effects were observed for grain yield in the two sets of maize varieties tested. Grain yield was significantly higher in the northern/southern Guinea savanna agro ecologies when compared to the other agro ecologies. Significant genotype x location interaction was also observed for both sets of maize varieties. The best hybrid (8522-2) combined stability with high grain yield and wide adaptability.

Burak and Broccoli (2001) evaluated fourteen pop corn hybrids in five locations for their adaptability and results revealed significant differences in genotype × environment interaction, genotypes and environments.

Using three test-cross populations of Tainan-white (TNW) maize as materials (T9-9 x TNW, H95 x TNW and A632 x TNW), the variation of stability and performance of 15 agronomic characters affected by meteorological factors in different locations was investigated by Sheng *et al.* (2002).

Dodiya and Joshi (2003) studied eighty-six genotypes of maize (*Z. mays*) for genotype x environment (G x E) interaction and stability parameters with respect to yield and maturity over three locations (Udaipur, Banswara and Pratapgarh) in Rajasthan, India. G x E interaction was significant for both characters studied (days to 50% brown hush and grain yield per plant). More number of genotypes was found to be stable for maturity compared to grain yield across the environment as indicated by the non-significant deviation from regression in stability analysis. Ten genotypes for grain yield and 19 genotypes for maturity were the most adaptable with desirable mean performance for better environments.

An analysis of combined variance through the localities and an analysis of stability was performed according to the additive main effects and multiplicative interactions model to evaluate the yield stability of seven maize cultivars in seven maize farms in Venezuela by Medina *et al*. (2003). The study of the interaction between the genotype and the location provided different patterns of responses among cultivars and hybrids.

Kumar and Singh (2004) conducted an experiment where a total of seven inbred maize parents and their twenty one single crosses and two standard checks were used for estimating the stability parameters (days to 50% tasselling, silking and maturity; plant and ear height; ear length and girth; number of kernel rows per ear; number of kernels per row, hundred kernel weight; and grain yield per plant) based on Eberhart and Russels' model by raising the crop in Ajitmal (Uttar Pradesh), Delhi, Banswara (Rajasthan) and Uchani (Haryana), India, during the 1998 kharif season. The stability analysis exhibited highly significant variation for genotypes (G), environment (E), G x E, environment (linear), G x E (linear) and pooled deviation for most of the characters.

AMMI (Additive Main effects and Multiplicative Interaction) analysis was carried out by Reddy *et al.* (2004) in maize yield trials of forty five hybrids over four environments (years/locations) to identify the suitable and stable hybrids. Grain yield data were subjected to the AMMI analysis. Analysis revealed significant G x E interaction which could be attributed to differential ranking of the genotypes across the environments. The G x E interaction was further partitioned into PCA axes, of which the first PCA axis captured 53.35% to the total G x E variance. Perusal of the biplot analysis indicated that six hybrids (H26, H17, H2, H3, H21 and H38) were identified as having a general adaptability with high mean yields and PCA scores nearer to zero. Similarly, among the environments, DEL95, with PCA score nearer to zero, was found ideal for stable performance of the hybrids.

Twenty five maize genotypes were evaluated in three different environmental conditions to estimate the relative stability of grain yield and days to maturity. The genotypes differed significantly for both the characters and significant genotype environment interactions also occurred for both the characters studied (Miah *et al.* 2004).

The stability and adaptability of forty six maize cultivars were evaluated at eleven locations in the Brazilian Northeast Region by Carvalho *et al.* (2005). The performance of the cultivars significantly varied in all environments. Shehata *et al.* (2005) constructed an index which combined the mean yield and two parameters of stability, i.e. bi and S^2 of the regression of variety mean on environmental index and it was designated as a superiority index. They reported that a superiority index could be used in estimating the degree of desirability for the different hybrids.

An experiment was established by Mendoza *et al*. (2006) across nine contrasting environments in Azuero, Panama during 2005-06, to select maize hybrids with the best stability and adaptability on the Azuero Region. The genetic materials comprised 14 white and yellow maize hybrids. A combined analysis of variances was done and the means was separated by LSD. To estimate the adaptability and stability of hybrids and environments, AMMI and GGE Bi-plot and SREG technique were used. The statistical analysis indicated significant differences ($P<0.01$) among genotypes, environments and the genotype-environment interaction, indicating the differential response of hybrids confronted with different environments. The hybrid P-0105 was superior to all others, with mean yield of 8.01 t/ha. This genotype was followed by the hybrid group formatted by 30S-40, PB-0103, P-0512, P-0102, 30F-80 and DK-466 with yields above 7 t/ha. The stability analysis identified the hybrid P-0102 like the most stable.

Soliman (2006) conducted a study to estimate stability degree of twenty four promising yellow maize single crosses. High significant genotype x environment interaction was detected for yield & yield contributing traits. A large portion of this interaction was accounted for the linear regression on the environmental means. The magnitude of non linear components was considerably small. Stability parameter indicated that five single crosses possessed high yield potential and earliness. These hybrids were more responsive to a wide range of environments.

Akanda *et at.* (2007) carried out stability analysis with fifteen maize hybrids under four different environments for grain yield and its components. The genotype x environment interaction indicated difference response of hybrids with respect to environments for these characters. Linear component towards hybrid x environment interaction for grain yield, days to maturity, plant height, ear length, ear girth, no. of kernel rows/ear and no. of kernels/row suggested more precise prediction of performance of the hybrids across environments based on these characters.

Abdulai *et al.* (2007) studied nine genotypes for four year at eight locations in Ghana. Stability analysis identified seven genotypes were stable, when b values alone were considered. When the b values and the deviations from regression (S^2d) were considered (GH24 × 1368) × 5012 and (GH22 × 1368) × 5012 were the most stable, but when coefficient of determination was added to the b value and S^2d, GH132-28 was the most stable genotype.

Admassu *et al.* (2008) tested fifteen maize genotypes at nine different locations to determine stable maize genotypes for grain yield and determine genotypes with high yield and form homogenous grouping of environments and genotypes. Based on the stability analysis, genotypes 30H83, BH-540, Ambo Synth-1, AMH-800 and BHQP-543 were found to be stable for grain yield. The first two Interaction Principal Component axis (IPCA1 and IPCA2) were significant ($p<0.01$) and cumulatively contributed 70.27% of the total genotype by environment interaction. The coefficient of determination (R^2) for genotypes 30H83 was as high as 0.92, confirming its high predictability to stability. Among the genotypes, the highest grain yield was obtained from genotype 30H83 and BH-541 (8.98 and 8.05 t ha^{-1}) across environments. Clustering of AMMI-estimate values grouped genotypes in to four clusters and the environment in to three clusters.

Kadir (2010) studied thirteen hybrids over four different environments and found significant differences among the test environments, genotypes and genotype x environment interaction. The presence of significant genotype x environment interaction showed the inconsistency of performance of maize hybrids across the environments. Variation due to genotype was highly significant. Variances due to environments were also significant suggesting that these traits were influenced significantly by environments

An experiment was conducted by Sadek *et al*. (2011) to investigate the performance and stability across four environments i.e. Gemmeiza, Sakha, Sids and Mallawy of eighteen genotypes of maize and two commercial checks hybrids (SC 155 and SC 3084). Combined analysis of variance of stability across environments indicated that significant genetic variability for all studied traits, as well as the environment indicating differential effect of each environment. Sakha location produced the highest grain yield. Most of the hybrids had a significant deviation mean square from linear regression for grain yield implying that these hybrids were unstable across environments except for seven hybrids Gm 1, Gm 2, Gm 6, Gm 9, Gm 14, Gm 17 and Gm 18 which showed small and insignificant S^2di estimates, indicating that these hybrids could be considered to be stable hybrids.

Mosa *et al.* (2012) found that genotype x environment (G x E) interaction and their partitions, E (linear), G x E (linear) and pooled deviations nonlinear) were significant for grain yield. They added that the coefficient of determination (R^2) values ranged from 0.58 to 0.91 for grain yield.

Lata *et al.* (2013) tested thirty maize hybrids in randomized complete block design with three replications to study genotype x environment (G x E) interactions and stability for yield and related traits across six locations in Himachal Pradesh. Combined analysis of variance across locations showed highly significant differences among locations, genotypes and their interactions for all the traits studied. Significant G x E interactions for all the traits depicted that these traits were important determinants of G x E for yield in specific area. Among six locations, Hi Shell (91.44 q/ha) ranked first followed by DKC 7074 (91.25 q/ha), 900 M Gold (89.74 q/ha) and VMH 4102 (89.38 q/ha).

Using Additive Main Effects and Multiplicative Interaction (AMMI) a field experiment was executed at two locations, Shambat and Elrawakeeb, Sudan to identify the yield stability and adaptability of the grain maize genotypes by Abuali *et al*. (2014). The results showed that, highly significant differences were detected among genotypes, environments and for G x E interaction, indicated differential performance of genotypes over environments. Considering mean grain yield, and the Linear Regression parameters bi and S^2d values jointly, the F_1 hybrids 160x2, 160x3 and 6x3 gave above average mean of grain yield/ha and were most stable for grain yield/ha. AMMI analysis differentiated the genotypes (parental inbred lines and F_1 hybrids), based on their grain yield into different adaptation pattern and stability. Based on AMMI analysis, the F_1 hybrids 66y x 6 and 6 x 3 were highly stable with considerable high yield and adapted to favorable environments.

Sudan *et al*. (2016) evaluated eleven experimental hybrids including a check (Kanchan-612) for stability and adaptability of grain yield and its component traits in experimental maize hybrids using AMMI based stability analysis. This study comprised of the ANOVA (Analysis of Variance) indicated significant effects of genotypes (G), environments (E) and their interaction (GE). The two principal components in AMMI analysis were significant, explaining 65.99% (37.87% PC1 and 28.12% PC2) of interaction variation. The AMMI biplot clearly showed that certain genotypes in one year have higher yield than in other.

Matin *et al.* (2017) evaluated twenty one hybrids along with two check varieties of maize were assessed for genotype environment interaction (GEI) and stability for selection of the best hybrid maize in three different Agro-Ecological Zones (AEZ) of Bangladesh during rabi season 2014/2015. The mean sum of square for genotypes was highly significant for the studied characters. Similarly, environmental variances were also highly significant for all characters. AMMI Component 1 showed variation for TSW. But AMMI Component 2 and G×E (Linear) revealed insignificant variation for all the characters. The highly significant effects of environment indicated high differential genotypic response across the different environments. The environments of Gazipur (Ij=-1.42**) and Barisal (Ij=-0.068) were poor but Rangpur (Ij=1.49) was a favorable environments due to positive environmental index for tested maize hybrids. The AMMI biplot showed four grouping of genotypes having none of them, low yielding and unstable; one hybrid was low yielding but moderately stable; eight were high yielding and stable hybrids, and fourteen were high yielder but highly unstable.

CHAPTER III
MATERIALS AND METHODS

The details of materials used and methods followed in carrying out the present investigation are presented in this chapter.

3.1 Experiment 1: Characterization and maintenance of maize inbred lines

A field experiment was conducted at Regional Agricultural Research Station, Rahmatpur, Barishal during the period from November 2015 to April 2016 to characterize collected materials based on various morphological traits and to identify potential genotypes.

3.1.1 Materials

Fifty-eight maize inbred lines developed by CIMMYT were used for conducting experiment to identify distinguished morphological characters among the genotypes. The list of inbred lines which were used, are mentioned in the Table 1.

3.1.2 Location and duration

The first experiment was carried out at Regional Agricultural Research Station, Rahmatpur, Barisal during rabi 2015-2016. The location of the site is 22^0 42″ North latitude and 90^o23″ East longitude at an elevation of 4 meter above the sea level. It belongs to the Non-calcareous Grey Floodplain Soils (Non saline, Ganges Tidal Alluvium) under AEZ 13.

3.1.3 Weather condition of the experimental site

The geographical situation of the experimental site was under the subtropical climate, characterized by three distinct seasons, the monsoon or rainy season from November to February and the pre-monsoon period or hot season from March to April and monsoon period from May to October (Edris *et. al.,* 1979). During the rabi season the rainfall generally is scant and temperature moderate with short day length. Meteorological data on rainfall, temperature, relative humidity from November 2015 to March 2016 were obtained from the Department of Meteorological Centre, Dhaka-1207, Bangladesh (Appendix I).

Table 1. List of maize inbred lines used in the 1st experiment

SL. No.	Inbred	Source	SL. No.	Inbred	Source
1	CML126	CIMMYT	30	CML332	CIMMYT
2	CML127	CIMMYT	31	CML333	CIMMYT
3	CML128	CIMMYT	32	CML334	CIMMYT
4	CML129	CIMMYT	33	CML367	CIMMYT
5	CML132	CIMMYT	34	CML368	CIMMYT
6	CML133	CIMMYT	35	CML369	CIMMYT
7	CML135	CIMMYT	36	CML370	CIMMYT
8	CML136	CIMMYT	37	CML371	CIMMYT
9	CML137	CIMMYT	38	CML372	CIMMYT
10	CML138	CIMMYT	39	CML373	CIMMYT
11	CML242	CIMMYT	40	CML375	CIMMYT
12	CML243	CIMMYT	41	CML376	CIMMYT
13	CML249	CIMMYT	42	CML377	CIMMYT
14	CML263	CIMMYT	43	CML378	CIMMYT
15	CML264	CIMMYT	44	CML379	CIMMYT
16	CML311	CIMMYT	45	CML380	CIMMYT
17	CML312	CIMMYT	46	CML381	CIMMYT
18	CML313	CIMMYT	47	CML382	CIMMYT
19	CML314	CIMMYT	48	CML383	CIMMYT
20	CML315	CIMMYT	49	CML384	CIMMYT
21	CML316	CIMMYT	50	CML385	CIMMYT
22	CML317	CIMMYT	51	CML482	CIMMYT
23	CML318	CIMMYT	52	CML483	CIMMYT
24	CML319	CIMMYT	53	CML484	CIMMYT
25	CML320	CIMMYT	54	CML485	CIMMYT
26	CML321	CIMMYT	55	CML512	CIMMYT
27	CML322	CIMMYT	56	CML517	CIMMYT
28	CML330	CIMMYT	57	CML518	CIMMYT
29	CML331	CIMMYT	58	CML519	CIMMYT

3.1.4 Characteristics of soil

The soil of the experimental plots were clay loam, land was medium high with medium fertility level. The Physical and Chemical characteristics of initial soil in the experimental field are presented in Appendix II.

3.1.5 Methods

The following precise methods have been followed to carry out the experiment:

3.1.5.1 Preparation of the main field

The plot selected for the experiment was opened in the first week of November 2015 with a power tiller, and was exposed to the sun for a week. After one week the land was harrowed, ploughed and cross-ploughed several times followed by laddering to obtain a good tilth. Weeds and stubbles were removed, and finally obtained a desirable tilth of soil for sowing of maize seeds.

3.1.5.2 Experimental design

The inbred lines were sown separately respectively, on 21 November, 2015. Unit plot size for each of the inbred line was 1 row 3 m long and maintaining 75 cm and 25 cm spacing between rows and hills, respectively, in both the cases. Fertilizers were applied @ 120, 35, 70, 40, 5 and 1.5 kg/ha of N, P, K, S, Zn and B respectively. After proper thinning, one healthy plant was kept in each hill. Undesirable and off type plants from the each line were rouged out before flowering. Standard agronomic practices were followed to raise a good crop. At flowering stage healthy, disease free desirable plants were selected and selfed carefully by hand pollination. Field view of maintenance breeding is presented in Plate 1.

3.1.5.3 Collection of data

Data were recorded according to the maize descriptor during vegetative, flowering, harvesting and post harvesting stage.

Plate 1. Field view of first experiment showing maintenance breeding of maize

The procedure of collecting data for each category of characters are given below

A. Eleven qualitative characters were recorded according to the maize descriptors (IBPGR, 1991)

i). Leaf attitude - a. Rectilinear b. Slightly recurved c. Recurved d. Strongly recurved e. Very strongly recurved

ii). Anthocyanin in anther (Tassel) - a. Absent or very weak b. Weak c. Medium d. Strong e. Very strong

iii). Anthocyanin in silk (Ear) - a. Absent or very weak b. Weak c. Medium d. Strong e. Very strong

iv). Anthocyanin in glume (Tassel) - a. Absent or very weak b. Weak c. Medium d. Strong e. Very strong

v). Anthocyanin in ring glume (tassel) - a. Absent b. Present

vi). Anthocyanin in nodes (stem) - a. Absent or very weak b. Weak c. Medium d. Strong e. Very strong

vii). Anthocyanin coloration of internodes - a. Absent or very weak. Weak c. Medium d. Strong e. Very strong

viii). Anthocyanin coloration of sheath - a. Absent or very weak b. Weak c. Medium d. Strong e. Very strong

ix). Angle between main axis and lateral branches - a. Very small b. Small c. Medium d. Large e. Very large

x). Number of primary lateral branches - a. Absent or very few b. Few c. Medium d. Many e. Very many

xi). Types of grain - a. Flint b. Flint-like c. Intermediate d. Dent-like e. Dent

B. Quantitative characters

i) Days to 50 per cent tasseling

The Number of days taken from date of sowing to date of 50 per cent plants shedding pollen was recorded.

ii) Days to 50 per cent silking

The number of days from sowing upto the day on which 50 per cent of plants showed silk emergence (2-3 cm) was recorded as days to 50 per cent silking.

iii) Plant height (cm)

The height of plant from ground level upto the base of the tassel, where branching of tassel started was recorded as plant height in centimeters when plants were matured.

iv) Ear height (cm)

Height from ground level upto the base of the upper most bearing internode was recorded as ear height in centimeters.

v) Ear length (cm)

Length of the ear was measured and recorded in centimeters at the time of harvest as its total length (from the base to the tip of the ear).

vi) Ear diameter (cm)

Ear girth was measured in centimeters at a point of maximum diameter after de husking of the ear.

vii) Number of kernel rows per ear

Number of kernel rows per ear was recorded by counting the number of rows per ear at the middle of the ear for five randomly selected ears.

viii) Number of kernels per row

Number of kernels per row was counted and average was recorded as number of kernels per row.

ix) Thousand grain weight (g)

Random sample of one thousand kernels was taken and the weight was recorded with the help of electronic top pan balance.

x) Grain weight/selfed ear/plot

Grain weight of selfed ear from each plot were taken and kept for maintenance purpose.

3.1.5.4. Statistical analysis

Collected data were subjected to Microsoft Software for analysis.

The data gathered were analyzed for:

Mean (X) = $\Sigma X_i/n$

Variance (V_x) = $\Sigma (X_i – X)^2 / (n-1)$

Variance of the mean (Vx) = Vx/n

Coefficient of Variation (CV %) = $\sqrt{}$ (Vx) / Mean x 100

The significance of the difference among the treatments means was estimated by the least significant difference (LSD) test at 5% level of probability (Gomez and Gomez, 1984).

3.2 Experiment 2: Study of inter-genotypic variability and genetic diversity for morphological and agronomic traits in maize inbred lines

A field experiment was conducted at Regional Agricultural Research Station, Rahmatpur, Barisal during the period from November 2015 to April 2016 to study on the inter genotypic variability and genetic divergence in inbred lines of maize and to screen out the suitable parents group which are likely to provide superior segregates on hybridization.

The materials and methods of this experiment are presented under the following headings:

3.2.1 Materials

The experiment material consisted of fifty eight white maize inbred lines. The maize inbred lines received from CIMMYT (International Wheat and Maize Improvement Centre), Mexico. The description of the genotypes was given in Table 1.

3.2.2 Methods

The following precise methods have been followed to carry out the experiment.

3.2.2.1 Preparation of the main field

The plot selected for the experiment was opened in the first week of November 2015 with a power tiller, and was exposed to the sun for a week. After one week the land was harrowed, ploughed and cross-ploughed several times followed by laddering to obtain a good tilth. Weeds and stubbles were removed, and finally obtained a desirable tilth of soil for sowing of maize seeds.

3.2.2.2 Application of manures and fertilizers

The fertilizers N, P, K, S, Zn and B in the form of urea, TSP, MP, Gypsum and borax, were applied @ 120, 80, 80, 20, 5 & 1 kg/ha of N, P_2O_5, K_2O, S, Zn and B, respectively. One third of Urea and the entire amount of TSP, MP, Gypsum, Zinc Sulphate and Borax was applied during the final preparation of land. Remaining two third of Urea was applied in two equal installments at floral initiation (knee height stage) and at about one week before silking.

3.2.2.3 Experimental design and layout

Field lay out was done after final land preparation. Fifty eight inbred lines from CIMMYT were used in this experiment following Alpha lattice design with two replications. Seeds of the inbred lines were sown on 21 November, 2015 at two seed per hill and each line was sown in one row plot with 3m long. The size of the unit plot was 3m×0.6m. A distance of 1.5 m from block to block, 60 cm from row to row and 25 cm from plant to plant was maintained. The seeds were placed at about 5 cm depth in the soil. After sowing the seeds were covered with soil carefully so that no clods were on the seeds. Seed germination started after 7 days of sowing on 28th November 2015.

3.2.2.4 Intercultural operations

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

i). Irrigation

One irrigation was provided at each of these growth stages i.e. within a day of planting, at knee height stage of the crop growth, a week before silking and about two weeks after silking for proper growth and development of the plants. Field view of maize at flowering stage is presented in Plate 2.

Plate 2. Field view of second experimental field at flowering stage

ii). Thinning and gap filling

Necessary gap filling were made within ten days of sowing. Thinning was done to keep one plant per hill after two weeks of emergence.

iii). Weeding and mulching

Weeding and mulching were done to keep the plots free from weeds, easy aeration of soil and to conserve soil moisture, which ultimately ensured better growth and development. When seedlings are about two weeks old, first weeding was done. Second weeding was done at knee height stage. Breaking the crust of the soil, when needed was done through mulching.

iv). Earthing up

Eathing up was done twice during growing period. The first earthing up was done at 45 days after sowing and second earthing up was done at the time of application of second dose of N at knee height stage of the crop.

3.2.2.5 Harvesting

Harvesting was started from 20th April, 2016 depending upon the maturity of the plants i.e. when plants showed distinct signs of drying, the husk cover was completely dried and the grains were fully matured. Grain maturity was identified from the milk line of kernels or the formation of a black layer at the junction of grain and placenta.

3.2.2.6 Collection of data

Five plants were tagged randomly for recording observations for each entry for all the quantitative characters except for days to 50 per cent tasseling and silking. Mean of five plants for each entry in each replication was worked out for each character and used for statistical analysis.

3.2.2.7 Observations recorded

Observations on the following quantitative characters were recorded at appropriate stages of plant growth and and details of data collection methods are furnished below.

3.2.2.7.1 Days to 50 per cent tasseling

The Number of days taken from date of sowing to date of 50 per cent plants shedding pollen was recorded.

3.2.2.7.2 Days to 50 per cent silking

The number of days from sowing upto the day on which 50 per cent of plants showed silk emergence (2-3 cm) was recorded as days to 50 per cent silking.

3.2.2.7.3 Plant height (cm)

Height of the plant from ground level upto the base of the tassel where branching of tassel started was recorded in centimeters as plant height when plants were matured.

3.2.2.7.4 Ear height (cm)

Height from ground level upto the base of the upper most bearing internode was recorded as ear height in centimeters.

3.2.2.7.5 Ear length (cm)

Length of the ear was measured and recorded in centimeters at the time of harvest as its total length (from the base to the tip of the ear).

3.2.2.7.6 Ear diameter (cm)

Ear diameter was measured in centimeters at a point of maximum diameter after de husking of the ear.

3.2.2.7.7 Number of kernel rows per ear

Number of kernel rows per ear was recorded by counting the number of rows per ear at the middle of the ear for five randomly selected ears.

3.2.2.7.8 Number of kernels per row

Number of kernels per row was counted and average was recorded as number of kernels per row.

3.2.2.7.9 Thousand grain weight (g)

Random sample of one thousand kernels was taken and the weight was recorded with the help of electronic top pan balance.

3.2.2.7.10 Grain yield per ha (t)

Grain yield was calculated by the following formula:

Grain yield (GY) = $\text{AFW} \times (100-\text{MC}) \times 0.8 \times 10{,}000/\text{Plot area} \times 85$

$\text{AFW}= \text{CF} \times \text{FW}$

$\text{CF}=\text{M}-0.3 \times \text{N}/\text{M}-\text{N}$

Where grain yield is in kg/ha, CF=Correction Factor, M=Optimum number of plants, N=No. of missing plants, 0.3=constant factor, AFW= Adjusted Field Weight, FW = Fresh weight of ears/plot, MC = Percent moisture content, 0.8 is the shelling percentage, 10,000 is the area in m^2 for one hectare and 85 is the factor for grains stored at 15% moisture content.

3.2.2.8 Statistical analysis

The data obtained for different characters were statistically analyzed to find out the significance of the difference among the maize genotypes. The mean values of all the characters were evaluated and analysis of variance was performing by the ‘F’ test. Correlation coefficient was estimated according to Singh and Chaudhury (1985b).

3.2.2.9 Estimation of variability

The data were analyzed for different components. Phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985a) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952).

3.2.2.9.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al*. (1955). The genotypic variance (σ^2_g) was estimated by subtracting error mean square (σ^2_e) from the genotypic mean square and dividing it by the number of replication (r).

This is given by the following formula -

a. Genotypic variance,

$$\sigma^2 g = \frac{MSG - MSE}{r}$$

Where, MSG = Mean square of the genotypes

MSE = Mean square of the error

r = Number of replications

b. Phenotypic variance, $\sigma^2 p = \sigma^2 g + \sigma^2 e$

Where, $\sigma^2 g$ = Genotypic variance,

$\sigma^2 e$ = Environmental variance = Mean square of error

3.2.2.9.2 Estimation of Genotypic and Phenotypic Co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the following formula (Burton, 1952) and expressed as percentage.

$$GCV = \frac{\delta g \times 100}{\bar{x}}$$

$$PCV = \frac{\delta p \times 100}{\bar{x}}$$

Where, GCV = Genotypic co-efficient of variation

PCV = Phenotypic co-efficient of variation

δg = Genotypic standard deviation

δp = Phenotypic standard deviation

$\bar{x}$ = Population mean

PCV and GCV were classified as per Sivasubramanian and Menon (1973) as shown below:

0-10%- low; 10.1-20%- moderate; >20.1%- high

3.2.2.9.3 Estimation of heritability

Haritability in broad sense (h^2b) was estimated by the formula as suggested by Johnson *et al*. (1955).

$$\% h_b^2 = \frac{\sigma^2 g}{\sigma^2 p} x \quad 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

h^2b = Heritability in broad sense.

The heritability percentage was categorized as low, moderate and high as followed by Robinson *et al*. (1949), as follows

0-30%: Low; 30-60%: Moderate; >60%: High

3.2.2.9.4 Estimation of Genetic Advance

The expected genetic advance (G.A.) for different characters under investigation was estimated according to the formula used by Johnson *et al.* (1955) and Allard (1960).

i. Genotypic Advance (G.A.) = K. h^2b.Sph

Where, h^2b = Heritability in broad sense,

Sph = phenotypic standard deviation

K = Selection intensity which is equal to 2.06 at 5% selection intensity

ii. Genetic advance in percent of mean $G.A.(\%) = \frac{GA}{\bar{x}F_1} \quad X \quad 100$

Where, GA = Genetic advance, $\bar{x}$ F_1 = Population mean of F_1

The GA as per cent of mean was categorized as low, moderate and high as following by Johnson *et al.* (1955) as follows

0-10 %: Low; 10-20%: Moderate; 20 and above: High

3.2.2.9.5 Estimation of genotypic and phenotypic correlation coefficient

Genotypic and phenotypic correlation coefficients for different characters in all possible combinations were done with the formula given by Miller *et al*. (1958).

i. Genotypic correlation co-efficient $(r_g) = \dfrac{COV.\,g(XY)}{\sqrt{\sigma^2(g)X} \bullet \sqrt{\sigma^2(g)Y}}$

Where, COV. g(XY) = Genotypic covariance between the characters X and Y.

$\sigma^2(g)X =$ Genotypic variances of the characters X

$\sigma^2(g)Y =$ Genotypic variances of the characters Y

ii. Phenotypic correlation co-efficient $(r_p) = \dfrac{COV.\,p(XY)}{\sqrt{\sigma^2(p)X} \bullet \sqrt{\sigma^2(p)Y}}$

Where, COV. p(XY) = Phenotypic covariance between the characters X and Y.

$\sigma^2(p)X =$ Phenotypic variances of the characters X

$\sigma^2(p)Y =$ Phenotypic variances of the characters Y

The calculated value of ‘r’ was compared with table ‘r’ value with n-2 degree of freedom at 5% and 1% level of significance, where, n refers to number of pairs of observation.

3.2.2.9.6 Estimation of path co-efficient

Path coefficient analysis was done according to the procedure stated by Singh and Chaudhury (1985b) and Dabholkar (1992) which was originally suggested by Dewey and Lu (1959). The following sets of simultaneous equations were obtained depending upon the cause and effect relationship:

$r_{1y} = P_{1Y} + r_{12} P_{2Y} + r_{13} P_{3Y} + r_{14} P_{4Y} + r_{15} P_{5Y} + r_{16} P_{6Y} + r_{17} P_{7Y} + r_{18} P_{8Y}$

$r_{2y} = P_{2Y} + r_{21} P_{1Y} + r_{23} P_{3Y} + r_{24} P_{4Y} + r_{25} P_{5Y} + r_{26} P_{6Y} + r_{27} P_{7Y} + r_{28} P_{8Y}$

$r_{3y} = P_{3Y} + + r_{31} P_{1Y} + r_{32} P_{2Y} + r_{34} P_{4Y} + r_{35} P_{5Y} + r_{36} P_{6Y} + r_{37} P_{7Y} + r_{38} P_{8Y}$

$r_{4y} = P_{4Y} + r_{41} P_{1Y} + r_{42} P_{2Y} + r_{43} P_{3Y} + r_{45} P_{5Y} + r_{46} P_{6Y} + r_{47} P_{7Y} + r_{48} P_{8Y}$

$r_{5y} = P_{5Y} + r_{51} P_{1Y} + r_{52} P_{2Y} + r_{53} P_{3Y} + r_{54} P_{4Y} + r_{56} P_{6Y} + r_{57} P_{7Y} + r_{58} P_{8Y}$

$$r_{6y} = P_{6Y} + r_{61} P_{1Y} + r_{62} P_{2Y} + r_{63} P_{3Y} + r_{64} P_{4Y} + r_{65} P_{5Y} + r_{67} P_{7Y} + r_{68} P_{8Y}$$

$$r_{7y} = P_{7Y} + r_{71} P_{1Y} + r_{72} P_{2Y} + r_{73} P_{3Y} + r_{74} P_{4Y} + r_{75} P_{5Y} + r_{76} P_{6Y} + r_{78} P_{8Y}$$

$$r_{8y} = P_{8Y} + r_{81} P_{1Y} + r_{82} P_{2Y} + r_{83} P_{3Y} + r_{84} P_{4Y} + r_{85} P_{5Y} + r_{86} P_{6Y} + r_{87} P_{7Y}$$

Where, r_{iy} = Genotypic correlation coefficient between the ith characters (i = 1..... 2, 8.) and Y = Seed yield per plant

P_{iy} = Path coefficient y to ith character (i = 1, 2, 3…………10.)

1 = Days to 50% tasseling
2 = Days to 50% silking
3 = Plant height
4 = Ear height
5 = Ear length
6 = Ear diameter
7 = number of row per ear
8 = number of kernel per row
9 = Thousand grain weight
10 = Yield (t/ha)

Total genotypic correlation was thus partitioned as follows:

P_{1Y} = The direct effect of 1 only
$r_{12} P_{2Y}$ = The direct effect of 1via 2 on Y only
$r_{13} P_{3Y}$ = The direct effect of 1via 3 on Y only
$r_{14} P_{4Y}$ = The direct effect of 1via 4 on Y only
$r_{15} P_{5Y}$ = The direct effect of 1via 5 on Y only
$r_{16} P_{6Y}$ = The direct effect of 1via 6 on Y only
$r_{17} P_{7Y}$ = The direct effect of 1via 7 on Y only
$r_{18} P_{8Y}$ = The direct effect of 1via 8 on Y only

After calculating the direct and indirect effects of the characters, residual effect (R) was calculated by using the following formula (Singh and Chaudhary, 1985)

$$P^2 R_Y = 1- \sum P_{Iy} r_{iY}$$

Where, $P^2 R_Y = R^2$ and P_{iY} = Direct effect of the characters on yield

r_{iY}= Correlation coefficient on the characters with yield

Therefore, Residual effect R = $\sqrt{P^2}\,RY$

Direct or indirect effects are categorized as given below as suggested by Lenka and Mishra 1973.

Negligible - 0.00 to 0.09; Low - 0.10 to 0.19; Moderate 0.20 to 0.29; High - 0.30 to 0.99; Very high - 1.00

3.2.2.10 Estimation of diversity

The genetic divergence among the fifty eight maize inbreds were assessed by Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). For determination of group constellations Tocher's Method (Rao, 1952) was followed. Canonical analysis was also done according to Rao (1986) for confirmation of the results of cluster and D^2 analysis. Mean data for each trait were subjected to multivariate analysis technique for principal component analysis (PCA), principal coordinate analysis (PCO) and canonical variate analysis (CVA**).**

3.2.2.10.1 Principal component analysis (PCA)

To examine the inter-relationship among several characters principal component analysis (PCA), one of the multivariate techniques, is used and can be done from sum of squares and product matrix for the characters. Therefore, Principal Component were computed from the correlation matrix and genotypes scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than unity (Jager *et al.*1983). The latent roots are called 'Eigen values'. Most of the original variability in a smaller number of dimensions is displayed by PCA. From the latent vectors of the first two principal components contribution of the different morphological characters towards divergence is discussed.

3.2.2.10.2 Principal coordinate analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but to calculate inter-unit distances it is used. It gives the maximum distances between each pair of the n point using similarity matrix (Digby *et al.*, 1989) through the use of all dimensions of P. Inter distance between genotypes were studied by PCO.

3.2.2.10.3 Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering was done using non-hierarchical classification. The algorithm repeatedly transfers genotypes from one group to another which are started from some initial classification of the genotypes into required groups, so long as such transfers improve the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swapping two genotypes of different classes and so on.

3.2.2.10.4 Canonical variate analysis (CVA)

Canonical variate analysis (CVA) complementary to D^2 statistic is a sort of multivariate analysis where canonical vector and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively and derieved**.** Canonical vector analysis a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing the ratio among groups to the within group variations.

3.2.2.10.5 Computation of average intra-cluster distances

When the clusters were formed, the average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the principal coordinate analysis (PCO). The square root of the average D^2 values represents the distances (D) within cluster.

The average intra cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

Square of intra cluster distance = $\Sigma Di^2 / n$

Where,

ΣDi^2 = sum of distance between all possible combinations.

n = Number of all possible combinations between the population in a cluster.

3.2.2.10.6 Computation of average inter-cluster distances

The average inter cluster distance were calculated by the formulae described by Singh and Chaudhary (1977).

Square of inter cluster distance = $\Sigma Di^2 / n_i n_j$

Where,

ΣDi^2 = sum of distances between all possible combinations ($n_i n_j$) of the entries included in the cluster study.

n_i = Number of entries in cluster i.

n_j = Number of entries in cluster j.

3.2.2.10.7 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using the method given by Singh and Chaudhary (1977). In all the combinations, each character was ranked on the basis of di = $y_i^j - y_i^k$ values.

Where,

di = mean deviation

y_i^j = mean value of the j_{th} genotype for the i_{th} character and

y_i^k = mean value of the k_{th} genotype for the i_{th} character.

Rank 'I' is given to the highest mean difference and rank 'P' is given to the lowest mean difference

Where,

P is the total number of characters.

Finally, the number of times that each character appeared in the first rank is computed and per cent contribution of characters towards divergence was estimated.

3.2.2.10.8 Cluster diagram

Cluster Diagram was drawn as suggested by Singh and Chaudhary (1977) using the intra and inter cluster distance. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.3 Experiment 3: Heterosis and combining ability for yield characters in maize

The field experiment was conducted at Regional Agricultural Research Station, Rahmatpur, Barishal during the period from November 2016 to April 2017 for making the cross among the selected inbred lines. During November 2017 to April 2018 for studying the general combining ability (GCA) of parents, specific combining (SCA) ability of crosses, determining combined heterotic effect of the crosses and selecting better cross combinations experiment was conducted at five location.

The materials and methods of these experiments are presented under the following headings:

3.3.1 Experiment 3 (i): Production of single cross hybrids

3.3.1.1 Materials and methods

The experimental material consisted of one set of seven white kernelled maize inbred lines (CML 330, CML 332, CML 322, CML 311, CML 331, CML 518, CML 383) based on diversity analysis. The lines were crossed in a half diallel fashion excluding reciprocals to produce 21 F_1's. Seeds of inbred lines were sown in three different dates (1st December, 4th December and 8th December 2016) for synchronization. Each inbred line was sown in one row plot with 5m long. Spacing was maintained at 75cm × 25cm (one plant/hill). Fertilizers were applied @ 120, 80, 80, 20, 5 and 1 kg/ha of N, P_2O_5, K_2O, S, Zn and B, respectively. Standard agronomic practices were followed to raise good crop according to procedure in experiment 2. Undesirable plants from the each line were rouged out before flowering. Name and characteristics of parental genotypes are shown in Table 2.

3.3.1.2 Crossing technique

Crossing was made by hand pollination in desirable plants and lines to fulfill the desired combinations. Tassel bag method was used for making hand pollination (Plate 3). Ethyl alcohol was used for hand washing during crossing. At flowering time, female and male organ (silk & tassel) of the plants of female and male parents were covered by special silk and tassel bag. The desired twenty-one F_1's combinations were made. At the same time and seed increase of the inbred parents were also done.

Table 2. List of selected parental inbred line for crossing program

SL. NO.	Parents	Criteria for selection
1	P1(CML 330)	Earliness
2	P2(CML 332)	Yield and plant height
3	P3(CML 322)	Yield
4	P4(CML 311)	Yield and late maturity
5	P5(CML 331)	Yield
6	P6(CML 518)	Yield
7	P7(CML 383)	Yield

Plate 3. Tassel bag method for making hand pollination

3.3.1.3 Crossing mode

The parents were crossed in all possible combination in half diallel fashion. There were no reciprocal crosses.

Parents							
P1	**Cross**						
P2	P1×P2	**Cross**					
P3	P1×P3	P2×P3	**Cross**				
P4	P1×P4	P2×P4	P3×P4	**Cross**			
P5	P1×P5	P2×P5	P3×P5	P4×P5	**Cross**		
P6	P1×P6	P2×P6	P3×P6	P4×P6	P5×P6	**Cross**	
P7	P1×P7	P2×P7	P3×P7	P4×P7	P5×P7	P6×P7	

3.3.1.3 Location and duration

The experiment was carried out at Regional Agricultural Research Station, Rahmatpur, Barishal during rabi 2016-2017 and it lies at 22^0 42″ North latitude and 90^o23″ East longitude at an elevation of 4 meter above the sea level.

3.3.1.4 Seed collection

After harvesting, selection of ears within each cross was done carefully. The seeds of each cross were shelled and maintained separately and stored for evaluation in the next season.

3.3.2 Experiment 3 (ii): Evaluation of single cross hybrids

A field experiment was conducted during the period from November 2017 to April 2018 to study combining ability of parents and crosses for yield and its component and to estimate the magnitude of heterosis for important characteristics. The materials and methods of this experiment are presented under the following headings

Table 3. List of hybrids used in the 3rd experiment

SL. NO.	Hybrids	SL. NO.	Hybrids
1	CML 330× CML 332(E1)	13	CML 322×CML 331(E13)
2	CML 330× CML 322(E2)	14	CML 322×CML 518(E14)
3	CML 330× CML 311(E3)	15	CML 322×CML 383(E15)
4	CML 330× CML 331(E4)	16	CML 311×CML 331(E16)
5	CML 330× CML 518(E5)	17	CML 311×CML 518(E17)
6	CML 330× CML 383(E6)	18	CML 311×CML 383(E18)
7	CML 332× CML 322(E7)	19	CML 331×CML 518(E19)
8	CML 332× CML 311(E8)	20	CML 331×CML 383(E20)
9	CML 332×CML 331(E9)	21	CML 518×CML 383(E21)
10	CML 332×CML 518(E10)	22	BHM-12(E22)
11	CML 332×CML 383(E11)	23	BHM-13(E23)
12	CML 322×CML 311(E12)	24	BHM-14(E24)

3.3.2.1 Materials

Twenty one F_1 white maize hybrids and three checks (BHM 12, BHM 13 and BHM 14) were used in this study. List of hybrids which were used are mentioned in the table 3**.**

3.3.2.2 Location

The experiments were carried out at Regional Agricultural Research Station (RARS), Rahmatpur, Barishal; Regional Agricultural Research Station (RARS), Jashore; Regional Agricultural Research Station (RARS), Jamalpur; Regional Agricultural Research Station (RARS), Hathazari, Chattogram and Wheat Research Centre (WRC), Nashipur, Dinajpur. during rabi 2017-2018.

3.3.2.3 Experimental design and layout

The experiment under each environment was laid out in a Alpha lattice design with three replications. The tested hybrids were allotted randomly to the twenty-one plots of each replication. The plot size was 4.0 m × 1.2 m with inter and intra row spacing of 60 and 25 cm, respectively. The recommended package of practices for respective environment at each location was followed in full to raise good crop.

3.3.2.4 Application of manures and fertilizers

The fertilizers N, P, K, S, Zn and B in the form of urea, TSP, MP, Gypsum and borax, were applied @ 250,120, 120,40 and 5 kg/ha of N, P_2O_5, K_2O, S, Zn and B, respectively. One third of Urea and the entire amount of TSP, MP, Gypsum, Zinc sulphate and borax were applied during the final preparation of land. Remaining two third of Urea was applied in two equal installments at floral initiation (knee height stage) and at about one week before silking.

3.3.2.5 Seed Sowing

Two seed per hill and each line were sown in two row plot with 4m long. The size of the unit plot was 4m×1.2m. A distance of 1.5 m from block to block, 60 cm from row to row and 25 cm from plant to plant was maintained. The seeds were placed at about 5 cm depth in the soil.

3.3.2.6 Intercultural operations

When the seedlings started to emerge in the plot it was always kept under careful observation. After emergence of seedlings, various intercultural operations were accomplished which was mentioned in 3.2.5.4 were followed for better growth and development of the maize seedlings.

3.3.2.7 Harvesting

Harvesting was started from 20th April, 2018 depending upon the maturity of the plants i.e. when plants showed distinct signs of drying, the husk cover was completely dried and the grains were fully matured. Grain maturity was identified from the milk line of kernels or the formation of a black layer at the junction of grain and placenta.

3.3.2.8 Collection of data

Five plants were tagged randomly for recording observations for each entry in each replication for all the quantitative characters except for days to 50 percent tasseling and silking. Mean of five plants for each entry in each replication was worked out for each character at each location and used for statistical analysis.

3.3.2.9 Observations recorded

Similar observations that were recorded in the second experiment such as days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm) and kernel row arrangement (number of row per ear and number of kernel per row), thousand kernel weight and grain yield (ton/ha) were also recorded in this experiment.

3.3.2.10 Statistical analysis

3.3.3.10.1 Combining ability analysis

Analysis of combining ability was carried out following Method-4, Model-I (fixed effects) of Griffing (1956) using software “diallel analysis” by Mark D. Burrow and James G. Coors, version 1.1 (Copyright© 1993). This method was most suitable for the present study where only one set of F_1s (without reciprocals) were included. Data were analyzed using combined analysis of variance (ANOVA), with environments, genotypes, GCA, SCA and interactions among them being the focus of both environments and genotypes according to Steel and Torrie (1980). Data were subjected to analysis of variance General Linear Model of SAS program (SAS, 2011). Significant genotypic variance of each trait was further partitioned to GCA, SCA and experimental error. From the mean sum of squares, estimates of GCA-effects (g_i) for each parent and SCA-effects (s_{ij}) for each cross combination were calculated according to Singh and Chaudhary (1985).

The statistical model for the mean value of a cross (i x j) is:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + 1/b\ \Sigma\Sigma\ e_{ijkl}$$

Where:

Y_{ij}	=	Mean of (i x j) th cross over replications k (k = 1, 2,..., b)
μ	=	General mean
g_i and g_j	=	GCA-effects of ith and jth parent, respectively
s_{ij}	=	SCA-effect for the cross involving ith and jth parent
$1/b\ \Sigma\Sigma\ e_{ijkl}$	=	Mean error effect

Estimation of standard errors (S.E.s)

S.E. (g_i) = $[(n-1)\ \sigma^2_e/n(n-2)]^{1/2}$

S.E. (S_{ij}) = $[(n-3)\ \sigma^2_e/n(n-1)]^{1/2}$

The estimates of genetic components were obtained based on the expectations of the mean squares as:

$$\sigma^2_g = \frac{1}{p-2}(M_g - M_s)$$

$$\sigma^2_s = M_s - M_e$$

Where:

σ^2_g = Variance due to gca

σ^2_s = Variance due to sca

M_g = Mean square due to gca

M_s = Mean square due to sca

M_e = Error mean square

3.3.3.10.2 Estimation of heterosis

Heterosis concerns with the superior performance of a hybrid relative to its parents, it is usually measured in two ways. When performance of hybrid is compared with the average performance of its parents, it is known as mid-parent heterosis or relative heterosis. Other term to express heterosis is heterobeltiosis which refers to the comparison of the performance of hybrid with that of the superior parent in the cross. Another term, known standard or economic heterosis is frequently used to represent heterosis in terms of heterotic performance of hybrid over the check variety. Heterosis or hybrid vigor is the better performance of hybrid relative to the parents and the outcome of the genetic and phenotypic variation. It is the superiority of first Filial generation over the standard commercial checks variety; hence it is also called economic superiority over checks (Sharief *et al*., 2009). The commercial usefulness of a hybrid would primarily depend on its performance in comparison to the best commercial variety of the concerned crop species. In maize, the superior parent of the hybrid usually found inferior to the best commercial hybrid variety. So, it is desirable to estimate heterosis in relation to the best commercial variety and for this reason here only hybrids (crosses) were evaluated against a number of commercially cultivated hybrid varieties. Using the mean data of all the single cross hybrids and check variety, the standard heterosis was estimated against three standard checks viz. BHM 12, BHM 13 and BHM 14 (BARI developed hybrid). The data were tested according to Singh and Singh (1994). Percent heterosis was calculated by using the following formula:

$$\text{Standard heterosis (\%)} = [(\overline{F_1} - \overline{CV}) / \overline{CV}] \times 100$$

Where, $\overline{F_1}$ and $\overline{CV}$ represented the mean performance of hybrid and standard check variety. The significance test for heterosis was done by using standard error of the value of check variety.

3.4 Experiment 4: Adaptation of single cross white maize hybrids in different agro-ecological zones

A field experiment was conducted during the period from November 2017 to April 2018 to study the performances of developed hybrids and crosses for yield and its component and evaluate the hybrids under five agro-ecological zones. The materials and methods of this experiment are presented under the following headings:

3.4.1 Materials

Twenty one F_1 white maize hybrids and three checks (BHM 12, BHM 13 and BHM 14) were used in this study. List of hybrids which were used are mentioned in the Table 3**.**

3.4.2 Location

The present study was carried out by undertaking multi-location trials of above said 24 hybrids in five locations *viz.*, Regional Agricultural Research Station (RARS), Rahmatpur, Barisal; Regional Agricultural Research Station (RARS), Jessore; Regional Agricultural Research Station (RARS), Jamalpur; Regional Agricultural Research Station (RARS), Hathazari, Chittagang and Wheat Research Centre (WRC), Nashipur, Dinajpur. Field view of experimental plot at five locations is presented in Plate 4.

3.4.3 Experimental design and layout

The experiment under each environment was laid out in a Alpha lattice design with three replications. The genotypes were allotted randomly to the twenty four plots of each replication. The recommended package of practices for respective environment at each location was followed in full to raise good crop.

3.4.4 Collection of data

Five plants were tagged randomly for recording observations for each entry in each replication for all the quantitative characters except for days to 50 per cent tasseling and silking. Mean of five plants for each entry in each replication was worked out for each character at each location and used for statistical analysis. The experimental field is visited by member of advisory committee (Plate 5).

3.4.5 Observations recorded

Observations that are recorded in these experiments were days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm) and kernel row arrangement (number of row per ear and number of kernel per row), thousand grain weight and grain yield (ton/ha) in all the five locations.

Plate 4. Field view of third and fourth experiment at different locations

Plate 5.The experimental field visited by the honorable members of the advisory committee and the researcher at RARS, Barishal.

3.4.6 Statistical analysis

The recorded data were analyzed statistically according to the design used in the experiment. The analysis of variance (ANOVA) was used and the GXE interaction was estimated by the AMMI model (Zobel *et al*., 1988). They stated that only a small portion of the interaction sum of squares is accounted by linear regression models. But AMMI analysis reveals a highly significant interaction component that has a clear agronomic meaning and it has no specific design requirements, except for a two-way data structure. The AMMI method is used for the following purposes. For initial statistical analysis of yield trials AMMI is more appropriate, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets (Gauch, 1988). Secondly, the G x E interaction is clarified and summarized patterns and relationships of genotypes and environments by AMMI (Zobel *et al*., 1988; Crossa *et al*., 1990). In this procedure, by using of the biplot graph the contribution of each genotype and each environment to the GXE interaction is assessed in which the means of traits are plotted against the scores of the first principal component of the interaction (IPCA1) of the same traits. The stability parameters, regression coefficient (bi) of the genotype over environmental indices and deviation from regression (S^2di) were estimated according to Eberhart and Russel (1966). Significance of differences among bi value and unity was tested by t-test, between S^2di and zero by F-test. All data were processed and analyzed using Cropstat 7.2 program.

3.4.6.1 Eberhart and Russell model

According to Eberhart and Russel (1966) model, a genotype with high mean, unit regression co-efficient (bi=1.00) and least deviation from regression ($S^2di=0$) is considered as an ideal as an ideal widely adopted and stable genotype. The following statistical model was used to study the stability of genotypes under different environments:

$$Y_{ij} = m + b_i I_j + \delta_{ij} \quad (i = 1,2, ------n, j=1,2, ---------1)$$

Where

Y_{ij} = Mean of the i^{th} variety in the j^{th} environment

M = Mean of all the varieties over all the environments

b_i = Regression coefficient of the ith genotype on the environmental index that measures the response of this genotype to varying environments

I_j = Environmental index which is defined as the deviation of the mean of all the genotypes at a given location from the overall mean

$$Ij = \frac{\sum_i Yij}{t} - \frac{\sum_i \sum_j Yij}{ts} \quad \text{with } \sum I_j = 0$$

Here, t = Number of genotypes

S = Number of locations

δ_i = Deviation from regression of the ith genotype at jth environment

3.4.6.2 Estimation of stability parameters

Two parameters of stability i.e. regression of co-efficient (bi) and deviation from regression (S^2di) were estimated as follows:

$$b_i = \frac{\sum_j y_{ij} I_j}{\sum_j I_j^2}$$

Where

$\sum_j Y_{ij} I_j$ = The sum of product between genotypes and environmental indices

$\sum_j^j I^2{}_j$ = The sum of squares due to environmental indices

$$S^2{}_{di} = \frac{\sum_j \delta_{ij}}{S-2} - \frac{S^2{}_e}{r}$$

$\sum_j \delta_{ij} = (\sum Y^2 ij - Y^2 i. /t) - (\sum_j Yij \; I_j)^2 / \sum_j I^2{}_j$

S^2di = Mean square deviation from linear regression

S^2e = Estimate of pooled error

3.4.6.3 Estimation of phenotypic index (Pi)

The phenotypic index (P_i) can be considered as one of the stability parameters in place of overall variety mean. A phenotypic index is calculated for easy interpretation and rapid decision (Ram and Panwar, 1970). The formula is given below:

$$P_i = \overline{Y}_{i.} - \overline{Y}_{..}$$

Where

$\overline{Y}_{i.}$ = is the mean of i^{th} variety over environments
$\overline{Y}_{..}$ = is the grand mean

i.e. phenotypic index (P_i) is the deviation of the genotype mean over environmental grand mean.

3.4.6.4 Estimation of sum of squares

SS due to environment + (genotype x environment) = $\sum Y^2ij - (\sum Y^2i./s)$

SS due to environment (linear) = $(1/t)\ (\sum Y.jIj)^2 / \sum I^2j$

SS due to genotype x environment (linear) = $\sum(YijIj)^2/\sum I^2j)$ - SSL(linear)

SS due to pooled deviation the sum of SS due to deviation for individual genotype for (s^2) degrees of freedom each

Pooled error mean square = S^2e/r

Here, S^2e/r was obtained by adding error sum of squares from individual analysis and dividing the sum by degrees of freedom of individual environments

3.4.6.5 Additive main effects and multiplicative interaction method (AMMI)

The AMMI model was used to investigate the agronomic nature of G x E interaction which combines the standard analysis of variance with principal component analysis (Zobel *et al.*, 1988). The AMMI model first fits additive effects for the main effects of genotypes and environments, using the additive analysis of variance procedure. Subsequently the program fits multiplicative effects for G x E by principal component analysis (Zobel *et al.*, 1988). For illustrating the relationships among genotypes, environments and between genotypes and environments Biplots (Biplot, 2007) were used. AMMI combines analysis of variance (ANOVA) into a single model with additive and multiplicative parameters.

The model equation is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda k \, \alpha ik \, \gamma jk + e_{ij}$$

Where:

Yij is the average yield of the ith genotype in the jth environment and is the overall mean yield;

μ is the grand mean;

Gi is the effect of genotype i;

Ej is the effect of environment j;

λ_k is the k^{th} singular value of the original matrix interaction;

α_{ik} and γ_{jk} are the genotype and environment principal component scores for axis k;

n is the number of principal components retained in the model and

eij is the average experimental error associated with observation, assumed to be independent.

The advantages of the AMMI model or its variants are that, they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (Freeman, 1990). In the form of a biplot display the interaction is explained where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the G x E interaction components. Integrating biplot display and genotypic stability statistics enable genotypes to be grouped based on similarity of performance across diverse environments (Tsige, 2002).

CHAPTER IV
RESULTS AND DISCUSSION

To achieve the objectives of the study four separate experiments were conducted. The results of the research works are presented experiment wise with relevant sub heads as follows

4.1. Experiment 1: Characterization and maintenance of maize inbred lines

This experiment was conducted to identify distinguished morphological characters among the genotypes. Morphologically fifty-eight inbred lines of maize were characterized on the basis of qualitative and quantitative characters in this study.

4.1.1 Qualitative characters

The results of characterization on different qualitative traits in fifty-eight inbred lines are presented in Table 4 and Table 5. Total eleven characters were evaluated to screening the inbred lines into different groups.

i). Leaf attitude

Leaf attitude of different genotypes exhibited wide variation (Table 5). Among the inbreds about 43.10% genotypes had recurved leaf attitude, 34.48% genotypes had slightly recurved, 15.52% and 6.89 % genotypes had strongly recurved and rectilinear leaf attitude pattern, respectively (Table 4). These results were in consonance with Akhi *et al.* (2014) and Begum *et al.* (2018). Different types of leaf attitude observed in maize inbreds are presented in Plate 6.

ii). Anthocyanin in anther (tassel)

The anthocyanin coloration in anther is an easily identifiable character which was absent in 34.48% genotypes, weak and medium pigmentation were in 24.14% and 22.41% genotypes, respectively and rest 18.97% had strong anthocyanin colour in anther (Table 4). This finding was according to Akhi *et al.* (2014) and Begum (2016). Different types of anther color found in different maize inbreds are presented in Plate 7.

Table 4. Frequency distribution of inbred lines belonging to different phenotypic classes

SL. No.	Characteristics	State of expression	No. of inbred lines belonging to each class	Frequency (%)
1	Leaf attitude	Rectilinear	4	6.89
		Slightly recurved	20	34.48
		Recurved	25	43.10
		Strongly recurved	9	15.52
2	Anthocyanin in anther (Tassel)	Absent	20	34.48
		Weak	14	24.14
		Medium	13	22.41
		Strong	11	18.97
3	Anthocyanin in silk (Ear)	Absent	22	37.93
		Weak	17	29.31
		Medium	9	15.52
		Strong	10	17.24
4	Anthocyanin in glume (Tassel)	Absent	33	56.90
		Weak	9	15.52
		Medium	10	17.24
		Strong	6	10.34
5	Anthocyanin in ring glume (tassel)	Absent	50	86.21
		Present	8	13.79
6	Anthocyanin in nodes (stem)	Absent	45	77.59
		Weak	11	18.97
		Medium	1	1.72
		Strong	1	1.72
7	Anthocyanin coloration in internodes	Absent	55	94.83
		weak	3	5.17
8	Anthocyanin coloration in sheath	Absent	47	81.03
		Weak	9	15.52
		Medium	2	3.45
9	Angle between main axis and lateral branches	Very small	18	31.03
		Small	19	32.76
		Medium	10	17.24
		Large	9	15.52
		Very large	2	3.45
10	Number of primary lateral branches	Few	22	37.93
		Medium	20	34.48
		Many	16	27.58
11	Types of grain	Dent	1	1.72
		Semi dent	13	22.41
		Flint	44	75.86

Rectilinear **Slightly recurved**

Recurved **Strongly recurved**

Plate 6. Different types of leaf attitude observed in maize inbred lines

Absent

Weak

Medium

Strong

Plate 7. Different types of anther color found in different maize inbred lines

Absent **Weak**

Medium **Strong**

Plate 8. Different types of anthocyanin pigmentation of silk found in maize inbred lines

iii). Anthocyanin in silk (ear)

Based on anthocyanin coloration in silk inbred lines were grouped as absent, weak, medium and strong. Among them 37.93% genotypes were expressed as absent, 29.31% were weak while 15.52% genotypes produced medium and 17.24% genotypes produced strong coloration in silk (Table 4). These results were consistent with of anthocyanin pigmentation of silk found in maize inbred lines are observations of earlier workers (Begum, 2016 and Begum *et al.* 2018). Different types presented in Plate 8.

iv). Anthocyanin in glume (tassel)

Four types variation was observed in anthocyanin coloration at glume base (Table 4). More than half of the genotypes (56.90%) had no coloration in glume followed by medium coloration (17.24%) while 15.52% had weak pigmentation and only strong anthocyanin were present in 10.34% genotypes. These results were in line with Akhi *et al.* (2014) and Begum *et al.* (2018).

v). Anthocyanin in ring glume (tassel)

On the basis of anthocyanin in ring glume genotypes were categorized into two groups in which coloration was absent in the maximum genotypes (86.21%) while 13.79% had anthocyanin in ring glume (Table 4). This was in conformity with the findings of Akhi *et al. (*2014) and Begum (2016).

vi). Anthocyanin in nodes (stem)

The maximum genotypes (77.59%) had no pigmentation in nodes followed by weak (18.97%) and only 1.72% had medium and strong presence, respectively (Table 4). Our results were in line with those of Akhi *et al.* (2014) and Begum (2016).

vii). Anthocyanin coloration in internodes

Based on this character the inbred lines were classified into two groups. Among them pigmentation was absent in 94.83% genotypes and the rest 5.17% had color in internode (Table 4). This study was also in accordance with Begum (2016) and Begum *et al.* (2018).

viii). Anthocyanin coloration in sheath

The anthocyanin coloration in sheath is an easily identifiable character which were absent in 81.03% genotypes, 15.52% showed weak and only 3.45% showed medium expression (Table 4). Akhi *et al.* (2014) and Begum *et al.* (2018) also reported same observations.

ix). Angle between main axis and lateral branches

The inbred lines were classified on the basis of angle between main axis and lateral branches into five groups i.e very small (31.03%), small (32.76%), medium (17.24%), large (15.52%) and very large (3.45%) (Table 4). These results were in harmony with that of Akhi *et al.* (2014) and Begum (2016).

x). Number of primary lateral branches

Three classes of number of primary lateral branches were observed (Table 4). Among the inbred lines, 37.93% showed few branches, 34.48% had medium branches and 27.58% had many branches. Begum (2016) and Begum *et al.* (2018) also observed different types of branches. Different number of lateral branches observed in maize genotypes is presented in Plate 9.

xi). Types of grain

Based on the types of grain, the inbreds were classified into flint, semi dent and dent. Among the inbreds, only 1.72% had the dent type (Table 4). Maximum (75.86%) were flint type and 22.41% were semi dent. Similar conclusions were also drawn by other workers (Akhi *et al.*, 2014 and Begum, 2016). Pictorial view is presented different types of grain found in maize inbred lines (Plate 10).

4.1.2 Quantitative characters

i). Days to 50% tasseling

Days to tasseling varied widely among the tested inbreds. Tasseling duration was 70 days to 90 days with an average of 84 days (Table 6). The line CML 243 took 70 days to reach tasseling stage compared to other genotypes. Due to genetic characters, specific life cycle and growth periods of different inbred lines this variation may arise. For different morphological traits, significant amount of variation was also confirmed by Ihsan *et al.* (2005) and Begum (2016) in their study.

ii). Days to 50% silking

The findings of the study showed that inbred took the highest 92 days for days to silking where as lowest duration was 72 days (Table 6). All the genotypes showed

Few **Medium**

Many

Plate 9. Different number of lateral branches observed in maize inbred lines

Dent **Flint**

Semi dent

Plate 10. Different types of grain found in inbred lines of maize

Table 5. Characterization of fifty eight inbred lines of maize based on qualitative characters

Lines	Leaf attitude	Anthocyanin in anther (Tassel)	Anthocyanin in silk (Ear)	Anthocyanin in glume (Tassel)	Anthocyanin in ring glume (tassel	Anthocyanin in nodes (stem)	Anthocyanin coloration of internodes	Anthocyanin coloration of sheath	Angle between main axis and lateral branches	Number of primary lateral branches	Types of grain
CML 126	Recurve	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Small	Many	Flint
CML 127	Slightly recurved	Absent	Strong	Medium	Present	Weak	Absent	Absent	Small	Many	Semi dent
CML 128	Recurve	Medium	Weak	Absent	Absent	Absent	Absent	Absent	Very small	Medium	Flint
CML 129	Recurve	Weak	Medium	Medium	Absent	Absent	Absent	Weak	Small	Medium	Flint
CML 132	Slightly recurved	Strong	Weak	Absent	Absent	Absent	Absent	Absent	Very small	Many	Flint
CML 133	Recurve	Absent	Absent	Absent	Absent	Weak	Absent	Absent	Small	Medium	Semi dent
CML 135	Recurve	Strong	Weak	Absent	Present	Absent	Absent	Medium	Medium	Medium	Dent
CML 136	Slightly recurved	Medium	Weak	Medium	Absent	Absent	Absent	Absent	Very small	Many	Semi dent
CML 137	Slightly recurved	Medium	Absent	Weak	Absent	Absent	Absent	Absent	Large	Few	Flint
CML 138	Recurve	Medium	Medium	Weak	Absent	Weak	Absent	Absent	Small	Many	Flint
CML 242	Slightly recurved	Medium	Strong	Absent	Present	Absent	Absent	Weak	Small	Few	Flint
CML 243	Slightly recurved	Medium	Medium	Absent	Absent	Weak	Absent	Weak	Small	Medium	Flint
CML 249	Slightly recurved	Absent	Medium	Absent	Absent	Absent	Absent	Absent	Large	Many	Flint
CML 263	Slightly recurved	Absent	Weak	Absent	Absent	Absent	Absent	Absent	Small	Many	Semi dent
CML 264	Slightly recurved	Medium	Absent	Medium	Absent	Absent	Absent	Absent	Large	Medium	Flint

Table 5 (cont’d).

Lines	Leaf attitude	Anthocyanin in anther (Tassel)	Anthocyanin in silk (Ear)	Anthocyanin in glume (Tassel)	Anthocyanin in ring glume (tassel	Anthocyanin in nodes (stem)	Anthocyanin coloration of internodes	Anthocyanin coloration of sheath	Angle between main axis and lateral branches	Number of primary lateral branches	Types of grain
CML 311	Recurve	Strong	Strong	Strong	Present	Absent	Absent	Medium	Very small	Few	Flint
CML 312	Slightly recurved	Medium	Strong	Medium	Absent	Absent	Absent	Absent	Very small	Few	Flint
CML 313	Recurve	Weak	Weak	Absent	Absent	Weak	Absent	Weak	Very small	Many	Flint
CML 314	Recurve	Absent	Strong	Absent	Present	Weak	Absent	Absent	Very small	Many	Flint
CML 315	Recurve	Absent	Medium	Absent	Absent	Absent	Absent	Absent	Small	Many	Flint
CML 316	Strongly recurved	Medium	Strong	Weak	Absent	Absent	Absent	Absent	Very large	Medium	Flint
CML 317	Recurve	Absent	Absent	Absent	Absent	Absent	Absent	Weak	Very large	Few	Flint
CML 318	Recurve	Absent	Absent	Weak	Absent	Absent	Absent	Absent	Large	Medium	Flint
CML 319	Recurve	Strong	Strong	Strong	Present	Strong	Absent	Absent	Large	Few	Semi dent
CML 320	Recurve	Absent	Absent	Weak	Absent	Absent	Absent	Absent	Very small	Medium	Semi dent
CML 321	Recurve	Weak	Absent	Absent	Absent	Absent	Absent	Absent	Small	Medium	Flint
CML 322	Recurve	Absent	Absent	Absent	Absent	Absent	Absent	Weak	Large	Few	Flint
CML 330	Slightly recurved	Strong	Medium	Absent	Present	Absent	Absent	Absent	Medium	Many	Semi dent
CML 331	Strongly recurved	Weak	Weak	Medium	Absent	Medium	Absent	Absent	Large	Medium	Flint
CML 332	Recurve	Weak	Weak	Absent	Absent	Absent	Absent	Absent	Medium	Medium	Flint

Table 5 (cont'd).

Lines	Leaf attitude	Anthocyanin in anther (tassel)	Anthocyanin in silk (ear)	Anthocyanin in glume (tassel)	Anthocyanin in ring glume (tassel)	Anthocyanin in nodes (stem)	Anthocyanin coloration of internodes	Anthocyanin coloration of sheath	Angle between main axis and lateral branches	Number of primary lateral branches	Types of grain
CML 333	Recurve	Weak	Strong	Absent	Absent	Absent	Absent	Absent	Very small	Many	Flint
CML 334	Recurve	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Very small	Many	Flint
CML 367	Strongly recurved	Medium	Medium	Medium	Absent	Absent	Absent	Absent	Medium	Few	Flint
CML 368	Recurve	Weak	Medium	Strong	Present	Absent	Absent	Absent	Medium	Medium	Semi dent
CML 369	Recurve	Weak	Absent	Weak	Absent	Weak	Absent	Absent	Large	Few	Semi dent
CML 370	Strongly recurved	Weak	Absent	Medium	Absent	Absent	Absent	Weak	Small	Few	Flint
CML 371	Slightly recurved	Strong	Absent	Strong	Present	Absent	Absent	Absent	Very small	Medium	Flint
CML 372	Strongly recurved	Medium	Absent	Absent	Absent	Absent	Absent	Absent	Small	Medium	Semi dent
CML 373	Rectilinear	Strong	Absent	Weak	Absent	Absent	Absent	Absent	Small	Few	Flint
CML 375	Slightly recurved	Medium	Weak	Absent	Absent	Absent	Absent	Absent	Small	Few	Flint
CML 376	Slightly recurved	Weak	Absent	Absent	Absent	Weak	Absent	Absent	Very small	Many	Flint
CML 377	Rectilinear	Absent	Weak	Absent	Absent	Absent	Absent	Absent	Very small	Few	Flint
CML 378	Strongly recurved	Absent	Weak	Strong	Absent	Absent	Absent	Absent	Medium	Few	Semi dent
CML 379	Slightly recurved	Medium	Weak	Medium	Absent	Absent	Absent	Weak	Small	Few	Flint
CML 380	Slightly recurved	Strong	Weak	Strong	Absent	Absent	Absent	Absent	Very small	Few	Semi dent

Table 5 (cont'd).

Lines	Leaf attitude	Anthocyanin in anther (tassel)	Anthocyanin in silk (ear)	Anthocyanin in glume (tassel)	Anthocyanin in ring glume (tassel)	Anthocyanin in nodes (stem)	Anthocyanin coloration of internodes	Anthocyanin coloration of sheath	Angle between main axis and lateral branches	Number of primary lateral branches	Types of grain
CML 381	Strongly recurved	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Medium	Few	Flint
CML 382	Recurved	Absent	Weak	Weak	Absent	Absent	Absent	Absent	Medium	Few	Flint
CML 383	Rectilinear	Absent	Absent	Absent	Absent	Absent	Weak	Absent	Very small	Medium	Flint
CML 384	Rectilinear	Absent	Weak	Absent	Absent	Absent	Absent	Absent	Very small	Few	Flint
CML 385	Slightly recuved	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Very small	Few	Flint
CML 482	Strongly recurved	Weak	Absent	Weak	Absent	Weak	Weak	Absent	Large	Medium	Flint
CML 483	Strongly recurved	Weak	Absent	Absent	Absent	Absent	Absent	Absent	Small	Few	Semi dent
CML 484	Recurved	Weak	Weak	Absent	Absent	Absent	Absent	Absent	Small	Medium	Semi dent
CML 485	Recurved	Weak	Weak	Absent	Absent	Weak	Weak	Absent	Medium	Many	Flint
CML 512	Slightly recurved	Strong	Strong	Absent	Absent	Absent	Absent	Absent	Very small	Few	Flint
CML 517	Recurved	Strong	Strong	Medium	Absent	Weak	Absent	Absent	Small	Medium	Flint
CML 518	Slightly recurved	Strong	Medium	Absent	Absent	Absent	Absent	Weak	Small	Medium	Flint
CML 519	Slightly recurved	Absent	Absent	Absent	Absent	Absent	Absent	Absent	Medium	Medium	Flint

statistically significant difference for days to silking. The inbred line CML 243 was a good inbred line for early maturity because this inbred lines required the minimum days for silking and line CML 483 required the maximum days. Due to the difference in genetic makeup among the tested genotypes variation in maturity duration was observed. Shah *et al.* (2000) and Begum (2016) also reported similar observation among maize for different maturity traits.

iii). Plant height

Plant height is an important identifiable character for maize. Always medium height maize is desirable to prevent lodging. In this observation lowest plant height value was observed in 91.7 cm and the highest value was 186.3 cm (Table 6). The highest value for plant height was recorded in line CML 334 and lowest in line CML 137. For plant height and ear height Dijak *et al.* (1999) reported significant variability among long and short stature maize.

iv). Ear height

Generally having ear in the middle of the plant is preferable. Average height of ear was 56.3 cm where line CML 319 showed the highest ear height and value was 79.8 cm and lowest value was found 30.5 cm in line CML 135 (Table 6). Ullah (2004) and Shah *et al.* (2000) have also reported variability for ear height among different maize.

v). Ear length

The observation of the study showed that the maximum ear length was 17.8 cm and 10.0 was the minimum which implied that wide variations were existed among the tested materials (Table 6). The inbred line CML 132 had the longest length of ear and line CML 381 had shortest ear length. Significant amount of variability for different morphological traits in maize inbred lines also reported by Sokolov and Guzhva (1997) and Begum *et al.* (2018).

vi). Ear diameter

Highly significant difference was recorded for this trait when means were compared for this trait. Ear diameter ranged from 3.3 to 5.3 cm in this study (Table 5). CML 535 was regarded as the best inbred for ear diameter among the genotypes tested (Table 6) Morphological variation mainly governed by genetic factor as well as environmental factors. Similar findings were also recorded by Begum (2016) and Huda *et al.* (2016).

Table 6. Quantitative characters and mean performance of fifty eight inbred lines of maize

Inbred lines	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of row per ear	No. of kernel per row	Thousand grain weight (g)	Grain yield (t/ha)
CML 126	84	88	130.67	39.33	13.17	3.33	11	25	150.0	3.22
CML 127	82	86	167.67	64.83	14.00	3.87	13	25	295.0	3.22
CML 128	81	84	102.33	31.67	11.83	3.98	13	24	330.0	3.05
CML 129	85	88	121.67	35.00	12.50	3.82	13	18	342.5	3.20
CML 132	82	87	101.17	31.17	17.83	3.63	13	28	350.0	4.82
CML 133	85	88	172.17	55.33	11.17	3.85	14	18	270.0	4.38
CML 135	80	84	106.33	30.50	11.17	4.10	15	19	250.0	2.88
CML 136	80	84	100.50	45.33	11.17	4.23	13	19	350.0	2.35
CML 137	77	81	91.67	30.67	10.50	3.85	16	19	265.0	2.28
CML 138	82	86	104.83	45.33	11.67	4.22	13	21	280.0	2.05
CML 242	72	74	128.17	41.17	11.08	3.87	14	19	300.0	2.64
CML 243	70	72	135.33	33.17	11.83	3.83	14	20	285.0	3.90
CML 249	88	90	145.00	78.00	15.50	4.33	13	29	340.0	5.47
CML 263	89	91	166.83	78.33	13.33	3.32	10	16	120.0	5.01
CML 264	84	86	145.33	53.50	12.33	4.13	13	19	305.0	4.17
CML 311	85	88	141.83	63.33	14.00	4.52	14	25	370.0	6.58
CML 312	85	88	181.50	55.33	14.67	4.67	14	25	395.0	5.40
CML 313	87	90	164.17	55.83	15.00	4.42	13	24	330.0	5.46
CML 314	82	86	139.50	53.67	12.83	4.25	14	21	295.0	5.57
CML 315	87	89	167.17	71.67	12.83	3.82	14	24	220.0	4.83
CML 316	85	88	179.00	72.17	10.33	4.22	14	20	240.0	3.96

Table 6 (Cont'd)

Inbred lines	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of row per ear	No. of kernel per row	Thousand grain weight (g)	Grain yield (t/ha)
CML 317	82	86	179.33	60.67	15.17	3.60	11	19	337.5	2.94
CML 318	80	84	166.8	46.17	13.00	3.80	13	21	360.0	2.77
CML 319	90	91	173.17	79.83	15.17	3.93	12	30	370.0	6.93
CML 320	87	89	139.00	54.33	12.67	3.88	13	24	270.0	4.16
CML 321	87	89	180.00	63.83	15.17	4.22	13	25	280.0	5.56
CML 322	85	87	122.50	58.17	11.33	4.87	13	23	395.0	6.60
CML 330	81	85	125.50	56.33	11.83	4.35	14	22	325.0	4.46
CML 331	85	88	156.17	63.50	14.33	4.45	12	22	410.0	6.99
CML 332	83	87	110.83	49.33	13.83	4.47	13	25	375.0	5.81
CML 333	86	88	141.83	71.00	14.17	3.78	13	25	300.0	4.49
CML 334	88	90	186.33	79.00	14.33	4.35	15	22	380.0	4.61
CML 367	84	87	110.00	46.67	10.00	3.82	13	21	155.0	2.32
CML 368	82	85	172.67	54.83	12.83	4.43	13	21	295.0	5.22
CML 369	78	86	139.33	54.00	13.00	3.37	12	22	280.0	3.12
CML 370	80	84	176.33	68.83	12.83	3.70	12	22	155.0	2.94
CML 371	86	88	133.17	56.67	12.83	3.93	13	23	310.0	4.46
CML 372	86	85	151.50	55.33	11.83	4.52	12	15	318.0	4.39
CML 373	85	88	151.33	52.67	13.67	3.90	13	19	365.0	3.32
CML 375	85	87	129.33	46.17	10.67	5.30	16	17	460.0	5.66
CML 376	87	89	123.83	46.67	14.17	4.12	13	28	285.0	5.34
CML 377	89	91	139.67	56.67	14.50	4.05	13	28	395.0	6.68

Table 6 (Cont'd)

Inbred lines	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of row per ear	No. of kerne per row	Thousand grain weight (g)	Grain yield (t/ha)
CML 378	90	92	116.67	54.67	13.67	4.13	13	31	350.0	4.75
CML 379	87	89	163.50	63.67	13.33	4.35	15	25	450.0	6.54
CML 380	89	91	137.00	60.00	12.17	4.83	15	18	425.0	6.81
CML 381	87	89	124.50	60.00	10.00	4.13	15	19	330.0	4.90
CML 382	82	85	130.50	62.67	15.67	4.42	14	26	420.0	6.79
CML 383	89	91	152.50	62.17	14.83	4.10	11	23	365.0	6.14
CML 384	89	91	145.67	63.00	13.33	3.93	11	27	340.0	6.83
CML 385	88	90	139.67	50.00	14.50	3.62	11	19	330.0	4.72
CML 482	81	85	164.83	68.00	11.00	4.07	12	20	375.0	3.84
CML 483	90	92	174.17	72.33	14.17	4.33	12	20	350.0	3.21
CML 484	85	89	127.00	58.17	11.33	4.12	13	19	347.5	3.60
CML 485	80	85	117.00	51.50	12.33	3.80	13	21	332.5	4.32
CML 512	86	89	148.33	58.33	11.67	3.75	13	22	260.0	3.69
CML 517	86	88	170.83	68.17	11.83	4.15	13	21	385.0	5.16
CML 518	86	88	153.50	65.17	12.00	4.02	12	22	420.0	5.87
CML 519	90	91	136.83	60.67	12.83	3.87	11	21	330.0	4.08
Grand mean	84.05	86.94	143.17	56.29	12.94	4.08	13.0	22.11	322.68	4.55
Minimum	70	71.5	91.7	30.5	10	3.3	10	15.3	120	2.05
Maximum	90	92	186.3	79.8	17.8	5.3	16	31	460	6.99
CV%	1.90	1.90	7.76	14.78	7.75	5.65	7.38	7.79	9.71	13.05
LSD(0.05)	3.19	3.29	22.24	16.66	2.01	0.46	1.92	3.45	62.76	1.19

vii). Number of row per ear

Number of rows per ear is an important identifiable character for maize because it has a close relationship with maize yield. A wide variation was observed for this trait. The maximum number of row per ear was 16 and minimum was 10 (Table 6). Maximum numbers of kernel rows (16) was observed in CML 375 and minimum in CML 263. Our results are in line with those of Begum *et al.* (2018).

viii). Number of kernel per row

Number of kernel per row is directly correlated with grain filling with producing more kernel in ear. Significant amount of variation was also observed in case of number of kernel per row (Table 6). Number of kernel per row ranges from 15-31 among the inbreds and the average number was 22. Highest number of kernels produced on a row was measured in the inbred CML 378. Huda *et al.* (2016) also observed similar findings.

ix).Thousand grain weight (g)

Kernel or grain weight is main yield element which has significant contribution to final yield. Among the tested inbred lines considerable variation was exhibited by giving the thousand grain weight 120.0 g to 460.0 g with an average of 322.6 g. The highest thousand grain weight was recorded for CML 375 and lowest in CML 263. Bold grain could contribute for getting higher yield in maize (Table 6). This study was also in accordance with the result of Huda *et al.* (2016).

x). Grain yield (t/ha)

A highly significant difference for grain yield was observed in tested inbred lines under investigation (Table 6). Grain yield ranges from 2.05 t/ha to 6.99 t/ha. Inbred CML 331 gave the highest estimated grain yield of 6.99 t/ha followed by CML 319, CML 384, CML 380 and CML 382. The yield differences may be due to the different genetic makeup among the tested materials. So the inbred lines CML 319, CML 384, CML 380 and CML 382 were identified a valuable source for yield increase in hybrid combinations. Huda *et al.* (2016) and Begum *et al.* (2018) reported pronounced variation in grain yield.

4.1.3. Maintenance of inbred lines

Tassel bag method was used for making pollination during maintenance of inbred lines. Among fifty eight inbreds, five healthy and disease free plants were selected from each plot and self-pollinated. Waxy paper bags were placed over the ear shoot three days before the silk emerge to protect the silk from wind blow pollen. Tassel bags were placed over tassel one day previous to pollination and fastened with paper clip. Pollens were collected in this bag about twenty four hours after bagging the tassel. When silk brush grown out 1 to 2 inches shoot bags were removed without exposing the silks and collected pollens were dusted over the silk brush. Finally, tassel bags were placed over the pollinated ear shoot to protect and identify the developing ear. When ear was matured harvested and stored separately.

4.2 Experiment 2: Study of inter-genotypic variability and genetic diversity for morphological and agronomic traits in maize inbred lines.

In maize breeding programs genetic improvement of economically importance traits along with maintaining sufficient amount of variability is always the desired objective. This variability is a key to crop improvement. For the selection of desirable parent from diversed germplasm in a successful breeding program genetic diversity is one of the useful tools. The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce heterotic effect (Arunachalam, 1981; Ghaderi, *et al.*, 1984 and Mian and Bahl, 1989). The success of any crop improvement program with define objectives depends on the amount of diversity available in the crop, assigning inbreds to heterotic groups and planning an appropriate mating design. Progress from selection directly related to the magnitude of genetic variance in the population has been reported by several workers (Helm *et al.*, 1989; Hallauer and Miranda, 1995). Grzesiak (2001) observed considerable genotypic variability for different traits among various maize genotypes. Ihsan *et al.* (2005) also reported significant genetic differences for morphological parameter for maize genotypes. So this experiment was conducted to determine the genetic variation of important morphological, yield and yield contributing characters among the inbred lines and to screen out the suitable parents group which are likely to provide superior segregates on hybridization.

The results of genetic variability and divergence of fifty eight maize inbreds are presented simultaneously in different tables and figures.

4.2.1 Variability study

Variability plays an important role in crop breeding. The magnitude of variability present in crop species provides the basis of selection. The mean sum of squares due to genotypes showed significant differences for all the characters suggesting considerable genetic variation in respect of various characters (Appendix X). This indicated the presence of substantial genetic variability among the genotypes. The existence of variability is essential for resistance to biotic and abiotic factors as well as for wide adaptability of genotypes (Vashistha *et al.*, 2013). Similar results were reported by Saikia and Sharma (2000) for different maize characters i.e. plant height, ear height and grain yield per plant. Similar results were also reported by Rather *et al.*

(2003), Jawaharlal *et al.* (2011), Rajesh *et al.* (2013), Huda *et al.* (2016) and Hossain (2016).

The phenotypic and genotypic variability, heritability, co-efficient of variation, genetic advance and genetic advance in percentage of mean were accounted for ten characters in fifty eight maize inbreds are furnished in Table 7. The phenotypic variance was partitioned into genotypic and environmental variances for clear understanding the pattern of variation. For detecting the amount of variability present in a given characteristic the parameters such as genotypic and phenotypic coefficients of variation (GCV and PCV) are useful. Although GCV is indicative of the presence of high degree of genetic variation, the amount of heritable portion can only be determined with the help of heritability estimates and genetic gain (Rao and Rao, 2015). Bilgin *et al*, 2010 also reported the efficiency with which genotypic variability can be exploited by selection depends upon heritability and the genetic advance (GA) of individual trait. To plan an efficient breeding program, genetic improvement for quantitative traits requires reliable estimates of heritability (Akinwale *et al*, 2011). For the selection of the best genotypes for yield and its attributing traits heritability coupled with high GA would be more useful in predicting the resultant effect (Singh *et al*, 2011). Heritability provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations (Bello *et al*, 2012). But it does not provide the indication of genetic improvement which results from selection of individual genotypes. Hence, knowledge about genetic advance coupled with heritability is most useful. The mode of gene action in the expression of a trait is indicated by expected genetic advance as per cent of mean, which helps in choosing an appropriate breeding method.

4.2.1.1 Days to 50% tasseling

In respect of days to 50% tasseling, the phenotypic variance (12.90) was higher than the genotypic variance (10.36) which indicated that moderate environmental influences for the expression of this character which was supported by the less difference between the genotypic (3.83%) and phenotypic coefficient of variation (4.27%) (Table 7). Similar observations were also reported by Zahid *et al.* (2004) and Sesay *et al.* (2016). Similar findings in maize were also reported by Vashistha *et al*. (2013) and Kumar *et al.* (2014).

4.2.1.2 Days to 50% silking

Phenotypic and genotypic variance for days to 50% silking was observed 10.36 and 7.65, respectively indicating they had some sort of interaction with environment and narrow difference between values of genotypic (3.18%) and phenotypic coefficient of variation (3.70%) also indicative of less environmental influences (Table 7). These findings were in consonance with the reports made earlier in maize by Kumar *et al.,* (2014), Begum *et al.* (2016) and Sravanti *et al.* (2017). High heritability (73.86%) along with low genetic advance in percentage of mean (5.63) attributed to non additive gene action involvement in the expression of the character and this will limit the scope of improvement by direct selection. Vashistha *et al.* (2013) and Rajesh *et al.* (2013). also found similar findings while studying variability in maize.

4.2.1.3 Plant height (cm)

The difference in magnitude in between genotypic (360.89) and phenotypic variances (484.29) was relatively high for plant height indicating that they were responsive to environmental factors. The values of genotypic (13.27%) and phenotypic coefficient of variation (15.37%) indicated the existence of inherent variability among the studied genotypes (Table 7). The results of moderate PCV and GCV values observed in this study were reported by earlier researchers on plant height (Ogunniyan and Olakojo, 2014 and Nzuve *et al.*, 2014). Plant height showed high heritability (74.52%) coupled with high genetic advance in percentage of mean (23.60) which implied that this trait was governed by additive gene action and it was high potential for effective selection for further genetic improvement of this trait. Kumar *et al.* (2014) and Patil *et al.* (2016) also recorded high heritability percentage coupled with high genetic advance in percentage of mean for this trait.

4.2.1.4 Ear height (cm)

In case of ear height, the phenotypic variance (149.49) was considerably higher than genotypic variance (80.29) indicating environment had a great influence for the expression of this trait (Table 7). Rather *et al.,* (2003), Abirami *et al.* (2005), Yusuf (2010) and Nzuve *et al*. (2014) also found highest phenotypic and genotypic variances for ear height. The existence of inherent variability among the genotype with possibility of high potential for selection were due to the moderate genotypic (15.52%) and phenotypic coefficient of variation (21.72%). Moderate heritability (53.71%) coupled with high genetic advance in percentage of mean (24.03) exposed the action of both additive and non additive gene effect on the expression of this character as well as scope of improvement through selection. Langade *et al.* (2013) and Sesay *et al.* (2016) also reported similar observation.

4.2.1.5 Ear length (cm)

The difference between phenotypic variance (2.43) and genotypic variance (1.42) were relatively low for ear length suggesting low environmental influence on the expression of the genes controlling this traits as well as values of genotypic (9.22%) and phenotypic coefficient of variation (12.04%) indicating less variation exists among different genotypes (Table 7). Moderate GCV and PCV values of ear length were reported by Singh *et al.,* (2003) and Begum *et al* (2016). The possibility of predominance of both additive and non additive gene action in the inheritance of this trait due to moderate heritability (58.62%) coupled with moderate genetic advance in percentage of mean (14.54). Langade *et al.* (2013) and Kumar *et al.* (2014) also observed moderate heritability in maize for ear length.

4.2.1.6 Ear diameter (cm)

Ear diameter showed low values and little difference between genotypic (0.08) and phenotypic variance (0.13) which implied that environment play a minor role for the expression on this trait as well as the value of genotypic (6.73%) and phenotypic coefficient of variation (8.78%) also indicated less variation among the genotypes (Table 7). This result was in consistence with the results of Hefny (2011), Vashistha *et al.* (2013) and Sesay *et al.* (2016). Moderate heritability (58.66%) along with low genetic advance in percentage of mean (10.61) revealed the major role of non additive gene action in the transmission of this character from parents to offsprings. Moderate heritability for ear diameter was reported by Satyanorayana and Kumar (1995) and Langade *et al* (2013).

Table 7. Genetic parameters for yield attributes and yield of different maize inbred lines

Characters	Genotypic variance	Phenotypic variance	Genotypic Coefficient of variation (%)	Phenotypic Coefficient of variation (%)	Heritability (%)	Genetic advance (GA)	GA in percentage of mean (%)
Days to 50% tasseling	10.36	12.90	3.83	4.27	80.31	5.94	7.07
Days to 50% silking	7.65	10.36	3.18	3.70	73.86	4.90	5.63
Plant height (cm)	360.89	484.29	13.27	15.37	74.52	33.78	23.60
Ear height (cm)	80.29	149.49	15.92	21.72	53.71	13.53	24.03
Ear length (cm)	1.42	2.43	9.22	12.04	58.62	1.88	14.54
Ear diameter (cm)	0.08	0.13	6.73	8.78	58.66	0.43	10.61
Number of row per ear	0.67	1.59	6.29	9.70	42.08	1.09	8.41
Number of kernel per row	6.92	9.90	11.91	14.23	70.01	4.54	20.52
Thousand grain weight (g)	3062.04	4044.356	17.15	19.71	75.71	9.19	30.74
Grain yield (t/ha)	1.17	1.52	23.69	27.05	76.71	1.95	42.74

4.2.1.7 Number of row per ear

In case of number of row per ear, there was a little difference between the phenotypic and genotypic variance i.e 0.67 and 1.59, respectively which was a indication of less influence of environment on the expression of the genes controlling of this traits. According to Table 7 genotypic coefficient of variation (6.29%) and phenotypic coefficient of variation (9.70%) for number of row per ear indicating that the genotypes are considerably less variable for this traits. Low GCV and PCV values for number of grain rows per ear were also reported Kumar *et al.* (2014) and Begum *et al* (2016). Moderate heritability (42.08%) coupled with low genetic advance in percentage of mean (8.41) for this character discovered the action of non additive gene effect and selection may not be rewarding for the improvement of trait. Vashistha *et al.* (2013), Sesay *et al.* (2016) and Sravanti *et al.* (2017) also found similar findings while studying heritability in maize.

4.2.1.8 Number of kernel per row

For the expression of trait number of kernel per row, environment had a influence on the genotypes because phenotypic variance (9.90) was higher than genotypic variance (6.92) for this trait and the value of genotypic coefficient of variation (11.91%) and phenotypic coefficient of variation (14.23%) indicated that the considerable variation exists among the genotypes and the apparent variation not only due to the genotypes but also due to the environmental influences (Table 7). Kumar *et al.* (2014) and Sravanti *et al.* (2017) also reported similar observation for number of kernel per row. Number of kernel per row showed high heritability (70.01%) coupled with high genetic advance in percentage of mean (20.52) revealed the attributed to additive gene effect and selection may be effective. Vashistha *et al.* (2013) and Patil *et al.* (2016*)* also recorded high heritability percentage coupled with high genetic advance in percentage of mean for this trait.

4.2.1.9 Thousand grain weight (g)

In case of thousand grain weight (g), the phenotypic variance (4044.35) was considerably higher than genotypic variance (3062.04) indicating that large environmental influence on this character and the value of genotypic coefficient of variation (17.15%) and phenotypic coefficient of variation (19.71%) suggested a wide range of variation for this trait (Table 7). Begum *et al.* (2016) and Sesay *et al.*

(2016) also found high value of GCV and PCV. High heritability (75.71%) attached with high genetic advance in percentage of mean (30.74) exposed the action of additive gene interaction. As this trait possessed high genetic advance, it has high potential for effective selection for further genetic improvement for this trait. Similar observation was also reported by Patil *et al.* (2016).

4.2.1.10 Grain yield (t/ha)

The difference between phenotypic variance and genotypic variance (1.17 and 1.52) were relatively low for grain yield, suggested less influence of environment on the expression of genes controlling this trait as well as genotypic coefficient of variation (23.69%) and phenotypic coefficient of variation (27.05%) indicating presence of considerable variability among the genotypes (Table 7). Begum *et al.* (2016) and Sravanti *et al.* (2017) also observed the lowest amount of genotypic and phenotypic variance. Sesay *et al.* (2016) also recorded high genotypic coefficient of variation and phenotypic coefficient of variation. The magnitude of heritability was high (76.71%) which was coupled with very high genetic advance in percentage of mean (42.74). Vashistha *et al.* (2013) and Patil *et al.* (2016) also recorded high heritability percentage coupled with high genetic advance in percentage of mean for this trait. These findings were indicative of additive gene action as well as a scope of improvement through selection.

4.2.2 Association analysis

Although the information regarding the possibility of improvement of various characters provided by the variability estimation, but the extent of nature of relationship exists between the characters are not described. For fruitful selection during advance in generation variation and character association are checked in breeding methods. The direction of action of different characters is determined from association analysis and it will help to establish selection criteria for higher yield.

Grain yield is a complex character which is highly influenced by the environment and is the result of inter-relationships of its various yield components (Grafius, 1960). Among the various traits, grain yield in maize is the most important and complex quantitative traits controlled by numerous genes (Zdunic *et al.*, 2008). The genotypic and phenotypic correlation coefficients provide information of various traits of plant to ascertain the degree to which these are associated with economic productivity.

Phenotypic correlation implies the association between two characters that can directly be observed, while the extents to which two traits are genetically associated are expressed by genotypic correlation. Both genotypic and phenotypic correlations among and between pairs of agronomic traits provide scope for indirect selection in a crop breeding program (Pavan *et al.*, 2011). Therefore, for understanding the intricacy of the trait association analysis between yield and yield contributing characters through correlation coefficient studies would be effective. Therefore, for designing appropriate breeding programme and for simultaneous improvement of more than one character knowledge about the degree and direction of association between yield and its components traits, is of great significance to the breeders.

So, with a view to study the association of characters among maize inbreds the correlation coefficients were separated into genotypic and phenotypic level for clear understanding the results (Table 8 and Table 9). In most cases, the genotypic correlation was higher than that of phenotypic correlation; reveal that association may be largely due to genetic reason (strong coupling linkage) (Sharma, 1988). In this study most of the cases the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients indicating strong inherent association between the characters studied and phenotypic correlation values were reduced due to suppressive effect of the environment which modified the phenotypic expression of these characters. In few cases, however, phenotypic correlation coefficients were same with or higher than their corresponding genotypic correlation coefficients suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. Genotypic and phenotypic correlation coefficients between pairs of characters in the present study are presented in Table 8 and Table 9.

4.2.2.1 Association between grain yield and yield components

Grain yield had highly significant and positive correlation with thousand grain weight (0.606 and 0.462), days to 50% tasseling (0.551 and 0.461), ear diameter (0.535 and 0.451), ear height (0.503 and 0.392), number of kernel per row (0.496 and 0.361), days to 50% silking (0.481 and 0.462), ear length (0.475 and 0.370) at both genotypic and phenotypic level, respectively (Table 8 and Table 9). Similar findings were reported by Begum *et al.* (2016) where grain yield showed highly significant positive correlations with ear length, ear diameter and number of kernels per row. Batool *et al.* (2012) also found positive correlation of grain yield with ear length and Rafiq *et al.* (2010) for ear diameter and number of kernels per ear. In an investigation by Patil *et al.*(2016) also showed significant positive correlation with grain yield both at phenotypic and genotypic levels for the characters ear diameter, number of kernels per row, ear length and hundred grain weight indicating dependence of these characters on each other. Thus the association between characters which were positive and significant indicated additive genetic model and these traits were less affected by fluctuation of environments. The significant positive correlation and non-significant positive correlation of grain yield was observed with plant height (0.234 and 0.252) at phenotypic and genotypic level respectively. Inherent relation among the pairs of combination was suggested by positive and non-significant association between traits. Number of row per ear had non-significant negative association with grain yield both at genotypic and phenotypic level. While the negative and non-significant association suggested a complex linked of relation among the pair of combination.

4.2.2.2 Correlations among yield components

Studies on inter-character associations for yield components revealed positive and highly significant association of days to 50% tasseling with days to 50% silking, plant height, ear height, ear length and number of kernel per row at both level (Table 8 and Table 9). Begum *et al.* (2016) and Nataraj *et al.* (2014) found similar relations with days to 50% silking, plant height and ear height. Days to 50% tasseling also showed positive and insignificant correlation with ear diameter and thousand grain weight (gm). The result was supported by Begum *et al.* (2016) and they reported positive correlations of days to tasseling with ear diameter. Number of row per ear was negatively and significantly correlated with days to 50% tasseling (Table 8 and Table 9). Furthermore, days to 50% silking showed highly significant positive correlation with days to 50% tasseling, plant and ear height, ear length and number of kernel per row (Table 8 and Table 9). These results were in accordance with the findings of Nataraj *et al.* (2014). Negative and insignificant correlation was observed between days to silking and number of row per ear.

Table 8. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different inbred lines of maize

Characters	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel/row	Thousand grain weight (g)	Grain yield (t/ha)
Days to 50% tasseling	1									
Days to 50% silking	0.972**	1								
Plant height (cm)	0.354**	0.297*	1							
Ear height (cm)	0.678**	0.662**	0.759**	1						
Ear length (cm)	0.387**	0.436**	0.312*	0.282*	1					
Ear diameter (cm)	0.252	0.154	0.004	0.130	-0.108	1				
Number of row per ear	-0.326*	-0.330*	-0.332*	-0.371**	-0.440**	0.721**	1			
Number of kerne lper row	0.309*	0.340**	-0.037	0.228	0.769**	-0.021	-0.120	1		
Thousand grain weight (g)	0.190	0.153	0.048	0.122	0.236	0.708**	0.379**	0.174	1	
Grain yield (t/ha)	0.551**	0.481**	0.252	0.503**	0.475**	0.535**	-0.023	0.496**	0.606**	1

*and ** indicate significant at 5% and 1% level of probability, respectively

Table 9. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different inbred lines of maize

Characters	Days to asseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel/row	Thousand grain weight (g)	Grain yield (t/ha)
Days to 50% tasseling	1									
Days to 50% silking	0.942**	1								
Plant height (cm)	0.281**	0.232*	1							
Ear height (cm)	0.490**	0.460**	0.682**	1						
Ear length (cm)	0.273**	0.291**	0.261**	0.232*	1					
Ear diameter (cm)	0.131	0.071	0.033	0.120	-0.071	1				
Number of row per ear	-0.240*	-0.250**	-0.172	-0.191*	-0.270**	0.421**	1			
Number of kernel per row	0.241*	0.272**	-0.012	0.123	0.502**	-0.012	-0.040	1		
Thousand grain weight (g)	0.172	0.153	-0.013	0.081	0.221*	0.560**	0.191*	0.132	1	
Grain yield (t/ha)	0.461**	0.412**	0.234*	0.392**	0.370*	0.451**	-0.043	0.361**	0.462**	1

*and ** indicate significant at 5% and 1% level of probability, respectively

Plant height had the positive and highly significant correlations with days to 50% tasseling, ear height and ear length and significant positive correlation with days to silking both at genotypic and phenotypic level (Table 8 and Table 9). Nataraj *et al.* (2014) and Begum *et al.* (2016) also reported highly significant positive correlation of plant height with ear height. Negative correlation of plant height with number of row per ear, number of kernel per row and thousand grain weight were observed at phenotypic level, whereas the number of row per ear was negatively and significantly correlated with plant height at genotypic level.

Ear height showed positive and highly significant correlations with days to 50% tasseling, days to 50% silking and plant height and significant positive correlation with ear length, ear diameter, number of kernel per row and thousand grain weight both at genotypic and phenotypic level (Table 8 and Table 9). Number of row per ear had negative and significant correlation with ear height.

Positive and highly significant correlation was observed of ear length with days to 50% tasseling, days to 50% silking, plant height and number of kernel per row significant positive correlation with ear height at both level and (Table 8 and Table 9). These results were in harmony with that of Nataraj *et al.* (2014) who found positive correlation coefficient between ear length and number of kernel per row. Number of row per ear had negative and significant correlation and ear diameter had negative correlation with ear length. Ear length had significant positive relation with thousand grain weight at phenotypic level and positive correlation at genotypic level with thousand grain weight.

Ear diameter had positive and highly significant correlation with number of row per ear and thousand grain weight both at genotypic and phenotypic level. Negative and insignificant correlation was observed between ear diameter and number of kernel per row (Table 8 and Table 9). Such results were in harmony with the findings of Begum *et al.* (2016) and they found negative and insignificant correlations with number of kernel per row. Similar results were reported by Khazaei *et al.* (2010) and Wannows *et al.* (2010).

Number of row per ear showed positive and highly significant correlation with ear diameter and thousand grain weight both at genotypic and phenotypic level. Negative and significant correlation was observed of number of row per ear with days to 50% tasseling, days to 50% silking, ear height and ear length at both levels. Plant height had negative and significant correlation with number of row per ear at genotypic level. Number of kernel per row had negative correlation with number of row per ear (Table 8 and Table 9).

Positive and highly significant correlation was observed of number of kernel per row with days to 50% silking and ear length at both level. Ear height and thousand grain weight were positively correlated with number of kernel per row. Negative correlation was observed with plant height, ear diameter and number of row per ear (Table 8 and Table 9).

Significant positive correlation was observed among the two important yield components viz. ear diameter and number of row per ear with thousand grain weight at both level (Table 8 and Table 9). Ear length also showed significant and positive correlation with thousand grain weight at phenotypic level. Thousand grain weight also showed positive correlation with other traits except plant height at phenotypic level.

4.2.3 Path coefficient analysis

Association of character determined by correlations may not provide a clear picture of each component's importance in determining grain yield because yield components are inter-related and developed sequentially at different growth stages. Therefore, to reveal the nature of relationship between the variables analyze the cause and effect of relationship between dependent and independent variables are necessary. Path coefficient analysis furnishes a method of partitioning the correlation coefficient into direct and indirect effect and provides the information on actual contribution of a trait on the yield (Dewey and Lu, 1959). Path coefficient analysis provides more information among variables than correlation coefficients (Aycicek and Yildirim, 2006).The traits having high positive correlation along with high direct effects are expected to be useful as selection criteria in improvement program (Pavan *et al.*, 2011). Therefore, correlation and path coefficient analysis are effective tools to improve the efficiency of breeding programs through the use of appropriate selection indices (Mohammadi *et al.*, 2003). However path coefficient analysis helps in partitioning the correlation coefficient into direct and indirect effects, which also measured the relative importance of each component. Estimates of direct and indirect effect of path coefficient are presented in Table 10.

Path coefficient analysis revealed that among the studied characters except silking date and plant height other characters had the positive direct effect on grain yield. Days to tasseling had the highest positive direct effect (0.372) on grain yield followed by ear diameter (0.303), number of kernel per row (0.190), ear height (0.176) and thousand grain weight (0.173). Hossain (2016) assessed similar results for ear height, days to tasseling and ear diameter, Patil *et al.*(2016) for thousand grain weight. These findings were also in agreement with reports of Venugopal *et al.* (2003) for plant height, ear length, and number of kernel row per ear. Kumar *et al.* (2006) and Shakoor *et al.* (2007) for 100 grain weight. The genotypic and phenotypic correlation of thousand grain weight, days to tasseling, ear height, ear diameter, number of kernel per row, ear length were also high and positive. Such high positive correlation with grain yield was mainly due to the high positive direct effect and considerable indirect effects of these characters and selection for any of these independent characters leads to improving the genotypes for grain yield. On the other hand, days to 50% silking and plant height had negative direct effect on grain yield. Similar results were found by Hossain (2016). Restricted selection should be followed for these characters.

The residual effect observed in path analysis was 0.30, which permitted precise explanation about the pattern of interaction of other possible components of yield and indicating that the character under study contributed 70.0% of variability in grain yield. It was suggested that there were some other factors or characters those contributed 30.0% to the yield not included in the present study may exert insignificant effect on yield.

From correlation coefficient and path analysis studies, it was found that days to tasseling, ear height, ear diameter, number of kernel per row and thousand grain weight were the most important components for getting higher yield due to significant positive correlation with grain yield and had high direct positive effect on yield. Therefore, the present study suggested that these traits were important yield components and selection based on these traits would give better response for improving grain yield.

Table 10. Path analysis showing direct (Diagonal/bold) and indirect effects of different characters on grain yield of maize inbred lines.

Characters	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel/row	Thousand grain weight (g)	Genotypic correlation with grain yield (t/ha)
Days to 50% tasseling	**0.372**	-0.154	-0.001	0.086	0.046	0.039	-0.003	0.046	0.029	0.551**
Days to 50% silking	0.350	**-0.164**	-0.001	0.081	0.049	0.021	-0.004	0.051	0.026	0.481**
Plant height (cm)	0.104	-0.038	**-0.003**	0.120	0.044	0.009	-0.002	-0.002	-0.002	0.252
Ear height (cm)	0.182	-0.076	-0.002	**0.176**	0.039	0.036	-0.003	0.023	0.014	0.503**
Ear length (cm)	0.100	-0.048	-0.001	0.041	**0.169**	-0.021	-0.004	0.095	0.038	0.475**
Ear diameter (cm)	0.048	-0.011	-0.000	0.021	-0.012	**0.303**	0.006	-0.002	0.097	0.535**
Number of row/ear	-0.089	0.041	0.001	-0.033	-0.046	0.127	**0.014**	-0.008	0.033	-0.023
Number of kernel/row	0.089	-0.044	0.000	0.021	0.085	-0.003	-0.001	**0.190**	0.022	0.496**
Thousand grain weight (g)	0.063	-0.025	0.000	0.014	0.037	0.170	0.003	0.025	**0.173**	0.606**

*and ** indicate significant at 5% and 1% level of probability, respectively

Residual effect = 0.30

4.2.4 Multivariate analysis (D^2 Statistics)

Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and assessing relative contribution of different components to the total divergence both at the intra-cluster and inter cluster levels (Murthy and Arunachalam, 1996; Ram and Panwar, 1970; Sharma *et al*., 2003). These statistical techniques simultaneously analyze multiple measurements on each individual under investigation which are widely used in analysis of genetic diversity (morphological, biochemical or molecular marker-based); classify the collections of germplasm and could reduce the time period and crop improvement expenditure. Multivariate analysis based on principal component analysis (PCA) is mostly used to evaluate the magnitude of genetic diversity among the germplasm (Guedira, 2000). Among the multivariate techniques, principal component analysis (PCA), Principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis are most commonly employed and appear particularly useful (Mohammadi and Prasanna, 2003). Cluster analysis is one of the statistical techniques aimed in grouping objects in clusters so that the objects in one cluster have high similarities than those in other clusters. The information, thus obtained, would be helpful to develop an effective maize breeding programme and as such a quantification of the degree of divergence would be helpful for ongoing breeding programmes in choosing suitable genotypes and traits of interests.

The experiment results of the genetic divergence of fifty eight maize inbreds are presented under the following headings i.e principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis.

4.2.4.1 Principal component analysis (PCA)

The Principal Component Analysis is a powerful tool to obtain parental lines for a successful breeding programme (Akter *et al*., 2009). The study was undertaken to run a classificatory analysis on the maize genotypes by means of PCA which would enable us to classify the available germplasm into distinct groups on the basis of their genetic diversity. The result of the eigen values of principal component axis, percent of total variation and cumulative percentage of percent variation from principal component analysis are presented in Table 11. The analysis revealed that eigen value above unity for first four characters of the principal component axes explaining 82.67% of the total variation. The first principal axes which alone contributed 37.08% of the total variation while the rest of nine characters with eigen value accounted for 62.92% variations describing fifty eight maize inbred lines. Kamara *et al* (2003); used PCA to categorize traits of maize (*Zea mays* L.) that accounted for most of the variance in the data. Important contribution of the first PCs in total variability of different traits were reported by Chozin (2007); Mujaju and Chakuya (2008). Greenacre (2010) stated that eigen values (in PCA) have primary importance for numerical diagnostics to assess variation attributed by number of large variables on the dependent structure and their data matrix in a graphical display.

4.2.4.2 Construction of scatter diagram

Using principal component score I (PCA score-I) as “X” axis and principal component II (PCA score-II) “Y” axis, which reflects the relative position obtained from the principal component analysis a two dimensional scatter diagram (Z1 and Z2) was constructed that are presented in Figure 1. From the diagram it has been shown that the position of the genotypes were distributed into seven groups which revealed the presence of genetic diversity among the studied genotypes. Significant genetic diversity was also investigated by Azam *et al.* (2013); Zaman and Alam, (2013) and Alam *et al.* (2013).

4.2.4.3 Non hierarchical clustering

By the application of covariance matrix for non-hierarchical clustering, fifty eight maize genotypes grouped into seven different clusters based on various agro morphological traits where genotypes placed in different clusters were more divergent than the other genotypes grouped together. The distribution pattern of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. The grouping pattern obtained through principal component analysis was confirmed by these results of clustering. For this reason it can be said by non hierarchical clustering the results obtained through principal component analysis were established.

The clusters occupied by the fifty eight inbreds are represented by Table 12 and Figure 2. The maximum number of genotypes (13) was comprised into cluster II and cluster VII indicating overall genetic similarity among them, followed by ten in

Table 11. Eigen values and percentage of variation for corresponding ten component characters in fifty eighty maize inbred lines

Principle component axis	Eigen values	Percentage of total variation accounted	Cumulative percentage of percent variation
I	3.71	37.08	37.08
II	2.17	21.68	58.76
III	1.40	14.08	72.84
IV	0.98	9.83	82.67
V	0.62	6.2	88.87
VI	0.40	4	92.87
VII	0.29	2.91	95.78
VIII	0.22	2.2	97.98
IX	0.17	1.68	99.66
X	0.03	0.34	100.00

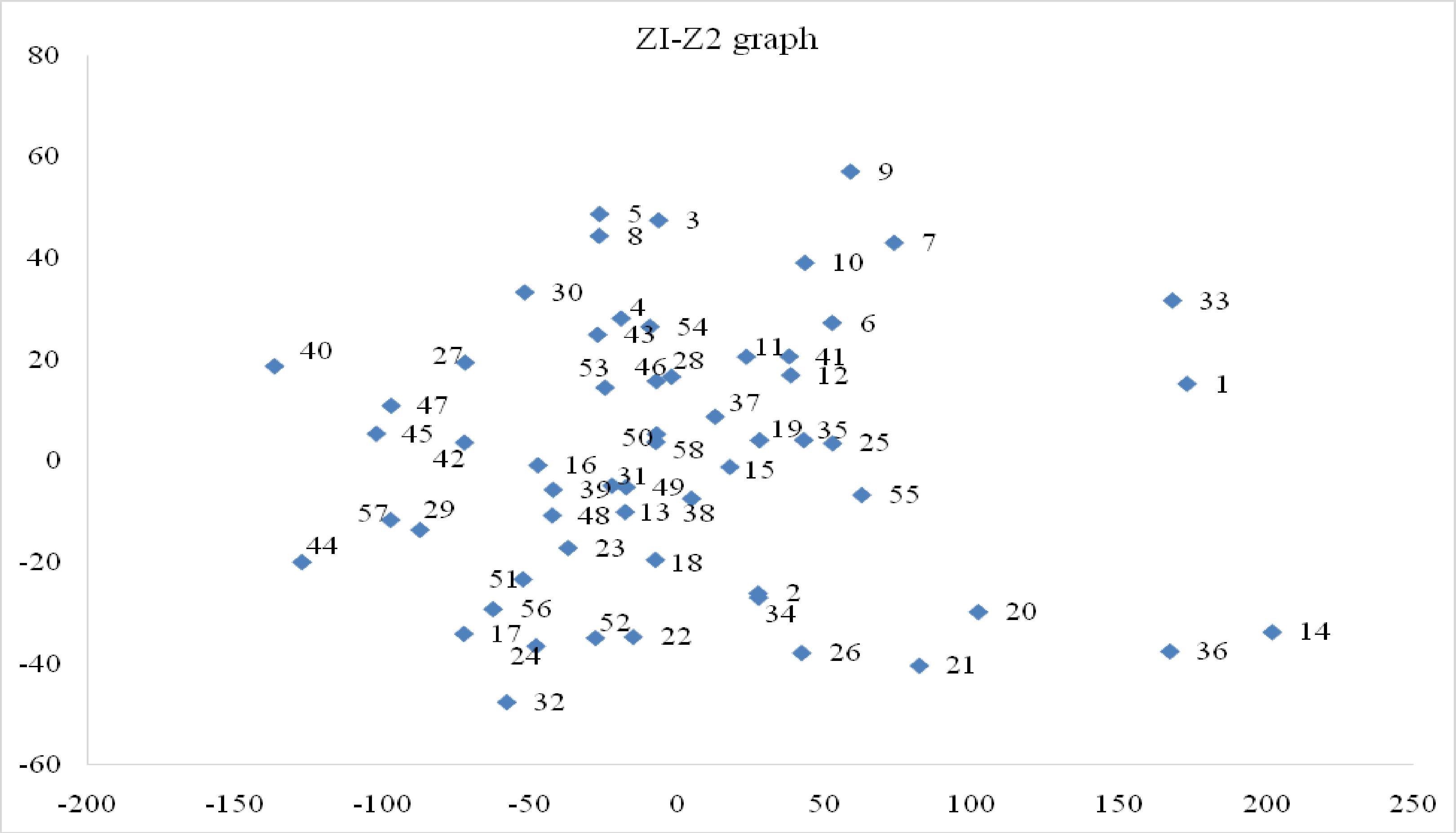

Figure 1. Scattered diagram of fifty eight maize inbreds based on their principal component score

Table 12. Distribution of fifty eight maize inbred lines in seven different clusters

Cluster	Number of inbreds	Inbred lines included in different clusters
I	10	CML 128, CML 129, CML 132, CML 136, CML 330, CML 332, CML 378, CML 381, CML 484, CML 485
II	13	CML 133,CML 135. CMnb L 137, CML 138, CML 242, CML 243, CML 264, CML 314, CML 320, , CML 369, CML 371, CML 376, CML 512
III	5	CML 127, CML 315, CML 316, CML 321, CML 368,
IV	5	CML 312, CML 319, CML 334, CML 482, CML 517
V	4	CML 126, CML 263, CML 367, CML 370
VI	8	CML 322, CML 331, CML 375, CML 377, CML 379, CML 380, CML 382, CML 518
VII	13	CML 249, CML 311, CML 313, CML 317, CML 318, CML 333, CML 372, CML 373, CML 383, CML 384,CML 385, CML 483, CML 519

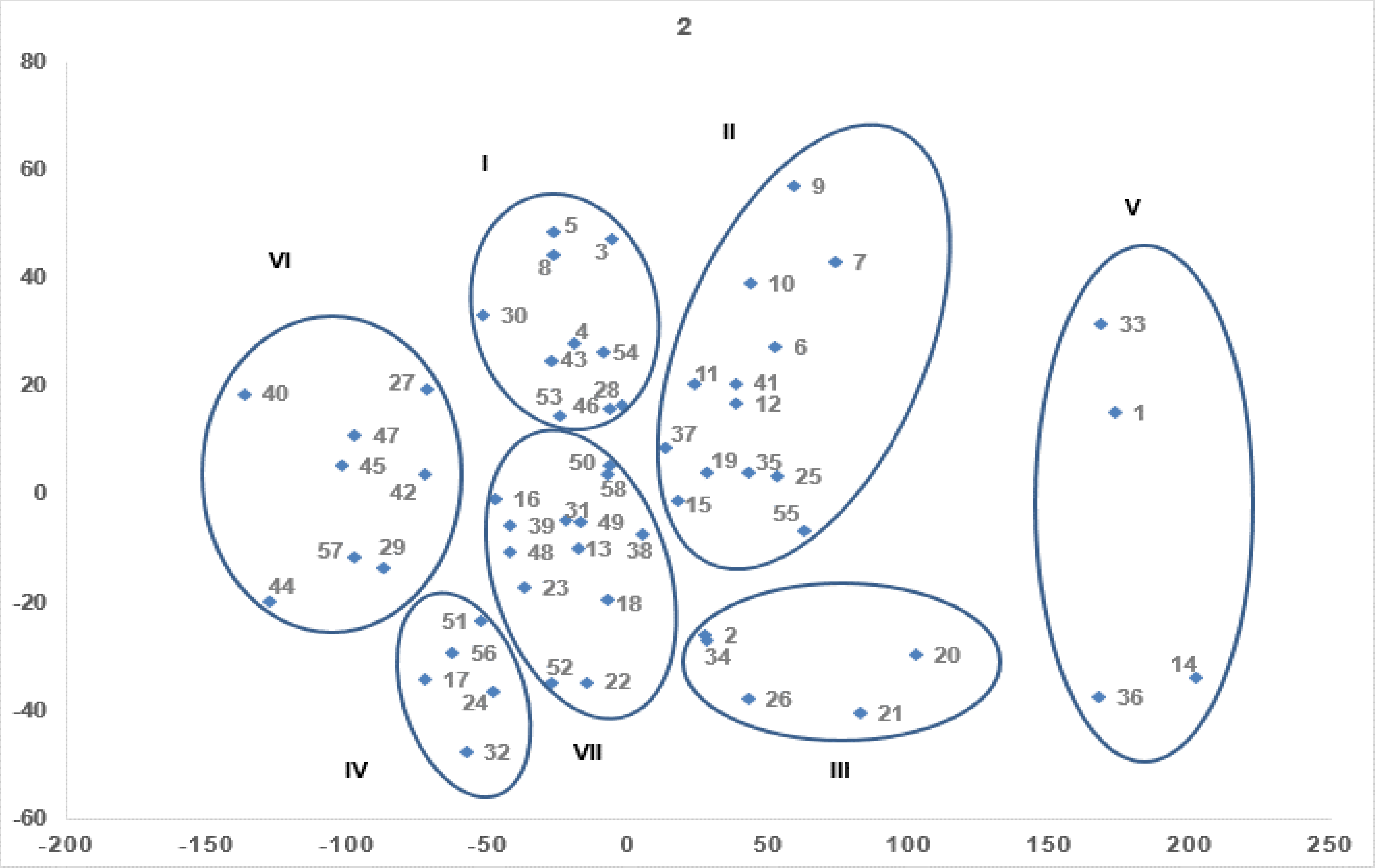

Figure 2. Cluster diagram of fifty eight maize inbreds based on their principal component score

cluster I. The cluster VI, III and V had eight, five and five genotypes, respectively where as cluster V contained four genotypes and occupied last position. This indicated that geographic diversity was not always related to genetic diversity. Crossa (1990), Khorasani *et al.* (2011) and Mostafavi *et al.* (2011) reported that making groups or clusters of under-study maize genotypes to minimize the plant pool is an efficient tool during selection process. Ivy *et al.* (2007) reported that twenty five genotypes divided into five clusters in a study of genetic divergence. Alam *et al.* (2013) made four groups when studying genetic diversity of seventeen inbred lines of maize. On the other hand, Azam *et al.* (2013) grouped into five clusters on forty nine genotypes. While assessing genetic diversity of sixty genotypes, Shrestha (2016) grouped them into six clusters. Rafique *et al* (2018) while assessing cluster analysis and genetic divergence of forty maize inbeds, grouped the genotypes into ten clusters.

4.2.4.4 Principal coordinate analysis (PCO)

Based on auxiliary of principal component analysis, principal coordinate analysis was performed. Between the pair of maize genotypes the inter-genotypic distance (D^2) was obtained by principal coordinate analysis (PCO) for all possible combination. Inter genotypic distance obtained from principal coordinate analysis showed (Table 13) that the highest distance (1.6183) was observed between the genotypes CML 263 & CML 132 followed by the genotypes CML 263 & CML 375 (1.5852), CML 263 & CML 137 (1.5704) and the lowest distance was obtained from the genotypic combination CML 371 & CML 330 (0.1666) which was followed by CML 371 & CML 320 (0.1772), CML 518& CML 517 (0.1946) and CML 382 & CML 311 (0.1973).

The prevalence of the genetic variability among the fifty eight genotypes of maize was indicated by the difference between the highest and lowest inter genotypic distance. From distance matrix by using these distance the intra cluster distance were calculated which was suggested by Singh and Chaudhary (1985), the magnitude of the intra cluster distance were not always proportional to the number of genotypes in the cluster.

Table 13. Ten of each higher and lower inter-genotypic distance (D^2) between pair of maize inbred lines

Inter-genotypic distance					
Sl. No.	**Genotypic combination**	**Highest distance**	**Sl. No.**	**Genotypic combination**	**Lowest distance**
1	CML 263 & CML 375	1.6183	1	CML 371& CML 379	0.1666
2	CML 263 & CML 132	1.5852	2	CML 371& CML 320	0.1772
3	CML 263 & CML 137	1.5704	3	CML 518 & CML 517	0.1946
4	CML 263 & CML 128	1.5586	4	CML 382 & CML 311	0.1973
5	CML 367 & CML 319	1.5147	5	CML 512 & CML 320	0.2032
6	CML 263 & CML 136	1.4797	6	CML 383 & CML 331	0.2042
7	CML 263 & CML 379	1.4745	7	CML 485 & CML 330	0.2061
8	CML 367 & CML 379	1.4744	8	CML 371& CML 264	0.2064
9	CML 263 & CML 382	1.4471	9	CML 377 & CML 311	0.2087
10	CML 263 & CML 129	1.4262	10	CML 382 & CML 383	0.2145

4.2.4.5 Canonical variate analysis (CVA)

The intra and inter cluster values worked out from canonical variate analysis within and among the cluster are presented in Table 14. The extent of genetic diversity among genotypes within the same cluster indicated by the magnitude of intra cluster distances The inter group distances in all cases appeared much greater than intra groups which indicated that a greater diversity existed among the lines of different cluster than those from same cluster. This was collaborated with the results of Ivy *et al.* (2007), Azam *et al.* (2013) and Alam *et al.* (2013). The inter cluster D^2 values ranges from 15.724 to 2.218. The highest inter-cluster distance was observed between clusters V and VI (15.724), followed by the distance between cluster IV and V (12.92), I and VI (11.554), V and VII (11.113) (Table 14) suggesting wide diversity between them and for getting transgressive segregates the genotypes in these cluster could be used as parents in hybridization programme. Clusters with comparatively less magnitude of divergence showed instability due to low divergence, while widely divergent clusters remained distinct in different environments (Somayajulu *et al*., 1970 and Raut *et al*., 1985). The lowest inter-cluster distance existed between cluster IV and VII (2.218), followed by I and VII (2.762) which indicated a close relationships between the same groups. These finding were supported by Zaman and Alam (2013), Datta and Mukherjee (2009) and Singh *et al*. (2005) that the greater genetic distances implying higher heterosis than those with similar genetic distances. The intra cluster D^2 value was the least in cluster VI (0.399) that was composed of eight genotypes and the highest in cluster V (0.741) that was four genotypes.

4.2.4.6 Performance of characters in clusters

Characterization of individual genotypes were made in respect of their mean value for different characters for getting idea whether the genotypes having similar characteristics which could be disseminated. In cluster means the genetic differences between clusters were reflected. The mean values of ten characters studied in maize genotypes for seven clusters are presented in Table 15. Enormous variations were observed in cluster mean for all characters. The results were described according to character wise. In case of days to tasseling and silking mean value was the minimum in cluster II (81 and 84 days, respectively). The second lowest value for early flowering appeared in cluster I (83 and 87 days) which was desirable and cluster I ranked the first for dwarf plant height (114.72 cm) and

Table 14. Average inter cluster distance (D^2) and Intra cluster distance (bold) for fifty eight maize inbred lines obtained by canonical variate analysis

Clusters	I	II	III	IV	V	VI	VII
I	**0.569**						
II	3.626	**0.578**					
III	6.452	3.501	**0.404**				
IV	4.453	6.038	6.578	**0.462**			
V	4.809	7.93	6.417	12.92	**0.741**		
VI	11.554	8.013	9.718	3.711	15.724	**0.399**	
VII	2.762	3.844	5.037	2.218	11.113	4.687	**0.511**

Table 15. Cluster means for ten characters of fifty eight maize inbred lines

Characters	I	II	III	IV	V	VI	VII
Days to 50% tasseling	83	81	85	86	84	86	86
Days to 50% silking	87	84	87	88	87	88	89
Plant height (cm)	114.72	127.36	169.57	175.33	145.96	141.52	154.07
Ear height (cm)	47.32	47.56	63.00	70.07	58.29	59.5	60.01
Ear length (cm)	12.63	12.35	12.57	13.4	12.33	13.00	13.99
Ear diameter (cm)	4.07	3.94	4.02	4.23	3.54	4.54	4.08
Number of row per ear	13.36	13.51	13.41	13.14	11.45	13.65	11.99
Number of kernel per row	22.48	21.76	21.93	23.42	20.9	22.53	21.82
Thousand grain weight g)	343.25	285.42	265.71	381.00	145.00	421.87	344.62
Grain yield (t/ha)	4.12	3.75	4.4	5.2	3.37	6.48	4.65

ear height (47.32 cm) also. Mean value for ear length was the highest (13.99 cm) in cluster VII followed by cluster VI. The inbred lines of cluster VI gave the highest yield (6.48 t/ha) and they also had the maximum value for ear diameter (4.54 cm), number of row per ear (13.65), thousand grain weight (421.87 gm). Selection on the basis of earliness and dwarfness genotypes in cluster I ranked first. Pattern of genotypes and contribution of characters towards divergence of the inbred lines, the D^2 analysis and principal component analysis were found to be alternative methods.

Considering yield and yield contributing character except ear length it appeared that the inbreds in the cluster VI performed better. The inbreds in this cluster had the highest value for ear diameter, number of row per ear, thousand grain weight and grain yield had compared to all other clusters. The genotypes of cluster VII were performed moderately in all the cases and had the highest value for ear length. Similar results have also been reported by Azad *et al.* (2012) and Zaman and Alam (2013). Hence, for the improvement of different characters viz. Days to tasseling, Days to silking, plant and ear height, yield and yield contributing characters under the present study, inbred lines should be selected from clusters I, cluster VI and VII.

4.2.4.7 Contribution of characters towards divergence of the inbred lines

Through canonical variate analysis contribution of characters towards divergence were estimated. For representing the genotypes in the graphical form (Rao, 1952) vectors of canonical roots were calculated by this method**.** The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 16. The positive absolute values of the two vectors for plant height and number of row per ear revealed that these characters contributed the maximum towards divergence among the ten characters of fifty eight genotypes. Ear diameter and thousand grain weight had negative value for two vectors which represent that these characters had the least responsibility of both the primary and secondary differentiation. The positive absolute values of vector 1 and negative absolute value for vector 2 for the characters like grain yield indicated the responsibility of primary differentiation. Responsibilities of secondary differentiation were noticed for days to tasseling, days to silking, ear height, ear length and number of kernel per row.

Table 16. Relative contributions of the ten characters of fifty eight inbred lines to the total divergence in maize

Characters	Vector 1	Vector 2
Days to 50% tasseling	-0.4373	0.0668
Days to 50% silking	-0.4245	0.0988
Plant height (cm)	0.2736	0.1845
Ear height (cm)	-0.3856	0.1327
Ear length (cm)	-0.3204	0.1215
Ear diameter (cm)	-0.1411	-0.5826
Number of row per ear	0.1455	0.5176
Number of kernel per row	-0.2592	0.0021
Thousand grain weight (g)	-0.2036	-0.4883
Grain yield (t/ha)	0.3907	-0.2714

4.2.4.8 Comparison of results based on different multivariate techniques

In Figure 1 and 2, the results observed from different multivariate technique were superimposed so it could be concluded that more or less similar results are given by all the techniques and the results of one technique supplemented and confirmed the results of the other. The clustering pattern of D^2 analysis through non-hierarchical clustering has taken care of simultaneous variations in all the characters under study. Through D^2 analysis in different clusters the distribution of inbred lines has followed the more or less similar of the Z_1 (principal component score I) and Z_2 (principal component score II) vectors of the principal component analysis. The information regarding the clustering pattern of genotypes and contribution of characters towards divergence of the inbred lines, the D^2 analysis and principal component analysis were found to be alternative methods.

Plate 11. Phenotypic appearance and ear of selected inbreds as parent from cluster I

Plate 12. Phenotypic appearance and ear of selected inbreds as parent from cluster VI

CML 383 **CML 311**

Plate 13. Phenotypic appearance and ear of selected inbreds as parent from cluster VII

4.3 Experiment 3: Heterosis and combining ability for yield characters in maize

Information about combining ability of parents and crosses facilitates breeders is the selection and development of single cross hybrids (Leta *et al.*, 2006). For establishing a sound basis for any breeding programme, information on the nature of combining ability of parents, their behaviour and performance in hybrid combinations is required. Combining ability studies provide information on the genetic mechanisms controlling the inheritance of quantitative traits and enable the breeders to select suitable parents for further improvement or use in hybrid breeding for commercial purposes (Hayder and Paul, 2014).

4.3.1 GCA and SCA Variance

Results from the pooled analysis of variance over five environments are presented in Table 17. The significant mean squares for general and specific combining abilities for studied characters indicated significant differences that suggested presence of notable genetic variability among the GCA as well as SCA effects. Narro *et al.* (2003), Akhi *et al.* (2018) and Murtadha *et al.* (2018) also reported highly significant differences for most of the sources of variation. For different traits in maize significant differences for GCA and SCA variances have also been reported earlier by (Mathur and Bhatnagar, 1995).

Environment played prominent role in phenotypic expression of agronomic characters. The progress and advances in selection would be reduced by ignoring environmental components which are important factors in breeding for desirable characters including grain yield. The results revealed significant mean square due to environments for all characters studied in this experiment which indicated the influence of differential environmental factors at different location on expression of different characters in maize. The analysis of variance also showed that genotypes differed significantly for all the characters except thousand grain weight. This suggested that significant differences existed among inbred lines, with respect to combining ability. These findings were similar to the earlier reports (Crossa, 1977; Vasal and Srinivasan, 1991; Spaner *et al.*, 1996; Joshi *et al.*, 1998; Nass *et al.*, 2000 and Matin *et.al.*, 2016). Highly significant genotype x

Table 17. Analysis of variance (MS value) including GCA and SCA for ten characters in 7X7 half diallel of maize pooled over five environments.

Source of variation	df	Mean sum of squares									
		Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel /row	Thousand grain weight (g)	Grain yield (t/ha)
Environment	4	2812.09**	2717.56**	5439.77**	2834.00**	33.82**	0.42**	4.22**	118.38**	64195.03**	7.44**
REP(Environment)	10	8.87**	15.72*	1316.12**	285.59**	1.33**	0.07**	0.64	8.20*	5355.45**	0.64
Cross (genotypes)	20	32.90**	37.82**	2643.94**	1348.78**	14.10**	0.52**	5.90**	33.47**	3313.15	16.29**
Genotypes X Environment	80	10.94**	11.66*	474.21	134.45**	1.11**	0.04**	0.62*	6.93**	1963.04	2.07**
GCA	6	80.82**	76.42**	6588.09**	3513.61**	25.06*	1.14**	12.83**	25.66	4227.39	17.71*
SCA	14	12.36	21.27*	953.59	421.00**	9.40**	0.25**	2.93**	36.82**	2921.34	15.68**
GCA X Environment	24	12.55	14.39	366.74	169.72	1.64*	0.03*	0.79	8.66*	1858.04	1.85
SCA X Environment	56	10.26**	10.49	520.27*	119.33**	0.89**	0.05**	0.55	6.19*	2008.04	2.17**
Residual	200	2.34	8.14	354.06	62.85	0.45	0.02	0.42	4.03	1498.14	0.39
GCA:SCA		6.54	3.59	6.91	8.35	2.67	4.56	4.39	0.70	1.45	1.13

environment effects suggested that maize genotypes significantly responded for yield and other characters to the environment and the need for selecting different parental lines for hybrids at specific environments. The effects of environment, entry and environment x entry interaction were highly significant for all characters were also reported by Murtadha *et al.* (2018).

The combining ability analysis of combined overall locations exhibited highly significant differences for GCA except number of kernel per row and thousand grain weights. Variance due to SCA were also significant for all the characters except days to tasseling, plant height and thousand grain weight which indicated that both types of gene actions i.e.additive and non-additive were involved for controlling these traits. Thus were agreeing with other findings (Nass *et al.,* 2000; Matin *et al*., 2016 and Begum, 2016). In maize the importance of both additive and non additive gene interactions were also reported by Rokadia and Koushik (2005).

GCA X Environment was significant for ear length, ear diameter, number of kernel per row and yield. In addition, the interaction of SCA by environment was significant for all traits except days to silking, number of row per ear and thousand grain weight which allows us to infer that the specific hybrid combinations were not performed same across environments (Aguiar *et al.*, 2003). This may be due to difference in the testing locations and the genetic materials studied. Non significant interaction effects of GCA and environment and also GCA and environment revealed the trend of GCA effects of parents and SCA effects of the crosss over the environments were similar. Ahmed *et al.* (2014) and Akhi *et al.* (2018) also reported that GCA and SCA can interact with environments.

In the present study ratio of GCA and SCA variance was observed close to unity for number of kernel per row, thousand grain weight and grain yield indicating equal importance of both additive and non additive gene effects. The closer the ratio of GCA: SCA is to unity; the greater the predictability of progeny performance based on the GCA alone and the better the transmission of trait to the progenies (Murtadha *et al.*, 2018). The ratio of the components revealed that GCA variance was higher than SCA for for days to tasseling days to silking, plant height, ear height, ear length, ear diameter and number of row per ear indicating the predominance of additive gene action for these traits and there is always a good chance of improving those traits by accumulation of favorable gene. These results were in agreement with earlier reports of Malik *et al.* (2004) for days to tasseling, plant height, ear height and grain yield. Matin *et al.* (2016) also reported predominant additive genetic variance in the inheritance of days to tasseling days to silking, plant height and ear height maize. Alika (1994) reported predominance of additive gene action for ear length and Vasal *et al.* (1993) reported high GCA effects for yield components in the same crop.

Combining ability analysis revealed that estimates of SCA variances were higher than GCA variances for the character number of kernel per row, suggesting predominance of non-additive or dominant gene action and ratio was almost unity for thousand grain weight and grain yield indicated equal importance of both additive and non-additive gene effects. Amiruzzaman *et al.* (2013) also found the importance of both additive and non-additive genetic variances with higher magnitude of SCA over GCA for yield-related characters of QPM in their study.

So the present study revealed that both additive and non-additive gene interaction influenced the expression of traits. The choice of efficient breeding method and incorporation of concerned genes into new materials are determined by the component of genetic variation which is estimated through combining ability analysis.

4.3.2 General combining ability (GCA) effects

The estimates of general combining ability effects for ten characters of the parental lines are presented in Table 18. Parents were grouped as good, average and poor general combiners based on their effects. A parent with higher significant GCA effects is considered as a good general combiner, whereas average parents as average combiners. Parents possessed significant but negative or undesirable GCA effects were designated as poor or low combiners (Ahmed *et al.*, 2014). But in case of days to tasseling, days to silking, plant height and ear height negative GCA effects were desirable.

Table 18. General combining ability (GCA) effects of parental inbreds for ten characters in 7X7 half diallel of maize pooled over five environments

Parents	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel/row	Thousand grain weight (g)	Grain yield (t/ha)
P1(CML 330)	-0.91**	-1.09**	-13.07**	-7.85**	0.19**	0.05**	0.05	-0.49*	11.02**	-0.38**
P2(CML 332)	-0.91**	-0.73*	-10.58**	-6.30**	-0.98**	0.01	-0.03	-0.44*	-6.85*	-0.74**
P3(CML 322)	1.00**	0.91**	6.40**	7.39**	-0.35**	0.01	0.27**	-0.52*	1.25	0.18**
P4(CML 311)	-1.22**	-1.20**	6.28**	2.89**	0.36**	0.06**	0.26**	0.20	-11.33**	0.13*
P5(CML 331)	1.36**	1.28**	-5.28**	-7.27**	0.05	-0.02*	-0.30**	-0.08	-2.27	-0.21**
P6(CML 518)	-0.03	0.14	6.69**	4.61**	-0.13*	0.15**	0.50**	0.22	4.94	0.75**
P7(CML 383)	0.70**	0.68*	9.56**	6.54**	0.86**	-0.25**	-0.74**	1.12**	3.23	0.27**
SE	0.12	0.22	1.42	0.60	0.05	0.01	0.05	0.15	2.93	0.05

4.3.2.1 Days to tasseling and days to silking

A significant and negative GCA effect for days to tasseling and days to silking was observed in P1 (CML 330), P2 (CML 332) and P4 (CML 311) but positive significant variation found in P3 (CML 322), P5 (CML 331) and P7 (CML 383) (Table 18). Due to importance of early maturity, lower values of days to tasseling and silking are desirable because as those were observed to be associated with earliness and indicating the potential advantage of inbred lines for development of early maturing hybrids. Significant negative GCA effects were considered as good combiners for this character. Early maturing inbred lines based on GCA effects were also noticed by Aminu *et al.* (2014), Sentayehu and Warsi (2015), Matin *et al.* (2016) and Amiruzzaman *et al.* (2013).

4.3.2.2 Plant height (cm) and ear height (cm)

Three parental lines i.e P1 (CML 330), P2 (CML 332) and P5 (CML 331) showed significant negative GCA effects and low mean values, indicated good combiner for short plant and low ear height (Table 18). The shorter plants with low ear height were associated with resistance to lodging (Matin *et al.* 2016). Rest four parental lines P3 (CML 322), P4 (CML 311), P6 (CML 518) and P7 (CML 383) had positive and significant GCA effects which contributed to taller plant type in their crosses. Good general combiner parents for short plant type in maize were also reported by Debnath and Sarker (1990), Uddin *et al.* (2006), Haydar and Paul (2014) and Ahmed *et al.* (2014). The results of significant and negative GCA effect for ear height also in accordance with previous report by Rodrigues and Chaves (2002), Malik *et al.* (2004), Amiruzzaman *et al.* (2010), Begum (2016), Kumar and Babu (2016).

4.3.2.3 Ear length (cm)

Out of seven parents three parents P1 (CML 330), P4 (CML 311), P7 (CML 383) showed significant GCA effects in a positive direction for ear length implying the tendency of the lines to increase ear length and positive but insignificant value of GCA was recorded in one parent P5 (CML 331) (Table 18). Positive GCA effect was also obtained by Rather *et al.*, (2009), Mohammad *et al.*, (2013), Azad *et al.*, (2014) and Purushottam and Shanthakumar (2017) for ear length in some maize inbred lines. However, P2 (CML 332), P3 (CML 322) and P6 (CML 518) revealed negative and significant GCA effect, suggesting that these lines were not good combiners. Negative GCA effect was also obtained by Bayissa *et al.* (2008) and Ahmed *et al.* (2014) for ear length.

4.3.2.4 Ear diameter (cm)

In case of ear diameter highly significant and positive value was identified in P1 (CML 330), P4 (CML 311) and P6 (CML 518) (Table 18). This finding was supported by Prodhan and Rai (1999), Lone (2006), Mohammad *et al.* (2013), Mousa (2014) and Zeleke (2015) whom reported significant GCA effects for cob diameter in maize. Positive but insignificant value of GCA was recorded in two parents P2 (CML 332) and P3 (CML 322). The rest of two parents P5 (CML 331) and P7 (CML 383) were identified undesirable significant negative value.

4.3.2.5 Number of row per ear

Number of row per ear is one of the yields contributing character for which positive and significant GCA effects are desirable. Parents P3 (CML 322), P4 (CML 311) and P6 (CML 518) had significant positive GCA effects for number of row per ear making them good combiners for improving the trait (Table 18). Similar observations were also made by Packiaraj (1995) and Mohammad *et al*. (2013). However, P5 (CML 331) and P7 (CML 383) revealed negative and significant GCA effect for number of row per ear.

4.3.2.6 Number of kernel per row

Out of seven parents only one parent P7 (CML 383) showed significant GCA effects in a positive direction for number of kernel per row implying the tendency of the lines to increase kernel number (Table 18). Premalatha *et al.* (2011), Abuali *et al.* (2012), Ahmed *et al.* (2014) and Purushottam and Shanthakumar (2017) also reported positive and significant GCA effects for this trait. Three parents P1 (CML 330), P2 (CML 332) and P3 (CML 322) revealed negative and significant GCA effect, suggesting that these lines were not good combiners.

CML 311 **CML 322**

CML 383 **CML 518**

Plate 14.The ear of four good general combiner parents

4.3.2.7 Thousand grain weight (g)

Positive estimates for this trait are desirable since bold grain directly contribute to yield in maize. Out of seven parents only P1 (CML 330) showed significant GCA effects in a positive direction for thousand grain weight (Table 18) implying the tendency of the lines to increase grain yield via bold grain and positive but insignificant value of GCA was recorded in P3 (CML 322), P6 (CML 518) and P7 (CML 383). This finding was in consistent with Ahmed *et al.* (2014). Two parental lines P2 (CML 332) and P4 (CML 311) had negative and significant value which contributed to gave lower yield.

4.3.2.8 Grain yield (ton/ha)

P6 (CML 518) was the best general combiner for grain yield, with highly significant and positive GCA effects followed by P7 (CML 383), P3 (CML 322) and P4 (CML 311) (Table 18). This indicated the potential advantage of the parents for development of high-yielding hybrids. Similar observations were also reported by Amiruzzamam *et al.* (2010), Hussain *et al.* (2003) and Ivy and Hawlader (2000). Three parents P1 (CML 330), P2 (CML 332) and P5 (CML 331) had significant, but negative GCA effects for grain yield. The estimate of GCA effects exhibited that the parent line P6 (CML 518) was considered as best general combiner for traits *i.e.* grain yield, ear diameter and number of row per ear and the parent P7 (CML 383), exhibited desirable GCA effects for grain yield, ear length and number of kernel per row. So, these parents could be used extensively in hybrid breeding programme to increase maize grain yield with superior ear traits. The parent P4 (CML 311) for both days to tasseling and silking exhibited significant negative GCA effects along with significant positive effect for yield, ear length, ear diameter, number of row per ear. So considering all traits P6 (CML 518), P7 (CML 383) P4 (CML 311) were good general combiners which could effectively be used in future breeding program for development of high yielding hybrids with desirable traits.

4.3.3 Specific combining ability (SCA) effects

The estimates of specific combining ability effects for ten characters of the parental lines are presented in Table 19. The SCA effects represent mainly dominance, additive × dominance, dominance × dominance effects. The crosses showing SCA effects involving parents with good GCA could be exploited.

4.3.3.1 Days to to tasseling and days to silking

Negative estimates are considered desirable for days to tasseling and silking, as they are observed to be associated with earliness. Four crosses viz. CML 331×CML 518 (E19), CML 331×CML 383 (E20), CML 322×CML 311 (E12) and CML 332×CML 311 (E8) showed desirable significant negative SCA effects for days to tasseling and one cross CML 331×CML 383 (E20) for days to silking indicating to have earliness (Table 19). CML 331×CML 383 (E20) was considered as best combination for early maturity due to its highest negative significant SCA value. Amiruzzamam *et al.* (2013) and Matin *et al.* (2016) observed earliness on different crosses.

4.3.3.2 Plant height (cm) and ear height (cm)

For plant height, cross combination CML 330×CML 311(E3) was the tallest cross showing the highest positive and significant SCA effect, while CML 332×CML 331(E9) exhibited highest negative and significant SCA effect (Table 19). Four crosses viz. CML 332×CML 331(E9), CML 322×CML 311(E12), CML 330× CML 332(E1) and CML 311×CML 383(E18) manifested significant SCA effects in desirable direction for ear height, indicating that the crosses had a good specific combination for shorter ear placement. Among all the cross combinations CML 332×CML 331(E9) showed desirable significant negative SCA effects both for plant and ear height, indicates dwarf type hybrids with lower ear placement. Ahmed *et al.* (2014) and Begum (2016) also found dwarf type plant in their observation.

4.3.3.3 Ear length (cm)

Out of twenty one cross combination, there were eight crosses found to have highly significant SCA effects for ear length in which five with positive value (Table 19). The cross combination CML 331×CML 518 (E19) produced the highest significant positive effects. The other combinations which produced highly significant and positive SCA effects were CML 330×CML 332 (E1), CML 331×CML 383 (E20), CML 311×CML 331 (E16) and CML 332×CML 311 (E8) considered as the best specific combiner for the trait concerned. So for obtaining desirable hybrid with longer ear length these cross combinations could be selected for future breeding program.

Table 19. Specific combining ability (SCA) effects of F$_1$'s for ten characters of maize pooled over five environments

Crosses	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel/row	Thousand grain weight (g)	Grain yield (t/ha)
1. CML 330× CML 332(E1)	-0.64	-0.71	-4.85	-4.85*	0.77**	-0.07*	-0.07	0.60	-7.97	-0.49**
2. CML 330× CML 322(E2)	0.79*	0.85	-7.11	1.26	-0.21	0.03	0.08	0.55	7.07	0.26*
3. CML 330× CML 311(E3)	0.20	-0.11	9.73*	-0.42	0.15	0.05	0.21	-1.26*	10.04	-0.04
4. CML 330× CML 331(E4)	0.76*	1.08	-4.99	2.93	-0.15	-0.02	-0.36*	0.33	-1.74	0.40*
5. CML 330× CML 518(E5)	-0.59	-0.84	7.10	1.36	-0.67**	0.00	0.43*	-1.51**	2.18	0.02
6. CML 330× CML 383(E6)	-0.52	-0.26	0.12	-0.28	0.11	0.01	-0.29*	1.29*	-9.58	-0.15
7. CML 332× CML 322(E7)	-0.35	0.09	9.26*	4.08*	0.29	0.05	0.18	-0.35	16.54*	0.09
8. CML 332× CML 311(E8)	-0.67*	-1.00	5.97	7.46**	0.59**	0.01	0.33*	1.22*	3.11	0.72**
9. CML 332×CML 331(E9)	1.36**	1.92*	-12.07*	-12.76**	-1.99**	-0.25**	-0.09	-2.65**	-30.74**	-2.31**
10. CML 332×CML 518(E10)	0.81*	0.66	-2.99	2.95	0.19	0.25**	0.26	0.55	5.78	1.11**
11. CML 332×CML 383(E11)	-0.52	-0.95	4.68	3.12	0.15	0.01	-0.61**	0.63	13.28	0.89**
12. CML 322×CML 311(E12)	-0.77*	-0.38	-7.13	-6.71**	0.06	-0.02	0.03	1.18*	-6.92	-0.47**
13. CML 322×CML 331(E13)	0.39	0.28	-1.16	1.93	-0.09	-0.06*	-0.07	-1.71**	-4.04	-0.24
14. CML 322×CML 518(E14)	-0.16	-0.98	5.09	-0.36	-0.18	-0.10*	-0.59**	0.29	-10.18	0.66**
15. CML 322×CML 383(E15)	0.11	0.14	1.06	-0.20	0.13	0.10*	0.37*	0.04	-2.48	-0.30*
16. CML 311×CML 331(E16)	-0.13	-0.28	4.46	4.79*	0.62**	0.15**	-0.23	2.03**	3.14	1.41**
17. CML 311×CML 518(E17)	0.19**	0.60	-6.30	-1.46	-0.23	-0.14**	-0.75**	-0.32	-0.14	-0.66**
18. CML 311×CML 383(E18)	1.19**	1.18	-6.73	-3.66*	-1.19**	-0.04	0.40*	-2.85**	-9.24	-0.97**
19. CML 331×CML 518(E19)	-1.19**	-1.15	4.99	-0.20	0.85**	0.12**	0.63**	1.05*	13.87	-0.46**
20. CML 331×CML 383(E20)	-1.19**	-1.83*	8.76*	3.30	0.75**	0.06	0.12	0.95*	19.51*	1.20**
21. CML 518×CML 383(E21)	0.93*	1.72*	-7.89	-2.29	0.05	-0.13**	0.01	-0.06	-11.50	-0.66**
SE	0.32	0.60	3.96	1.67	0.14	0.03	0.14	0.42	8.15	0.13

The results were agreement with the results of Premalatha *et al.* (2011), Zeleke (2015) and Aslam *et al.* (2017).

4.3.3.4 Ear diameter (cm)

In case of ear diameter the highest significant and positive SCA effects was obtained in the cross CML 332×CML 518 (E10) which was followed by CML 311×CML 331 (E16), CML 331×CML 518 (E19) and CML 322×CML 383 (E15). Thus the two combinations CML 332×CML 518 (E10) and CML 311×CML 331 (E16) were considered as the best specific combiner for this trait which indicated that these combinations would be effective for thick ear as well as higher yield (Table 19). Rather *et al.* (2009); Haydar and Paul (2014) and Purushottam and Shanthakumar (2017) also estimated maximum SCA effects for ear diameter. The negative and significant SCA effect for ear diameter contributed to lower yield.

4.3.3.5 Number of row per ear

The crosses CML 331×CML 518 (E19), CML 330×CML 518 (E5), CML 311×CML 383 (E18), CML 322×CML 383 (E15) and CML 332× CML 311 (E8) reported significant higher SCA effects for kernel rows per ear in positive direction which was desirable for getting higher yield (Table 19). Among five cross combination CML 331×CML 518 (E19) was the best specific combiner for number of row per ear. Similar results were also observed by Alamine *et al.* (2003), Todkar and Navale (2006), Zeleke (2015) and Aslam *et al.* (2017).

4.3.3.6 Number of kernel per row

In case of number of kernel per row, out of twenty one crosses six cross combinations viz. CML 311×CML 331 (E16), CML 330×CML 383 (E6), CML 332×CML 311 (E8), CML 322×CML 311 (E12), CML 331×CML 518 (E19) and CML 331×CML 383 (E20) produced the highest SCA effect which might be selected as the best specific combiner for one of the important yield contributing trait (Table 19). Negative and significant SCA effect was showed by five cross combinations CML 311×CML 383 (E18), CML 332×CML 331 (E9), CML 322×CML 331 (E13), CML 330×CML 518 (E5) and CML 330× CML 311 (E3) which were denoted as poor specific combiner for the character

Plate 15. The ear of top four hybrids having good SCA for yield

concerned. The results were agreement with the results of Premalatha *et al.* (2011), Abuali *et al.* (2012), Ahmed *et al.* (2014).

4.3.3.7 Thousand grain weight (g)

Bold grain is one of the most yield contributing traits for getting higher yield in maize. Esimates of positive significant SCA effects for thousand grain weight were more frequently associated with significant SCA effect of kernel yield (Table 19). Only two cross combinations CML 331×CML 383 (E20) and CML 332×CML 322 (E7) exhibited significant effect in positive direction and one cross CML 332×CML 331 (E9) gave significant effect in negative direction. This finding was in consistent with Ahmed *et al.* (2014), Begum (2016) and Matin *et al.* (2016).

4.3.3.8 Grain yield (t/ha)

Out of twenty one F_1, eight crosses viz. CML 311×CML 331 (E16), CML 331×CML 383 (E20), CML 332×CML 518 (E10), CML 332×CML 383 (E11), CML 332× CML 311(E8), CML 322×CML 518(E14), CML 330× CML 331(E4) and CML 330× CML 322(E2) showed significant positive SCA effects for yield. In most of the cases, one or both parents were good combiners, which indicated the vital role of parental lines' GCA (Table 19). Similar results were also reported by Xingming *et al.* (2002). Positive SCA indicate that lines were in opposite heterotic groups, while negative SCA effects indicate lines were in the same heterotic group (Vasal *et al.*, 1992). Vasal (1998) also revealed that enrollment of at least one good combiner in crossing program prioritize higher heterosis in maize which confirmed the findings of the present study. Among eight crosses, CML 311×CML 331 (E16) had high × low combiners; CML 322×CML 518 (E14) had high x high; CML 331×CML 383 (E20), CML 332×CML 518 (E10), CML 332×CML 383 (E11), CML 330× CML 322 (E2) and CML 332× CML 311 (E8) involved of low × high; CML 330× CML 331 (E4) had low × low general combiners. Roy *et al.* (1998) noticed that the best crosses for yield and yield contributing characters involved of high × high, high × low, high × average and low × average general combiners for SCA effects in their study. The observations of the above results indicated that additive × additive, additive × dominance and dominance × dominance gene interaction were responsible for derivation of good specific cross for higher grain yield.

In general, the GCA effects of the parents were reflected in the SCA effects of the crosses in most of the studied traits. Moreover, Amiruzzaman *et al*. (2011) also pointed out that the SCA was a result of the interaction of GCA effects of the parents and that it could improve or deteriorate the hybrid expression compared to the expected effect based on GCA only.

4.3.4 Heterosis

Generally standard heterosis is measured over a commercially cultivated popular variety or hybrid variety is integrated for comparison during release of new hybrid variety. In this experiment BHM 12, BHM 13 and BHM 14 were included as a check variety for better comparison of ten yield contributing characters of the twenty one experimental hybrids. Percent heterosis for different characters of the F_1 hybrids over standard check values are shown in Table 20, Table 21 and Table 22. The percent of heterosis in crosses varied from character to character or from cross to cross.

4.3.4.1 Days to 50% tasseling

Days to tasseling indicates the earliness or lateness of a hybrid. Negative heterosis is desirable for this trait. Twelve hybrids showed negative crosses which ranged from -3.31 to 2.46% and among them eight hybrids showed significant value. Highly negative significant heterosis (-3.31%) was provided by the hybrid CML 332× CML 311 (E8) for days to tasseling over BHM 12 (Table 20) which was followed by the crosses CML 330×CML 332 (E1), CML 330×CML 311 (E3), CML 330×CML 518 (E5) and CML 311×CML 518 (E17) and the other nine hybrids showed positive heterosis which was not desirable. When BHM 13 was considered as a check all the hybrids showed the significant negative heterosis except CML 322×CML 331 (E13) (Table 21). The highest significant standard heterosis was obtained from CML 332×CML 311 (E8) which showed -5.50% heterosis. Considering hybrid BHM 14 as a check no negative heterosis was observed there (Table 22). Earlier Maryam and Jones (1985), Ganguli *et al.* (1989), Amiruzzamam *et al.* (2013), Sentayehu and Warsi (2015) and Begum (2016) reported negative significant heterotic values for days to tasseling over check variety.

4.3.4.2 Days to 50% silking

Considering BHM 12 as a check, fifteen hybrids showed significant negative heterosis which was desirable for selection of hybrid with short duration (Table 20). The standard heterosis was in respect of days to silking from -5.33% to 0.14% over BHM 13 (Table 21). Among twenty one hybrids except four all the hybids produced significant negative heterotic value. The combination CML 332×CML 311 (E8) represented the highest negative heterosis (-3.99% and -5.33%) over BHM 12 and BHM 13, respectively. Hence for early maturity hybrid breeding this hybrid combination was marked as suitable When BHM 14 was considered as a check (Table 22) all the hybrids showed the significant positive heterosis which was not desirable for this trait. Ram *et al* (2015) and Matin *et al*. (2016) reported that earliness is associated with days to silking.

4.3.4.3 Plant height (cm)

Negative heterosis is also desirable for plant height which helps to develop short statured plant preventing lodging. For plant height except two all the hybrids expressed significant negative heterosis over BHM 12 (Table 19) which ranged from -22.70% (CML 330×CML 332) to -1.18% (CML 322×CML 518). Considering BHM 13 as a check, except two nineteen hybrids showed negative heterosis indicating dwarfness which was desirable for selection of hybrid (Table 20). All twenty one hybrids exhibited standard heterosis in positive direction in respect of plant height over the check variety BHM 14 (Table 22). Amiruzzamam *et al.* (2013) and Azad *et al*. (2014) found significant negative heterosis for this trait.

4.3.4.4 Ear height (cm)

Generally the shorter plants with low ear height are associated with resistance to lodging. Out of twenty one hybrid except six hybrids all of them showed significant negative heterotic value for ear height (Table 20) over BHM 12 where CML 332×CML 331(E9) produced the highest significant negative heterosis (-34.25%). Considering BHM 13 as a check, except two all the hybrids showed significant negative heterosis which was desirable for selection of hybrid. The standard heterosis ranged from -36.49% to 2.19% (Table 21). When BHM 14 was considered as a check negative heterosis which was desirable for selection of hybrid. The standard heterosis ranged from

Table 20. Percent heterosis over the check variety BARI Hybrid Maize 12 for different characters in 7x7 diallel crosses of maize over five environments

Crosses	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel /row	Thousand grain weight (g)	Grain yield (t/ha)
1. CML-330× CML-332(E1)	-2.95**	-3.58**	-22.70**	-27.75**	-14.29**	6.18**	1.96**	-12.12**	8.22**	-22.20**
2. CML-330× CML-322(E2)	0.56	-0.33	-16.40**	-5.20*	-15.96**	8.17**	5.23**	-12.97**	13.91**	-7.01**
3. CML-330× CML-311(E3)	-2.39**	-3.45**	-8.06**	-17.52**	-10.85**	9.36**	6.18**	-15.76**	11.55**	-10.10**
4. CML-330× CML-331(E4)	0.91*	0.27	-20.62**	-21.63**	-13.76**	6.57**	-2.11*	-12.38**	10.88**	-9.28**
5. CML-330× CML-518(E5)	-1.97**	-2.77**	-9.00**	-11.10**	-17.15**	10.36**	9.52**	-16.35**	13.61**	-4.09
6. CML-330× CML-383(E6)	-1.13**	-1.68**	-11.33**	-9.17**	-8.65**	2.39**	-4.80**	-6.89**	10.30**	-9.92**
7. CML-332× CML-322(E7)	-0.63	-0.74*	-7.06**	-3.79	-19.11**	7.77**	5.45**	-15.15**	11.84**	-11.83**
8. CML-332× CML-311(E8)	-3.31**	-3.99**	-10.00**	-7.1	-14.33**	7.97**	6.47**	-9.28**	5.45**	-6.46**
9. CML-332×CML-331(E9)	1.54**	1.49**	-21.80**	-34.25**	-28.09**	1.20	-0.65	-19.91**	-0.64	-37.12**
10. CML-332×CML-518(E10)	-0.50	-0.94*	-12.65**	-8.64**	-18.63**	14.34**	7.70**	-10.94**	10.11**	2.64
11. CML-332×CML-383(E11)	-1.13**	-2.03**	-7.87**	-5.25*	-14.09**	1.79*	-7.63**	-8.46**	11.53**	-3.73
12. CML-322×CML-311(E12)	-1.41**	-1.68**	-7.06**	-6.93**	-13.90**	7.57**	6.47**	-9.58**	4.98**	-9.83**
13. CML-322×CML-331(E13)	2.46**	1.49**	-9.15**	-5.62*	-16.01**	4.78**	1.60	-17.71**	7.91**	-10.01**
14. CML-322×CML-518(E14)	0.42	-0.94*	-1.18	2.71	-17.39**	7.57**	3.71**	-11.81**	8.17**	6.92**
15. CML-322×CML-383(E15)	1.54**	0.75*	-2.13	5.79*	-11.18**	3.59**	1.67	-10.15**	9.65**	-6.28**
16. CML-311×CML-331(E16)	-0.36	-1.22**	-6.82**	-10.53**	-9.27**	10.16**	0.44	-6.23**	6.58**	4.73*
17. CML-311×CML-518(E17)	-1.48**	-1.48**	-6.73**	-6.14**	-14.19**	7.57**	2.40*	-11.51**	7.55**	-5.46*
18. CML-311×CML-383(E18)	0.35	-0.33	-5.45**	-3.07	-14.05**	1.79*	1.82	-15.71**	4.90**	-12.74**
19. CML-331×CML-518(E19)	-0.21	-0.74*	-6.54**	-13.80**	-10.51**	11.16**	8.43**	-8.74**	13.22**	-6.82**
20. CML-331×CML-383(E20)	0.77*	-0.87*	-3.03*	-8.35**	-6.26**	1.99*	-4.29**	-6.69**	14.18**	4.00
21. CML-518×CML-383(E21)	1.33**	1.56**	-5.55**	-0.69	-10.51**	1.79*	0.73	-8.51**	8.34**	-4.28
Minimum	-3.31	-3.99	-22.70	-34.25	-28.09	1.20	-7.63	-19.91	-0.64	-37.12
Maximum	2.46	1.56	-1.18	5.79	-6.26	14.34	9.52	-6.23	14.18	6.92
CD (5%)	0.71	0.73	2.78	4.31	2.11	1.68	2.08	1.74	1.66	4.32
CD (1%)	0.97	1.00	3.80	5.88	2.87	2.29	2.83	2.38	2.27	5.90

Table 21. Percent heterosis over the check variety BARI Hybrid Maize 13 for different characters in 7x7 diallel crosses of maize over five environments

Crosses	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel /row	Thousand grain weight (g)	Grain yield (t/ha)
1. CML-330× CML-332(E1)	-5.15**	-4.93**	-20.52**	-30.21**	-1.81	5.54**	4.39**	-4.48**	-0.93	-20.76**
2. CML-330× CML-322(E2)	-1.72**	-1.73**	-14.04**	-8.43**	-3.72*	7.52**	7.74**	-5.40**	4.27**	-5.28**
3. CML-330× CML-311(E3)	-4.60**	-4.80**	-5.46**	-20.33**	2.13	8.71**	8.71**	-8.44**	2.11**	-8.43**
4. CML-330× CML-331(E4)	-1.38**	-1.13**	-18.37**	-24.31**	-1.20	5.94**	0.22	-4.76**	1.50	-7.60**
5. CML-330× CML-518(E5)	-4.19**	-4.13**	-6.43**	-14.13**	-5.09**	9.70**	12.13**	-9.08**	4.00**	-2.32
6. CML-330× CML-383(E6)	-3.37**	-3.06**	-8.82**	-12.27**	4.65**	1.78*	-2.53*	1.20	0.97	-8.25**
7. CML-332× CML-322(E7)	-2.88**	-2.13**	-4.43**	-7.07**	-7.33**	7.13**	7.96**	-7.77**	2.38**	-10.19**
8. CML-332× CML-311(E8)	-5.50**	-5.33**	-7.46**	-10.30**	-1.86	7.33**	9.00**	-1.39	-3.46**	-4.73*
9. CML-332×CML-331(E9)	-0.76*	0.07	-19.59**	-36.49**	-17.62**	0.59	1.71	-12.95**	-9.04**	-35.96*
10. CML-332×CML-518(E10)	-2.75**	-2.33**	-10.19**	-11.76**	-6.79**	13.66**	10.27**	-3.20**	0.79	4.54*
11. CML-332×CML-383(E11)	-3.37**	-3.40**	-5.26**	-8.48**	-1.59	1.19	-5.43**	-0.50	2.10**	-1.95
12. CML-322×CML-311(E12)	-3.65**	-3.06**	-4.43**	-10.10**	-1.37	6.93**	9.00**	-1.73*	-3.90**	-8.16**
13. CML-322×CML-331(E13)	0.13	0.07	-6.58**	-8.84**	-3.78**	4.16**	4.02**	-10.56**	-1.21	-8.34**
14. CML-322×CML-518(E14)	-1.85**	-2.33**	1.61	-0.80	-5.36**	6.93**	6.18**	-4.15**	-0.97	8.90**
15. CML-322×CML-383(E15)	-0.76*	-0.66	0.63	2.19	1.75	2.97**	4.09**	-2.34*	0.38	-4.54*
16. CML-311×CML-331(E16)	-2.62**	-2.60**	-4.19**	-13.59**	3.94**	9.50**	2.83*	1.92*	-2.43**	6.67**
17. CML-311×CML-518(E17)	-3.71**	-2.86**	-4.09**	-9.34**	-1.70	6.93**	4.84**	-3.82**	-1.55*	-3.71
18. CML-311×CML-383(E18)	-1.93**	-1.73**	-2.78*	-6.38**	-1.53	1.19	4.24**	-8.38**	-3.97**	-11.12**
19. CML-331×CML-518(E19)	-2.47**	-2.13**	-3.90*	-16.74**	2.52**	10.50**	11.01**	-0.81	3.64**	-5.10*
20. CML-331×CML-383(E20)	-1.51**	-2.26**	-0.29	-11.47**	7.39**	1.39	-2.01	1.42	4.53**	5.93*
21. CML-518×CML-383(E21)	-0.97**	0.14	-2.88*	-4.08	2.52*	1.19	3.13**	-0.56	-0.83	-2.50
Minimum	-5.50	-5.33	-20.52	-36.49	-17.62	0.59	-5.43	-12.95	-9.04	-35.96
Maximum	0.13	0.14	1.61	2.19	7.39	13.66	12.13	1.92	4.53	8.90
CD (5%)	0.69	0.72	2.86	4.16	2.41	1.67	2.13	1.89	1.52	4.40
CD (1%)	0.95	0.98	3.90	5.67	3.29	2.28	2.90	2.58	2.07	6.01

Table 22. Percent heterosis over the check variety BARI Hybrid Maize 14 for different characters in 7x7 diallel crosses of maize over five environments

Crosses	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel /row	Thousand grain weight (g)	Grain yield (t/ha)
1. CML-330× CML-332(E1)	4.86**	5.17**	1.39	40.45**	5.78**	5.34**	-2.03*	8.00**	5.31**	0.59
2. CML-330× CML-322(E2)	8.66**	8.71**	9.66**	84.28**	3.71**	7.31**	1.12	6.96**	10.84**	20.24**
3. CML-330× CML-311(E3)	5.47**	5.31**	20.62**	60.33**	10.02**	8.50**	2.03*	3.53**	8.54**	16.24**
4. CML-330× CML-331(E4)	9.03**	9.38**	4.13*	52.33**	6.43**	5.73**	-5.94**	7.69**	7.89**	17.29**
5. CML-330× CML-518(E5)	5.92**	6.06**	19.37**	72.81**	2.24	9.49**	5.24**	2.80*	10.55**	24.00**
6. CML-330× CML-383(E6)	6.83**	7.24**	16.32**	76.56**	12.74**	1.58*	-8.52**	14.43**	7.33**	16.47**
7. CML-332× CML-322(E7)	7.37**	8.27**	21.92**	87.02**	-0.18	6.92**	1.33	4.28**	8.83**	14.00**
8. CML-332× CML-311(E8)	4.48**	4.73**	18.06**	80.51**	5.72**	7.11**	2.30*	11.50**	2.61**	20.94**
9. CML-332×CML-331(E9)	9.72**	10.71**	2.57	27.81**	-11.26**	0.40	-4.54**	-1.57	-3.32**	-18.71**
10. CML-332×CML-518(E10)	7.52**	8.05**	14.58**	77.58**	0.41	13.44**	3.49**	9.45**	7.14**	32.71**
11. CML-332×CML-383(E11)	6.83**	6.86**	20.86**	84.19**	6.01**	0.99	-11.24**	12.50**	8.53**	24.47**
12. CML-322×CML-311(E12)	6.53**	7.24**	21.92**	80.92**	6.25**	6.72**	2.30*	11.12**	2.15**	16.59**
13. CML-322×CML-331(E13)	10.71**	10.71**	19.18**	83.46**	3.66**	3.95**	-2.37*	1.13	5.00**	16.35**
14. CML-322×CML-518(E14)	8.51**	8.05**	29.64**	99.65**	1.95	6.72**	-0.35	8.38**	5.26**	38.24**
15. CML-322×CML-383(E15)	9.72**	9.90**	28.39**	105.65**	9.61**	2.77**	-2.30*	10.43**	6.69**	21.18**
16. CML-311×CML-331(E16)	7.67**	7.75**	22.23**	73.91**	11.97**	9.29**	-3.49**	15.24**	3.71**	35.41**
17. CML-311×CML-518(E17)	6.46**	7.46**	22.36**	82.45**	5.90**	6.72**	-1.61	8.76**	4.65**	22.24**
18. CML-311×CML-383(E18)	8.43**	8.71**	24.04**	88.42**	6.07**	0.99	-2.16*	3.59**	2.07*	12.82**
19. CML-331×CML-518(E19)	7.82**	8.27**	22.61**	67.57**	10.44**	10.28**	4.19**	12.16**	10.17**	20.47**
20. CML-331×CML-383(E20)	8.88**	8.13**	27.21**	78.16**	15.68**	1.19**	-8.03**	14.68**	11.11**	34.47**
21. CML-518×CML-383(E21)	9.49**	10.78**	23.91	93.04**	10.44**	0.99	-3.21**	12.44**	5.42**	23.76**
Minimum	4.48	4.73	1.39	27.81	-11.26	0.40	-11.24	-1.57	-3.32	-18.71
Maximum	10.71	10.78	29.64	105.65	15.68	13.44	5.24	15.24	11.11	38.24
CD (5%)	0.77	0.80	3.65	8.37	2.60	1.67	2.00	2.14	1.62	5.59
CD (1%)	1.05	1.09	4.99	11.42	3.55	2.27	2.72	2.92	2.21	7.62

-36.49% to 2.19% (Table 21). When BHM 14 was considered as a check (Table 22) all the hybrids showed the positive heterosis which was not desirable for this trait. Sentayehu and Warsi (2015) and Ram *et al*. (2016) also observed heterosis value in negative direction for ear height.

4.3.4.5 Ear length (cm)

In case of ear length, none of the hybrids exhibited positive heterosis over BHM 12 (Table 20). The result of standard heterosis computed relative to BHM 13 among tested hybrids showed that five hybrids manifested significant positive heterosis and CML 331× CML 383 (E20) produced the highest positive heterotic value (Table 21). When BHM 14 was considered as a check (Table 22) sixteen hybrids showed the significant positive heterosis which was desirable for this trait and and the hetesosis ranged from -11.26% to 15.68%. Amiruzzamam *et al.* (2013), Sentayehu and Warsi (2015) and Begum (2016) reported positive and negative heterosis for ear length.

4.3.4.6 Ear diameter (cm)

The range of standard heterosis was 1.20% to 14.34%, 0.59% to 13.66% and 0.40% to 13.44% over BHM 12, BHM 13 and BHM 14, respectively and positive heterosis was expressed by all the hybrids (Table 20, Table 21 and Table 22). In all the cases CML 332×CML 518(E10) showed the highest significant positive heterotic value which was followed by the CML 331×CML 518(E19), CML 330× CML 518(E5) and CML 311×CML 331(E16). So these four hybrids might be selected for the getting the maximum ear diameter. Azad *et al*. (2014) and Hossain (2016) also observed positive heterosis for ear diameter.

4.3.4.7 Number of row per ear

Considering BHM 12 as a check, eleven hybrids showed positive heterosis which was desirable for selection of hybrid (Table 20) and the standard heterosis in respect of number of row per ear from -7.63% to 9.52% over BHM 12. Among twenty one hybrids all the hybids produced significant positive heterotic value over BHM 13 except five hybrids (Table 21). When BHM 14 was considered as a check (Table 22) six hybrids showed the significant positive heterosis. The combination CML

330×CML 518 (E5) represented the highest significant positive heterosis over all the checks for this trait. Azad *et al* (2014) and Mahmood *et al*. (2016) reported maximum number of row associated with higher yield.

4.3.4.8 Number of kernel per row

Among twenty one tested hybrids none of them showed significant positive heterosis over the check BHM 12 (Table 20). The result of standard heterosis computed relative to BHM 13 among tested hybrids showed that only one hybrid exhibited significant positive heterosis and the highest significant positve heterosis was shown by the cross combination CML 311×CML 331 (E16) (Table 21). When BHM 14 was considered as a check (Table 22) the range of standard heterosis was -1.57% to 15.24%, nineteen hybrids showed the significant heterosis in positive direction which was desirable for this trait and CML 311×CML 331 (E16) possessed the highest significant positive heterotic value. Positive and negative heterosis for number of kernel per row was also confirmed by Azad *et al*. (2014) and Mahmood *et al*. (2016).

4.3.4.9 Thousand grain weight (g)

For thousand grain weight the ranges of standard heterosis varied from -0.64% to 14.18%, -9.04% to 4.53% and -3.32% to 11.11% over BHM 12, BHM 13 and BHM 14, respectively. Among twenty one tested hybrids, all hybrids showed significant positive heterosis over the check BHM 12 except one (Table 20). When BHM 13 was considered as a check (Table 21) seven hybrids showed significant positive value. Considering BHM 14 as a check, except one cross combination all the hybrids showed significant positive heterosis and hybrid CML 331×CML 383 (E20) expressed highest significant positive heterotic value in all the cases (Table 22). Matin *et al*. (2016) and Begum (2016) also observed positive and negative heterosis for thousand grain weight (g).

4.3.4.10 Grain yield (ton/ha)

In case of grain yield out of twenty one hybrids, only two hybrids i.e CML 322×CML 518(E14) and CML 311×CML 331(E16) exhibited significant positive heterosis over BHM 12 (Table 20). The result of standard heterosis computed relative to BHM 13 among tested hybrids showed that four hybrids viz. CML 322×CML 518 (E14), CML 311×CML 331 (E16), CML 331×CML 383 (E20) and CML 332×CML 518 (E10) manifested significant positive heterosis and CML 322×CML 518 (E14) produced the highest significant positive heterotic value (Table 21). When BHM 14 was considered as a check (Table 22) nineteen hybrids showed the significant positive heterosis which was desirable for this trait and the hetesosis ranged from -18.71% to 38.24%. Appreciable percentage of heterosis for grain yield in maize was also reported by Amiruzzamam *et al.* (2013), Azad *et al* (2014), Sentayehu and Warsi (2015) and Begum (2016).

4.4 Experiment 4: Adaptation of single cross white maize hybrids in different agro-ecological zones.

In most breeding programmes one of the main complications for selection of broad adaptation genotypes with superior grain yield, quality and other desirable characteristics over a wide range of different environmental conditions is genotype x environment (G x E) interaction. It is known fact that due to genotype x environment interactions (G X E) the genotypes performing well under a particular environment may or may not perform well over the other environments. The development of variety with wide adaptability necessitates because if care is not taken to select for both yield and stability of performance, one may end-up with a high yielding genotype that is suitable only for a particular environment. For this reason this experiment was conducted with twenty one F_1 hybrid with three checks (BARI Hybrid Maize 12, BARI Hybrid Maize 13 and BARI Hybrid Maize 14) at five different locations; Barishal, Dinajpur, Chattogram, Jashore and Jamalpur. The data pertaining to maize hybrids for yield and yield contributing characters at different locations were computed and statistically analyzed. The results obtained from analysis are interpreted under the following headings

4.4.1 Combined analysis of variance

Results of combined analysis of variance for ten characters viz. days to 50% tasseling, days to 50% silking, plant height, ear height, ear length (cm), ear diameter (cm) and kernel row arrangement (number of row per ear and number of kernel per row), thousand grain weight and grain yield (ton/ha) of twenty four hybrids at five environments are presented in Table 23. The mean sums of squares for the genotypes were highly significant for all the traits which revealed the presence of genetic variability in the material under investigation for all the characters studied. Environments mean sum of squares were highly significant for all the characters except number of row per ear and thousand grain weight suggesting that these traits were significantly influenced by environments. The highly significant effects of environment indicate high differential genotypic response across the different environments. The variation in soil structure and moisture across the different environments were considered as a major underlying causal factor for the GXE interaction. Variance for genotype x environment interactions were significant for all characters except plant height and thousand grain weight

Table 23. Full joint analysis of variance including the partitioning of the G×E interaction of maize hybrids

Source of variation	df	Mean sum of squares									
		Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel /row	Thousand grain weight (g)	Grain yield (t/ha)
Genotypes (G)	23	61.75**	70.69**	3367.34**	2273.56**	11.11**	0.36**	4.37**	38.84**	4119.61**	16.66**
Environment (E)	4	3104.05**	3013.05**	6655.61**	2962.55**	75.63**	0.99**	1.06	226.26**	61779.08	7.35**
Interaction G x E	92	12.30**	13.84**	433.16	125.70*	1.96**	0.07**	0.73*	8.88**	2020.18	2.01**
AMMI Component 1	26	23.93**	23.34**	1010.59**	231.00**	2.30**	0.09**	0.93*	12.63**	2746.24	3.38**
AMMI Component 2	24	13.43**	17.01**	301.42	120.21	1.59**	0.04	0.70	9.57*	2055.92*	1.62
AMMI Component 3	22	5.04*	6.99	206.42	89.14	0.80	0.02	0.53	3.67	1727.53	1.54
AMMI Component 4	20	3.80	5.16	89.98	35.62	0.35	0.01	0.21	2.14	1355.33	1.23
Residuals	23	3.09	8.22	420.84	81.71	0.78	0.03	0.50	5.48	1754.16	1.79

it means that in different locations or environments genotypes exhibited different performance which is due to their different genetic makeup or the variation due to the environments or both. In this respect, Comstock and Moll (1963) defined the genotype x environment interaction as the differential response of phenotype to the change in environment, also, Freeman and Perkins (1971) demonstrated that the main cause of differences among genotypes in their yield stability traits were the wide occurrence of genotype x environment interaction. Similar results agreement with Ragheb *et al*. (1993), Mosa *et al*. (2009), Abdallah *et al*. (2011) and Mosa *et al*. (2012). Several investigators [Gamma and Hallaur (1980); Verma and Agarwal (1985) and Prasad and Singh (1991)] also reported the significant difference among genotypes, environments and genotype x environment interactions in maize. Eberhart and Russel (1966) stated that due to the occurrence of genotype x environment interaction the differences among genotypes in their stability arise. For development of high yielding and more uniform hybrids for varied environmental conditions maize breeders are encouraged by such significant interactions. According to Eberhart and Russel (1966) model the partitioning of G x E interactions provide information on predictable and unpredictable source of variation, respectively through the magnitude of linear and non-linear components of variations contributing to genotype x environment interactions for all characters. Since the G x E interactions was found significant for most of the characters, the data of all ten characters were subjected to stability analysis.

A box and whisker plot also called a box plot, created by John W. Tukey, are fantastic little graphs that provides a lot of statistical information in a cute little square and displays the five-number summary of a set of data. The five-number summary is the minimum, first quartile, median, third quartile, and maximum. In a box plot, a box was drawn from the first quartile to the third quartile. The inter-quartile range box represents the middle 50% of the data. At the median a horizontal line goes through the box. The median is a common measure of the center of data. The whiskers go from each quartile to the minimum or maximum i.e it indicates the range of data and they are usually represented as vertical lines ending in a small horizontal line. The whiskers extend from either side of the box. The whiskers represent the ranges for the bottom 25% and the top

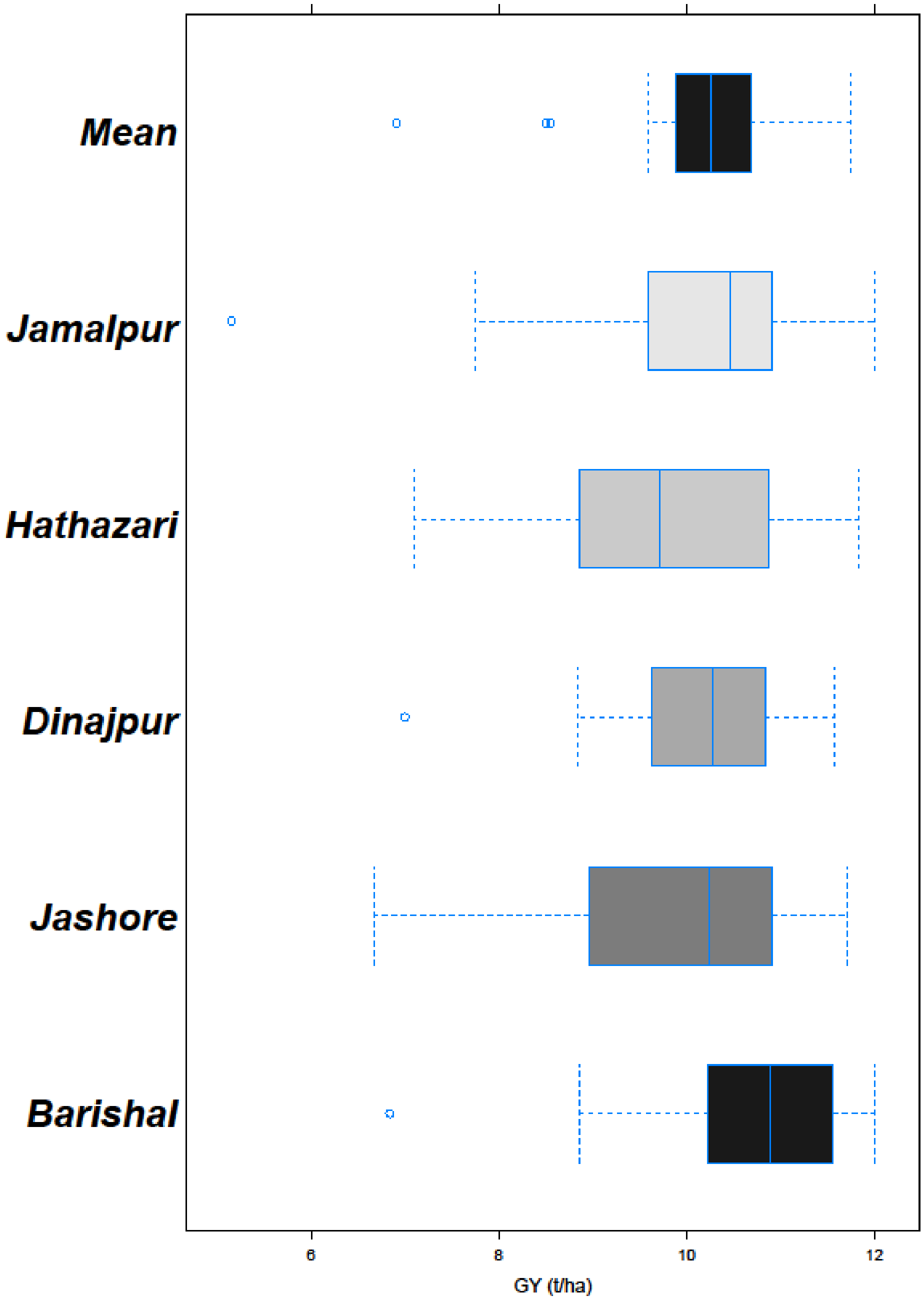

Figure 3. Box plot showing variability in yield in different locations

25% of the data values. Extreme values are also represented by the plot. So boxplot contains a lot of information in a very little space which are useful to show the distribution of a dataset at a glance. Figure 3 explained the phenomenon of heterogeneity of genetic variance in different environments. Heterogeneity implies the magnitude of genetic variance which was observed within individual environments will be changed from one environment to another. In most of the cases in better environment the genetic variance tends to be larger in better environments than in poorer environments, although the opposite can be observed (Przystalskietal *et.al*, 2008). In Figure 3, box plot showed that genotypic variation for grain yield was more at Jashore, Hathazari and Jamalpur where genotypic variation was less at Dinajpur and Barishal and the Barishal location gave the highest grain yield. In Barishal, Dinajpur and Jamalpur locations one genotype gave remarkably lower yield than other genotypes. In case of mean yield over the environment three genotypes gave noticeable lower performance than other.

4.4.2 Assessment of phenotypic index and stability parameters

For judgment of the phenotypic stability of a genotype Eberhart and Russel (1966) accentuated the necessitate of both linear and non linear components of G x E interactions. According to Eberhart and Russel (1966), regression coefficient (bi) is considered as parameter of response of the genotype to varying environments while deviation from regression (S^2di) as the parameter of stability. A variety is considered to be ideal widely adopted and stable one with a high mean yield, regression coefficient equals to one (bi=1) and deviation from regression equals to zero (S^2di=0). A genotype with regression coefficient value less than 1.0 has above average stability i.e comparatively insensitive to change in environment and is especially adaptable to low-performing environments. A genotype with bi value greater than 1.0 has below average stability which is a indication of their responsiveness and especially adaptable to high performing environments and a genotype with bi value equal to 1.0 has average stability and is well or poorly adaptable to all environments depending on high or low mean performance (Finlay and Wilkinson, 1963). However, in most cases, S^2di is considered as stability parameter rather than bi which are more about responsiveness of genotypes Eberhart and Russell, 1966; Becker and Léon, 1988). The linear prediction will invalidate if deviation from regression (S^2di) is significantly different from zero. The performances of a genotype for a given environment may be predicted if S^2di is non-significant. Assessment of phenotypic index (Pi) and stability parameters i.e. mean (x), regression coefficient (bi) and deviation from regression (S^2di) were estimated for characters, days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), ear length (cm), ear diameter (cm) and kernel row arrangement (number of row per ear and number of kernel per row), thousand grain weight and grain yield (ton/ha) and results are discussed in character wise.

4.4.2.1 Days to 50% tasseling

Days to 50% tasseling along with the value of mean performance, their response, phenotypic indices (P_i) regression coefficient (bi), deviation from regression (S^2di) are presented in Table 24. The genotypic mean ranged for days to 50% tasseling is 87.8 to 97.2. The mean value of this character indicated that the cross CML 322×CML 331 required more number of days (97.2), while the hybrid BHM 14 less and the minimum number of days (87.8) to 50 percent tasseling. Over the entire environment mean value for this trait was 94.37. Significant differences were observed for days to 50% tasseling for all locations. Among the tested hybrids, fourteen hybrids showed positive P_i index while the rest ten showed negative P_i index for 50% tasseling date. The genotypes which showed positive P_i index they took longer period for days to tasseling which represents undesirable genotypes and negative P_i index showing genotypes took shorter period for days to 50% tasseling were diserable. In case of environmental index, significant variations across the locations indicated by the range of environmental index (-2.69 to 11.68). For a character positive and negative environmental index (I_J) reflects the rich or favorable and poor or unfavorable environments, respectively. However, negative environmental index are favorable for days to 50% tasseling. Barishal took shorter (89.49 days) period and Dinajpur took longer (105.75 days) period for day to 50% tasseling. The bi and s^2di values range for days to 50% tasseling were 0.65 (CML 332× CML 311) to 1.29 (CML 322×CML 518) and -0.81 (CML 332× CML 311) to 11.77 (BHM 14) respectively. Due to non significant regression coefficient, equal to unity implied the adaptability of genotypes over the tested environments.

Table 24. Estimates of stability parameters for days to 50% tasseling

Crosses	Days to 50% tasseling					Overall mean	P_i	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	88	92	100	93	88	92.07	-2.30	0.69	4.93
2. CML 330× CML 322(E2)	90	93	108	94	92	95.40	1.03	1.09	2.26
3. CML 330× CML 311(E3)	88	92	106	88	89	92.60	-1.77	1.17	-0.47
4. CML 330× CML 331(E4)	92	94	109	92	91	95.73	1.37	1.15	2.65
5. CML 330× CML 518(E5)	89	92	101	92	91	93.00	-1.37	0.67	-0.19
6. CML 330× CML 383(E6)	88	93	105	92	91	93.80	-0.57	0.95	0.17
7. CML 332× CML 322(E7)	90	95	106	89	92	94.27	-0.10	1.05	0.66
8. CML 332× CML 311(E8)	88	92	99	89	90	91.73	-2.64	0.65	-0.81
9. CML 332×CML 331(E9)	91	99	110	89	93	96.33	1.96	1.25	4.55
10. CML 332×CML 518(E10)	90	95	106	92	90	94.40	0.03	0.99	1.17
11. CML 332×CML 383(E11)	87	92	109	89	91	93.80	-0.57	1.29	-0.24
12. CML 322×CML 311(E12)	89	94	104	89	92	93.53	-0.84	0.90	0.83
13. CML 322×CML 331(E13)	93	97	110	92	94	97.20	2.83	1.10	0.31
14. CML 322×CML 518(E14)	90	94	110	91	91	95.27	0.90	1.29	0.00
15. CML 322×CML 383(E15)	92	95	110	89	95	96.33	1.96	1.15	4.38
16. CML 311×CML 331(E16)	88	93	105	94	92	94.53	0.16	0.89	3.10
17. CML 311×CML 518(E17)	88	92	108	90	89	93.47	-0.90	1.25	0.02
18. CML 311×CML 383(E18)	89	94	105	93	94	95.20	0.83	0.87	1.59
19. CML 331×CML 518(E19)	90	96	104	92	92	94.67	0.30	0.85	0.33
20. CML 331×CML 383(E20)	90	96	108	89	95	95.60	1.23	1.11	3.01
21. CML 518×CML 383(E21)	92	96	107	89	95	96.13	1.76	0.99	4.75
22.BHM 12(E22)	87	97	105	90	95	94.87	0.50	0.95	7.46
23.BHM 13(E23)	91	97	108	94	96	97.07	2.70	0.99	0.53
24.BHM 14(E24)	85	84	97	90	83	87.80	-6.57	0.70	11.77
E.mean	89.49	93.94	105.75	90.97	91.68	**94.37**			
E.index (I_J)	-4.88	-0.43	11.38	-3.40	-2.69				
LSD(0.05)	1.22	1.59	4.4	2.33	2.84				

Two cross combinations CML 330×CML 383 (E6) and CML 332×CML 322(E7) were found stable for days to 50% tasseling under environmental changes having negative phenotypic index, near unit regression coefficient (bi), non significant deviation from regression (S^2di=0). These results are in line with the reports Sharma and Saikia (2001), Kumar and Singh (2004b) and Kaundal and Sharma (2006).

4.4.2.2 Days to 50% silking

Stability parameters in respect of days to 50% silking are given in Table 25. The genotypic mean ranged for days to 50% silking 90.33 to 100.7. The cross CML 518×CML 383 (E21) registered more number of days (100.7 days), while hybrid BHM 14 (E24) less number of days (90.33) to 50% silking. Whereas average mean value across five locations were 97.38 days. Significant variations were observed in regard of silking date in different environmemts. Fourteen hybrids showed positive P_i index while rest ten showed negative P_i index for 50% silking. The crossess showed negative P_i index which represents those genotypes that were desirable for early flowering. Significant differences were noticed for day to 50% silking across the environment as indicated by environment indices (-1.12 to 11.15). In case of environmental index, Barishal location (-5.46) was favorable followed by Hathazari location (-3.13) and in Dinajpur location late flowering were observed (108.5 days). The bi and S^2di values range for days to 50% silking were 0.63 (CML 332×CML 311) to 1.26 (CML 332×CML 383) and -2.54 (CML 332×CML 311) to 14.07 (BHM 14) respectively. The present findings were in agreement with Kumar and Singh (2004a), Soliman (2006), Akanda (2007), Rahman *et al*. (2010) and Kadir (2010).

4.4.2.3 Plant height (cm)

Plant height along with the value of phenotypic indices ($P_{i,}$) Regression coefficient (bi), stability (S^2di) is presented in Table 26. The genotypic mean and environmental mean ranged for plant height 160.7 cm to 211 cm and 178.8 cm to 203.3 cm, respectively. Highly significant differences were observed for this trait among the tested hybrids across five locations. The hybrid BHM 12 with mean plant height of 211.0 cm was the tallest and the hybrid BHM 14 with mean plant height of 160.7 cm was the shortest.

Table 25. Estimates of stability parameters for days to 50% silking

Crosses	Days to 50% silking					Overall mean	P_i	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	90	94	104	95	92	95.00	-2.38	0.80	1.50
2. CML 330× CML 322(E2)	92	96	112	97	95	98.20	0.82	1.18	-0.04
3. CML 330× CML 311(E3)	90	94	108	92	92	95.13	-2.25	1.09	-1.30
4. CML 330× CML 331(E4)	94	97	112	96	95	98.80	1.42	1.16	-0.36
5. CML 330× CML 518(E5)	91	95	103	95	94	95.80	-1.58	0.69	-2.04
6. CML 330× CML 383(E6)	91	95	107	96	95	96.87	-0.51	0.93	-0.55
7. CML 332× CML 322(E7)	92	97	109	92	99	97.80	0.42	1.05	2.77
8. CML 332× CML 311(E8)	91	94	102	92	94	94.60	-2.78	0.63	-2.54
9. CML 332×CML 331(E9)	94	102	113	93	98	100.00	2.62	1.19	4.91
10. CML 332×CML 518(E10)	92	97	109	95	95	97.60	0.22	0.98	-1.57
11. CML 332×CML 383(E11)	91	94	111	93	94	96.53	-0.85	1.26	-1.41
12. CML 322×CML 311(E12)	92	96	108	92	97	96.87	-0.51	0.97	-1.34
13. CML 322×CML 331(E13)	95	99	112	94	99	100.00	2.62	1.10	-0.28
14. CML 322×CML 518(E14)	93	96	112	93	94	97.60	0.22	1.24	-0.54
15. CML 322×CML 383(E15)	94	97	112	93	100	99.27	1.89	1.17	2.32
16. CML 311×CML 331(E16)	90	97	107	98	96	97.33	-0.05	0.91	3.34
17. CML 311×CML 518(E17)	91	94	111	96	94	97.07	-0.31	1.18	1.36
18. CML 311×CML 383(E18)	92	96	108	97	98	98.20	0.82	0.86	-1.07
19. CML 331×CML 518(E19)	92	100	107	94	96	97.80	0.42	0.84	0.66
20. CML 331×CML 383(E20)	92	98	110	93	96	97.67	0.29	1.14	-1.28
21. CML 518×CML 383(E21)	95	98	110	93	103	100.07	2.69	0.95	9.72
22.BHM 12(E22)	90	101	107	94	100	98.53	1.15	0.92	10.59
23.BHM 13(E23)	93	99	111	96	100	99.93	2.55	1.06	-0.73
24.BHM 14(E24)	88	86	99	93	86	90.33	-7.05	0.70	14.07
E.mean	91.92	96.26	108.53	94.25	95.92	**97.38**	-	-	-
E.index (I_J)	-5.46	-1.12	11.15	-3.13	-1.46		-	-	-
LSD(0.05)	3.51	1.90	4.93	1.40	4.95	-	-	-	-

Table 26. Estimates of stability parameters for plant height

Genotypes	**Plant height (cm)**					**Overall mean**	**P_i**	**bi**	**S^2di**
	Barishal	**Jashore**	**Dinajpur**	**Hathazari**	**Jamalpur**				
1. CML 330× CML 332(E1)	175.7	159.4	156.7	155.0	168.7	163.1	-27.89	0.75	99.86
2. CML 330× CML 322(E2)	186.7	175.9	158.3	187.1	174.0	176.4	-14.58	0.73	6.76
3. CML 330× CML 311(E3)	217.7	212.1	173.3	191.9	175.0	194.0	3.02	1.55	168.62
4. CML 330× CML 331(E4)	179.3	176.7	161.7	144.5	175.3	167.5	-23.47	1.16	10.43
5. CML 330× CML 518(E5)	217.7	185.6	200.0	169.2	187.3	192.0	0.99	0.90	225.53
6. CML 330× CML 383(E6)	194.7	181.6	160.0	212.3	187.0	187.1	-3.85	0.62	316.61
7. CML 332× CML 322(E7)	209.7	197.7	171.7	207.9	193.3	196.1	5.08	1.02	62.64
8. CML 332× CML 311(E8)	187.0	196.7	175.0	213.5	177.3	189.9	-1.05	0.02	146.52
9. CML 332×CML 331(E9)	157.3	149.4	161.7	181.2	175.3	165.0	-25.98	0.62	13.85
10. CML 332×CML 518(E10)	191.3	194.4	183.3	150.7	201.7	184.3	-6.68	1.10	225.49
11. CML 332×CML 383(E11)	228.0	205.7	191.7	152.8	194.0	194.4	3.47	2.10	334.11
12. CML 322×CML 311(E12)	210.3	203.5	185.0	181.5	200.0	196.1	5.08	1.22	101.66
13. CML 322×CML 331(E13)	205.3	205.3	175.0	167.3	205.7	191.7	0.76	1.66	26.45
14. CML 322×CML 518(E14)	224.3	214.9	185.0	205.8	212.7	208.5	17.58	1.46	90.80
15. CML 322×CML 383(E15)	222.7	213.5	186.7	202.1	207.7	206.5	15.55	1.40	108.53
16. CML 311×CML 331(E16)	211.0	200.1	178.3	191.5	202.3	196.6	5.67	1.24	114.49
17. CML 311×CML 518(E17)	214.7	200.9	185.0	185.7	197.7	196.8	5.80	1.26	114.66
18. CML 311×CML 383(E18)	202.3	203.6	190.0	200.5	201.0	199.5	8.52	0.45	106.13
19. CML 331×CML 518(E19)	221.3	198.9	196.7	167.3	201.7	197.2	6.20	1.43	125.61
20. CML 331×CML 383(E20)	207.0	207.5	193.3	208.2	207.0	204.6	13.64	0.40	90.07
21. CML 518×CML 383(E21)	195.3	202.6	188.3	195.4	214.7	199.3	8.30	0.44	26.26
22.BHM 12(E22)	236.3	217.9	191.7	191.9	217.0	211.0	19.99	1.95	104.46
23.BHM 13(E23)	219.7	210.7	193.3	204.1	198.0	205.2	14.19	1.01	114.77
24.BHM 14(E24)	164.3	161.9	150.0	150.8	176.5	160.7	-30.26	0.77	60.33
E.mean	203.3	194.9	178.8	184.1	193.8	**190.97**	-	-	-
E.index (Ij)	12.35	3.88	-12.15	-6.89	2.81		-	-	-
LSD(0.05)	22.01	14.35	27.30	22.88	10.30	-	-	-	-

The average plant height over the environment was 190.97 cm. Sixteen crosses showed positive P_i index while rest eight showed negative P_i index signifying short stature which were considered desirable as taller plants are more prone to lodging. Significant differences were noticed for plant height across the environment as indicated by environment indices (-12.15 to 12.35). As per indication of environmental index the present findings revealed that Dinajpur location was most favorable environment for plant height, whereas Barishal resulted in taller plant height. The bi values range for plant height was 0.02 to 2.1. Non-significant regression coefficient value of plant height indicated the average response of genotypes in environmental variation. Six tested hybrids BHM 14 (E24), CML 330×CML 332 (E1), CML 332×CML 331 (E9), CML 330×CML 331 (E4), CML 330×CML 322 (E2) and CML 332×CML 518 (E10) had highest negative phenotypic index with close to unit regression coefficient (bi) and non-significantly deviating from regression might be considered as stable ones for short plant. The findings of the current study were in consistent with Mahajan *et al.* (1991), Kumar and Singh (2004b), Kaundal and Sharma (2006) and Akanda (2007).

4.4.2.4 Ear height (cm)

Stability parameters in referring to this trait are given in Table 27. The mean of genotype over environment ranged for ear height 53.62 cm to 110.27 cm. Among the tested hybrids highest ear height was produced by CML 322×CML 383 (E15) and lowest ear height was produced by BHM 14 (E24). Sixteen crosses showed positive P_i index while the rest of eight crosses exhibited shorter ear height. The genotypes which showed positive pi index they represent taller ear height and negative pi index showing genotypes represent shorter ear height. Fluctuating environments for this trait were indicated by the range of environmental index (-3.72 to 5.99). It has been perceived from this study that in Barishal location maximum positive environmental indexed (5.99) indicating unsuitability of the environment for expression of the character. On the contrary the minimum environment index showed in Jashore location which indicated favorable condition for expression. The bi values range for ear height was 0.26 (BHM 14) to 2.25 (CML 330× CML 322). This trait was considered to be less affected by the environment because all the genotypes had regression coefficient (bi) not significantly different from one another and

Table 27. Estimates of stability parameters for ear height

Crosses	Ear height (cm)					Overall mean	P_i	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	83.67	70.93	70.93	76.33	74.67	75.31	-18.36	1.15	-21.31
2. CML 330× CML 322(E2)	103.00	92.73	92.73	111.23	94.33	98.81	5.14	2.25	73.50
3. CML 330× CML 311(E3)	96.33	81.13	81.13	84.23	87.00	85.97	-7.70	0.39	11.80
4. CML 330× CML 331(E4)	89.67	80.40	80.40	72.93	85.00	81.68	-11.99	0.71	12.88
5. CML 330× CML 518(E5)	109.33	87.07	87.07	86.83	93.00	92.66	-1.01	1.61	12.53
6. CML 330× CML 383(E6)	96.33	85.67	85.67	111.33	94.33	94.67	1.00	1.95	99.98
7. CML 332× CML 322(E7)	109.67	94.93	94.93	112.53	89.33	100.28	6.61	1.49	70.52
8. CML 332× CML 311(E8)	98.67	92.67	93.13	105.83	93.67	96.79	3.12	0.41	8.83
9. CML 332×CML 331(E9)	70.00	63.67	63.67	75.63	69.67	68.53	-25.14	1.13	2.26
10. CML 332×CML 518(E10)	100.33	92.53	92.53	96.70	94.00	95.22	1.55	0.77	-21.52
11. CML 332×CML 383(E11)	115.33	96.40	96.40	94.67	91.00	98.76	5.09	1.53	35.37
12. CML 322×CML 311(E12)	99.67	91.60	91.60	94.20	108.00	97.01	3.34	0.83	18.58
13. CML 322×CML 331(E13)	105.33	94.33	94.33	99.53	98.33	98.37	4.70	1.66	-16.43
14. CML 322×CML 518(E14)	114.67	104.80	104.80	104.33	106.67	107.05	13.38	1.24	-16.92
15. CML 322×CML 383(E15)	107.53	115.40	115.40	99.67	113.33	110.27	16.60	0.52	51.96
16. CML 311×CML 331(E16)	102.67	86.93	86.93	92.07	97.67	93.25	-0.42	0.95	-8.45
17. CML 311×CML 518(E17)	109.67	93.33	93.33	90.80	102.00	97.83	4.16	0.54	34.81
18. CML 311×CML 383(E18)	99.67	100.73	100.73	101.37	102.67	101.03	7.36	0.72	-6.26
19. CML 331×CML 518(E19)	99.67	86.27	86.27	87.40	89.67	89.85	-3.82	0.65	-4.53
20. CML 331×CML 383(E20)	99.67	89.20	89.20	103.27	96.33	95.53	1.86	0.81	-2.32
21. CML 518×CML 383(E21)	97.67	101.00	101.00	101.20	116.67	103.51	9.84	0.63	69.21
22.BHM 12(E22)	115.00	102.13	102.13	99.20	102.67	104.23	10.56	1.07	-2.69
23.BHM 13(E23)	111.33	107.07	107.07	103.40	110.67	107.91	14.24	0.71	-12.23
24.BHM 14(E24)	57.00	47.80	47.80	56.83	58.67	53.62	-40.05	0.26	-2.81
E.mean	99.66	89.95	89.97	94.23	94.56	**93.67**			
E.index (Ij)	5.99	-3.72	-3.70	0.56	0.89				
LSD(0.05)	13.90	11.12	16.01	16.52	9.64				

the results showed that all genotypes had non-significant deviation from regression coefficient (S^2di) indicating wider adaptability to the tested conditions. Stable maize hybrids for both short and long ear height were reported earlier by Kumar and Singh *et al.* (2004b) and Akanda *et al*. (2007).

4.4.2.5 Ear length (cm)

Mean performance of the tested hybrids, their response and stability parameters i.e phenotypic indices (P_i), regression coefficient (bi) and deviation from regression (S^2di) in respect of ear length are presented in Table 28. Significant differences were noticed for this trait in different location. The genotypic mean for ear length ranges from 15.05 to 20.93 cm. The average mean value across five locations was 18.05 cm while the hybrid BHM 12 (check) registered the highest mean value (20.93 cm) which was followed by CML 331×CML 383 (E20) by producing ear length 19.62 cm and CML 332×CML 331 (E9) genotype showed the lowest mean value (15.05cm) for this trait. Out of twenty four cross combinations, ten crosses had positive phenotypic index signifying longer length of ear and the rest of crosses exhibited shorter ear length which was indicated by negative phenotypic index. The environment varied by influencing on this trait ear length as showed the environmental index ranges from -1.17 to 0.72. The study revealed that as the maximum environmental index (0.72) was recorded in Jashore location so this location is the most ideal for expression of this trait. The lowest environmental index (-1.17) in Dinajpur location indicated that, this environment had suppressed the expression of this trait. All the genotypes exhibited non-significant regression coefficient (bi) which implied their adaptability over the tested location. Two crosses CML 311×CML 331 (E16) and CML 331×CML 518 (E19) showed high mean value as well as positive phenotypic index, non significant regression coefficient (bi) value and non-significant deviation from regression (S^2di) indicating wider adaptability to all locations. Stable maize genotypes for ear length were also observed by Kaundal and Sharma (2006) and Matin *et al*. (2017).

4.4.2.6 Ear diameter (cm)

Stability parameters i.e phenotypic indices (P_i), regression coefficient (bi) and deviation from regression (S^2di) in referring to this trait are given in Table 29. Among the

Table 28. Estimates of stability parameters for ear length (cm)

Crosses	Ear length (cm)					Overall mean	P_i	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	18.10	18.95	16.77	18.13	17.75	17.94	-0.11	1.03	-0.05
2. CML 330× CML 322(E2)	18.22	17.09	17.50	17.42	17.72	17.59	-0.46	0.02	0.41
3. CML 330× CML 311(E3)	18.05	20.07	17.87	18.75	18.55	18.66	0.61	0.78	1.45
4. CML 330× CML 331(E4)	18.14	18.55	17.47	17.92	18.18	18.05	0.00	0.51	-0.20
5. CML 330× CML 518(E5)	18.15	17.49	16.39	17.18	17.51	17.34	-0.71	0.77	0.12
6. CML 330× CML 383(E6)	17.92	20.08	19.39	19.56	18.65	19.12	1.07	-0.09	2.17
7. CML 332× CML 322(E7)	17.09	16.93	16.80	16.94	16.89	16.93	-1.12	0.11	-0.22
8. CML 332× CML 311(E8)	18.66	18.33	16.82	17.84	17.99	17.93	-0.12	0.92	-0.08
9. CML 332×CML 331(E9)	15.22	16.11	13.83	14.72	15.34	15.05	-3.00	1.08	-0.04
10. CML 332×CML 518(E10)	17.91	18.00	15.19	17.01	17.05	17.03	-1.02	1.55	-0.20
11. CML 332×CML 383(E11)	18.64	19.09	16.22	18.10	17.85	17.98	-0.07	1.51	-0.24
12. CML 322×CML 311(E12)	18.15	19.90	16.02	18.19	17.85	18.02	-0.03	1.78	0.64
13. CML 322×CML 331(E13)	18.76	17.70	16.64	17.54	17.24	17.58	-0.47	0.83	0.57
14. CML 322×CML 518(E14)	17.35	18.68	15.84	17.24	17.35	17.29	-0.76	1.29	0.29
15. CML 322×CML 383(E15)	18.34	19.01	18.44	18.49	18.68	18.59	0.54	0.17	-0.04
16. CML 311×CML 331(E16)	19.93	19.31	17.73	19.10	18.89	18.99	0.94	1.02	0.14
17. CML 311×CML 518(E17)	18.82	19.98	15.09	17.56	18.34	17.96	-0.09	2.48	-0.08
18. CML 311×CML 383(E18)	18.90	18.85	16.24	18.20	17.75	17.99	-0.06	1.47	-0.16
19. CML 331×CML 518(E19)	19.71	18.79	17.70	18.64	18.79	18.73	0.68	0.82	0.39
20. CML 331×CML 383(E20)	21.05	20.37	17.46	19.85	19.37	19.62	1.57	1.78	0.39
21. CML 518×CML 383(E21)	19.05	20.00	17.15	18.95	18.50	18.73	0.68	1.38	-0.05
22.BHM 12(E22)	22.39	21.13	19.29	21.28	20.57	20.93	2.88	1.31	1.01
23.BHM 13(E23)	18.58	19.00	17.23	18.04	18.50	18.27	0.22	0.89	-0.22
24.BHM 14(E24)	17.58	17.10	16.22	16.97	16.93	16.96	-1.09	0.60	-0.04
E.mean	18.53	18.77	16.89	18.07	18.01	**18.05**			
E.index (Ij)	0.48	0.72	-1.17	0.01	-0.04				
LSD(0.05)	1.36	1.67	1.08	1.03	1.25				

tested hybrids the maximum mean ear diameter (5.74 cm) was produced by the cross CML 332×CML 518 (E10). On the contrary the minimum ear diameter (5.02 cm) was produced by BHM 12 (E22). The phenotypic index for ear diameter ranges from -0.28 to 0.44. The desirable genotypes for higher ear diameter were indicated by the positive phenotypic index. Among the twenty four crosses twelve crosses had positive phenotype index and the rest crosses exhibited negative phenotype index which represented the undesirability of those genotypes for getting maximum ear diameter. Fluctuating environments for this trait were indicated by range of environmental indices (-0.08 to 0.14). The highest ear diameter was observed in Dinajpur location as indicated by higher environmental index (0.14) and lowest ear diameter was observed in Jashore location as environmental index is low (-0.08). So Dinajpur location was rich and Jashore location was poor for ear diameter. The differences in regression coefficient (bi) value ranges from -0.64 (CML 311×CML 518) to 3.39 (CML 332×CML 518).This differences in value was an indication of differential response of genotypes in different environment. The genotype CML 330× CML 331 (E4) with positive phenotypic index, non-significant for regression value (1.14) and non-significant deviation from regression value (0.00) was found stable for ear diameter. Significant observations were also made by Kumar and Singh (2004b), Kaundal and Sharma (2006) and Matin *et al.* (2017).

4.4.2.7 Number of row per ear

Stability parameters in respect of number of row per ear are given in Table 30. Significant differences were noticed for this trait in three locations (Barishal, Jashore and Dinajpur) and the other two locations Hathazari and Jamalpur were found to be non significant. The genotypic mean for number of row per ear ranges from 12.71 to 15.07. The average mean value across five locations were 14.06 cm while the cross CML 330×CML518 (E5) produced the maximum number of row per ear (15.07) which was followed by CML 331×CML 518 (E19) and CML 332×CML 518 (E10) by producing 14.92 and 14.82 number of row per ear, respectively. On the other hand, CML 332×CML 383 (E11) produced the lowest mean value (12.71) for this trait. In case of phenotypic index eleven crosses showed positive phenotypic index which is desirable for this trait while

Table 29. Estimates of stability parameters for ear diameter (cm)

Crosses	Ear diameter (cm)					Overall mean	Pi	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	5.42	5.19	5.40	5.35	5.29	5.33	0.03	0.58	0.01
2. CML 330× CML 322(E2)	5.39	5.41	5.50	5.45	5.41	5.43	0.13	0.46	-0.01
3. CML 330× CML 311(E3)	5.46	5.46	5.55	5.51	5.48	5.49	0.19	0.44	-0.01
4. CML 330× CML 331(E4)	5.23	5.30	5.51	5.42	5.27	5.35	0.05	1.14	0.00
5. CML 330× CML 518(E5)	5.65	5.27	5.72	5.49	5.55	5.54	0.24	1.48	0.05
6. CML 330× CML 383(E6)	5.22	5.07	5.15	5.18	5.10	5.14	-0.16	0.13	0.00
7. CML 332× CML 322(E7)	5.46	5.38	5.40	5.39	5.42	5.41	0.11	-0.07	-0.01
8. CML 332× CML 311(E8)	5.49	5.36	5.43	5.38	5.42	5.42	0.12	0.10	0.00
9. CML 332×CML 331(E9)	5.00	4.95	5.31	4.99	5.15	5.08	-0.22	1.66	-0.01
10. CML 332×CML 518(E10)	5.50	5.53	6.21	5.80	5.68	5.74	0.44	3.39	0.00
11. CML 332×CML 383(E11)	5.04	5.05	5.26	5.08	5.11	5.11	-0.19	1.03	-0.01
12. CML 322×CML 311(E12)	5.15	5.56	5.50	5.35	5.42	5.40	0.10	0.48	0.08
13. CML 322×CML 331(E13)	5.24	5.05	5.50	5.35	5.18	5.26	-0.04	1.83	0.00
14. CML 322×CML 518(E14)	5.35	5.41	5.44	5.35	5.45	5.40	0.10	0.23	-0.01
15. CML 322×CML 383(E15)	5.05	4.96	5.58	5.34	5.05	5.20	-0.10	2.84	-0.01
16. CML 311×CML 331(E16)	5.41	5.44	5.75	5.64	5.42	5.53	0.23	1.57	-0.01
17. CML 311×CML 518(E17)	5.49	5.42	5.32	5.38	5.41	5.40	0.10	-0.64	-0.01
18. CML 311×CML 383(E18)	5.27	4.91	5.13	5.20	5.02	5.11	-0.19	0.39	0.05
19. CML 331×CML 518(E19)	5.35	5.52	5.88	5.61	5.54	5.58	0.28	2.07	0.02
20. CML 331×CML 383(E20)	4.92	5.06	5.39	5.01	5.24	5.12	-0.18	1.87	0.01
21. CML 518×CML 383(E21)	5.18	5.13	5.03	5.17	5.04	5.11	-0.19	-0.56	-0.01
22.BHM 12(E22)	4.88	4.89	5.31	4.95	5.05	5.02	-0.28	2.09	-0.01
23.BHM 13(E23)	4.90	5.03	5.22	5.07	5.02	5.05	-0.25	1.21	0.00
24.BHM 14(E24)	5.04	5.04	5.10	5.03	5.07	5.06	-0.24	0.29	-0.01
E.mean	5.25	5.22	5.44	5.31	5.28	**5.30**			
E.index(Ij)	0.05	-0.08	0.14	0.01	-0.02				
LSD(0.05)	0.31	0.21	0.30	0.25	0.28				

Table 30. Estimates of stability parameters for number of row per ear

Crosses	Number of row per ear					Overall mean	Pi	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	14.00	14.00	14.50	14.13	13.53	14.03	-0.03	0.48	-0.16
2. CML 330× CML 322(E2)	14.67	14.13	14.70	14.71	14.19	14.48	0.42	1.04	-0.08
3. CML 330× CML 311(E3)	14.67	15.07	15.17	14.04	14.11	14.61	0.55	-2.35	-0.01
4. CML 330× CML 331(E4)	13.33	12.67	14.10	14.09	13.17	13.47	-0.59	1.54	0.36
5. CML 330× CML 518(E5)	16.00	14.67	15.61	14.49	14.57	15.07	1.01	-2.19	0.42
6. CML 330× CML 383(E6)	14.00	12.60	12.30	13.78	12.80	13.10	-0.96	5.92	0.43
7. CML 332× CML 322(E7)	15.33	14.27	14.05	14.89	14.01	14.51	0.45	4.32	0.33
8. CML 332× CML 311(E8)	14.67	14.27	15.20	14.75	14.34	14.65	0.59	-0.25	-0.05
9. CML 332×CML 331(E9)	13.33	13.60	14.50	13.73	13.17	13.67	-0.39	-0.74	-0.06
10. CML 332×CML 518(E10)	14.00	15.20	15.40	14.98	14.52	14.82	0.76	-0.34	0.30
11. CML 332×CML 383(E11)	12.00	12.80	13.16	13.38	12.21	12.71	-1.35	2.60	0.17
12. CML 322×CML 311(E12)	14.67	14.93	14.30	14.98	14.35	14.65	0.59	3.12	-0.07
13. CML 322×CML 331(E13)	14.00	14.00	14.05	14.36	13.48	13.98	-0.08	2.67	-0.16
14. CML 322×CML 518(E14)	14.00	14.93	14.30	14.13	13.97	14.27	0.21	0.18	0.14
15. CML 322×CML 383(E15)	14.00	13.20	14.94	14.31	13.49	13.99	-0.07	0.00	0.31
16. CML 311×CML 331(E16)	14.00	14.40	13.40	13.78	13.52	13.82	-0.24	1.87	0.20
17. CML 311×CML 518(E17)	14.00	14.53	14.50	13.82	13.59	14.09	0.03	-0.80	-0.03
18. CML 311×CML 383(E18)	14.67	13.73	13.60	14.53	13.51	14.01	-0.05	4.70	0.15
19. CML 331×CML 518(E19)	14.67	15.47	15.00	14.84	14.61	14.92	0.86	0.40	0.05
20. CML 331×CML 383(E20)	12.67	12.80	13.85	13.87	12.67	13.17	-0.89	2.17	0.19
21. CML 518×CML 383(E21)	13.33	13.87	14.50	14.22	13.36	13.86	-0.20	0.93	0.04
22.BHM 12(E22)	14.00	13.73	14.00	13.51	13.57	13.76	-0.30	-2.36	-0.14
23.BHM 13(E23)	13.33	13.47	14.05	13.42	12.94	13.44	-0.62	-0.40	-0.15
24.BHM 14(E24)	14.00	14.80	14.30	14.49	14.02	14.32	0.26	1.50	0.02
E.mean	14.06	14.05	14.31	14.22	13.65	**14.06**			
E.index(Ij)	0.00	-0.01	0.25	0.16	-0.40				
LSD(0.05)	1.47	0.87	0.88	ns	ns				

the other thirteen crosses had negative phenotypic index for number of row per ear. The environment varied with regard to number of row per ear as seen from environment indices (-0.40 to 0.25). High environmental index of 0.25 in Dinajpur location represented favourable condition for expression of this character, while Jamalpur location showed low environment index of - 0.40 indicating unsuitability of environment for expression of this character. The bi value range for number of row per ear were -2.36 (BHM 12) to 5.92 (CML 330× CML 383). Non significant regression coefficient implied the adaptability of genotypes over the tested environments. The hybrid CML 518×CML 383 (E21) was found stable for number of row per ear under environmental changes which was having unit regression coefficient (bi=0.93), non significant deviation from regression (S^2di=0.04). Kumar and Singh (2004b) and Kaundal and Sharma (2006) were also made similar observations.

4.4.2.8 Number of kernel per row

Mean performance of the tested hybrids, their response and stability parameters i.e phenotypic indices (P_i), regression coefficient (bi) and deviation from regression (S^2di) in regard of number of kernel per row are presented in Table 31. Significant variations were observed for this trait in Barishal, Jashore and Dinajpur location and non-significant variation was in Hathazari and Jamalpur location. The genotypic mean ranges from 31.25 to 39.02 for number of kernel per row. The average mean value for this trait across five locations was 34.57 while the hybrid BHM 12 (check) registered the highest mean value (39.02) which was followed by CML 311×CML 331 (E16) and CML 331×CML 383 (E20) by producing 36.59 and 36.41 kernel per row, respectively and CML 332×CML 331 (E9) cross gave the lowest mean value (31.25) for this trait. Out of twenty four hybrids, twelve hybrids had positive phenotype index which was expected for this trait and the rest of hybrids produced lower number of kernel per row which was indicated by negative phenotypic index. The environment varied by influencing on this trait number of kernel per row as showed the environment index ranges from -1.86 to 2.65. The study perceived that as the maximum environmental index (2.65) was recorded in Barishal location so for expressions of trait number of kernel per row this location was the most ideal. The minimum environmental index (-1.86) in Hathazari location indicated that

Table 31. Estimates of stability parameters for number of kernel per row

Crosses	Number of kernel per row					Overall mean	P_i	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	36.14	34.40	33.27	34.82	32.79	34.29	-0.28	0.73	-1.29
2. CML 330× CML 322(E2)	36.44	31.87	35.17	31.87	34.45	33.96	-0.61	0.86	0.87
3. CML 330× CML 311(E3)	35.45	31.27	34.16	30.11	33.37	32.87	-1.70	0.91	0.79
4. CML 330× CML 331(E4)	35.84	32.20	34.39	33.82	34.68	34.19	-0.38	0.56	0.35
5. CML 330× CML 518(E5)	35.17	31.60	31.38	31.89	33.15	32.64	-1.93	0.95	-0.71
6. CML 330× CML 383(E6)	36.56	35.87	39.83	32.60	36.81	36.33	1.76	0.02	6.62
7. CML 332× CML 322(E7)	36.10	32.53	33.05	30.24	33.61	33.11	-1.46	1.13	-1.20
8. CML 332× CML 311(E8)	38.69	35.73	33.39	33.29	35.90	35.40	0.83	1.30	-0.46
9. CML 332×CML 331(E9)	32.99	30.93	28.61	31.98	31.75	31.25	-3.32	0.69	3.97
10. CML 332×CML 518(E10)	39.45	34.00	32.17	32.89	35.25	34.75	0.18	1.81	-0.67
11. CML 332×CML 383(E11)	39.78	35.93	34.83	31.85	36.22	35.72	1.15	1.57	-0.03
12. CML 322×CML 311(E12)	37.02	36.60	33.17	33.82	35.77	35.28	0.71	0.75	1.54
13. CML 322×CML 331(E13)	37.12	29.20	32.72	28.91	32.62	32.11	-2.46	1.80	2.14
14. CML 322×CML 518(E14)	37.29	35.20	31.72	32.93	34.89	34.41	-0.16	1.17	1.48
15. CML 322×CML 383(E15)	36.57	34.47	34.17	34.49	35.60	35.06	0.49	0.58	-0.94
16. CML 311×CML 331(E16)	38.09	35.80	35.83	36.18	37.04	36.59	2.02	0.56	-0.80
17. CML 311×CML 518(E17)	36.93	34.40	33.50	32.82	34.98	34.53	-0.04	0.93	-1.49
18. CML 311×CML 383(E18)	33.73	32.00	34.27	31.07	33.39	32.89	-1.68	0.27	-0.62
19. CML 331×CML 518(E19)	38.81	36.00	34.72	32.42	36.12	35.61	1.04	1.25	-0.56
20. CML 331×CML 383(E20)	43.47	33.40	37.49	30.76	36.92	36.41	1.84	2.58	7.40
21. CML 518×CML 383(E21)	38.25	37.47	31.61	34.96	36.20	35.70	1.13	1.10	7.94
22.BHM 12(E22)	43.07	39.47	37.83	35.22	39.50	39.02	4.45	1.58	0.13
23.BHM 13(E23)	36.98	34.93	35.50	35.73	36.35	35.90	1.33	0.38	-0.64
24.BHM 14(E24)	33.31	29.73	33.14	30.42	32.15	31.75	-2.82	0.50	0.78
E.mean	37.22	33.96	34.00	32.71	34.98	**34.57**			
E.index(Ij)	2.65	-0.61	-0.58	-1.86	0.41				
LSD(0.05)	4.24	3.58	2.23	ns	ns				

this environment had suppressed the expression of this trait. Non-significant regression coefficient (bi) is a indication of adaptability of genotypes over the tested location. Two crosses CML 518×CML 383(E21) and CML 322×CML 311(E12) showed high mean value as well as positive phenotypic index and non significant regression coefficient (bi) value equal to unity indicating wider adaptability to all locations. These were in accordance with observations which were made by Kumar and Singh (2004b) and Kaundal and Sharma (2006).

4.4.2.9 Thousand grain weight (g)

Stability parameters i.e phenotypic indices (P_i), regression coefficient (bi) and deviation from regression (S^2di) in referring to this trait are given in Table 32. Jashore, Dinajpur and Jamalpur locations were found to be significant in different genotypes while the other two locations Hathazari and Barishal found to be non-significant in case of thousand grain weight (g). The genotypic mean ranges from 407.00 to 464.73 with average mean value 441.64 across five locations. The cross CML 331×CML 383 (E20) produced bold grain which was weighted 464.73g for thousand grains. On the other hand, BHM 12 (E22) produced the lowest grain weight value (407.00g) for this trait. Among the twenty four crosses twelve hybrids had positive phenotype index which revealed higher thousand grain weight (g) and the rest of genotypes exhibited negative phenotypic index which represented those hybrids which had lower grain weight. The environment varied by influencing on this trait as showed the environment index range (-29.28 to 40.67). So, significant differences were noticed for thousand grain weight (g) across the environment. It has been perceived from the study Dinajpur location was favorable condition due to its maximum positive environmental index (40.67) for this trait and negative environmental index (-29.28) in Barishal location was an indication of unsuitability of this environment for expression of this character. The differences in regression coefficient (bi) value ranges from -0.17 (CML 311×CML 383) to 1.98 (CML 330×CML 331) which were an indication of differential response of genotypes in different environment. The crosse CML 330×CML 518 (E5), CML 332×CML 518 (E10), CML 331×CML 518 (E19) and CML 331×CML 383 (E20) were found fit to wide range of environments as indicated by regression coefficient (bi) value equal to unity

Table 32. Estimates of stability parameters for thousand grain weight (g)

Crossess	Thousand grain weight (g)					Overall mean	P_i	bi	S^2di
	Barishal	Jashore	Dinajpur	Hathazari	Jamalpur				
1. CML 330× CML 332(E1)	376.67	443.33	412.00	495.67	474.67	440.47	-1.17	1.22	800.61
2. CML 330× CML 322(E2)	406.67	510.00	453.33	508.00	440.00	463.60	21.96	1.44	-207.92
3. CML 330× CML 311(E3)	390.00	456.67	466.00	485.33	472.00	454.00	12.36	0.80	596.84
4. CML 330× CML 331(E4)	390.00	526.67	397.33	507.67	434.67	451.27	9.63	1.98	245.58
5. CML 330× CML 518(E5)	423.33	486.67	435.33	501.33	465.33	462.40	20.76	1.07	-367.62
6. CML 330× CML 383(E6)	396.67	476.67	432.00	515.33	424.00	448.93	7.29	1.59	-463.65
7. CML 332× CML 322(E7)	423.33	470.00	416.67	504.67	461.33	455.20	13.56	1.12	-223.59
8. CML 332× CML 311(E8)	440.00	436.67	425.33	426.67	417.33	429.20	-12.44	-0.01	-414.81
9. CML 332×CML 331(E9)	420.00	403.33	352.67	470.00	376.00	404.40	-37.24	1.02	959.82
10. CML 332×CML 518(E10)	420.00	470.00	461.33	481.33	408.00	448.13	6.49	0.86	15.55
11. CML 332×CML 383(E11)	413.33	510.00	421.33	481.00	444.00	453.93	12.29	1.21	35.27
12. CML 322×CML 311(E12)	380.00	483.33	411.67	473.33	388.00	427.27	-14.37	1.52	-79.77
13. CML 322×CML 331(E13)	413.33	473.33	424.00	484.00	401.33	439.20	-2.44	1.19	-301.22
14. CML 322×CML 518(E14)	403.33	453.33	436.00	500.67	408.00	440.27	-1.37	1.26	-267.14
15. CML 322×CML 383(E15)	400.00	433.33	431.33	529.33	437.33	446.27	4.63	1.42	350.88
16. CML 311×CML 331(E16)	413.33	443.33	419.33	485.00	408.00	433.80	-7.84	1.02	-375.43
17. CML 311×CML 518(E17)	423.33	496.67	368.00	471.33	429.33	437.73	-3.91	1.26	896.70
18. CML 311×CML 383(E18)	436.67	410.00	411.33	428.67	448.00	426.93	-14.71	-0.17	-201.49
19. CML 331×CML 518(E19)	420.00	473.33	467.33	510.00	433.33	460.80	19.16	1.08	-190.18
20. CML 331×CML 383(E20)	426.67	500.00	480.67	477.67	438.67	464.73	23.09	0.71	159.68
21. CML 518×CML 383(E21)	423.33	460.00	383.00	501.00	437.33	440.93	-0.71	1.29	127.30
22.BHM 12(E22)	423.33	410.00	378.00	426.33	397.33	407.00	-34.64	0.30	-98.66
23.BHM 13(E23)	423.33	443.33	438.33	488.67	429.33	444.60	2.96	0.79	-352.15
24.BHM 14(E24)	410.00	416.67	453.00	422.33	389.33	418.27	-23.37	0.05	181.38
E.mean	412.36	423.97	482.31	427.61	461.94	**441.64**			
E.index(Ij)	-29.28	-17.67	40.67	-14.03	20.31				
LSD(0.05)	ns	70.73	51.64	ns	5.53				

with high mean value. Kumar and Singh (2004b), Kaundal and Sharma (2006) and Matin *et al.* (2017) were also made significant observations.

4.4.2.10 Grain yield (ton/ha)

The grain yield along with the value of phenotypic indices (P_i), regression coefficient (bi) and deviation from regression (S^2di) are presented in Table 33. The genotypic mean ranged from 6.91 t/ha to 11.75 t/ha. Among the tested hybrids, the maximum yield was produced by CML 322×CML 518 (11.75 t/ha) which was followed by CML 311×CML 331 (11.51 t/ha), CML 331×CML 383 (11.43 t/ha) and CML 332×CML 518 (11.28 t/ha).. On the other hand, the minimum grain yield was produced by CML 332×CML 331 (6.91 t/ha). In case of phenotypic index, fourteen crosses showed positive phenotypic index while the other had negative phenotypic index for yield. Thus, positive phenotypic index represented the higher yield which was expected and negative represented the lower yield among the crosses. Again, positive and negative environmental index (Ij) reflected the rich or favorable and poor or unfavorable environments for this character, respectively. The range of environmental indices for grain yield was -0.37 to 0.51 which reflected the variation in performance from one location to another showed in Table 33. Thus the environment of Hathazari was the poorest, where as Barishal and Dinajpur were the most favorable environmental for maize production. The environmental mean for grain yield ranged from 9.79 t/ha to 10.67 t/ha. The differences in bi value ranges from 0.08 to 3.75 reflected the respose of tested hybrid and indicated that these materials responded differently in different environment. The adaptability in performance across the location for all the genotypes was indicated by the non significant regression coefficient value (bi) different from unity. When bi=1 and mean yield high, then the genotypes are well adapted to all environment; when bi=1 and mean yield low, the genotypes are poorly adopted to all environments. A regression coefficient value significantly less than unity indicate, either, a lower than average response to high yielding environments or a better than average performance in low-yielding environments. Among the hybrids, CML 322×CML 518 (11.75 t/ha), CML 311×CML 331 (11.51 t/ha), CML 331×CML 383 (11.43 t/ha) and CML 332×CML 518 (11.28 t/ha) produced higher yield than check BHM 12 and BHM 14. Considering higher

Table 33. Estimates of stability parameters for yield (t/ha)

Crosses	**Yield (t/ha)**					**Overall mean**	**Pi**	**bi**	**S^2di**
	Barishal	**Jashore**	**Dinajpur**	**Hathazari**	**Jamalpur**				
1. CML 330× CML 332(E1)	10.44	8.31	8.84	7.09	8.08	8.55	-1.60	3.75	0.48
2. CML 330× CML 322(E2)	10.50	8.86	11.17	9.61	10.97	10.22	0.07	1.25	0.46
3. CML 330× CML 311(E3)	10.68	10.99	10.21	7.58	9.93	9.88	-0.28	2.62	0.90
4. CML 330× CML 331(E4)	10.85	8.99	10.34	8.94	10.73	9.97	-0.18	2.26	0.10
5. CML 330× CML 518(E5)	11.79	8.92	11.33	10.83	9.84	10.54	0.39	1.90	0.73
6. CML 330× CML 383(E6)	9.31	10.29	10.74	9.70	9.47	9.90	-0.25	0.66	0.16
7. CML 332× CML 322(E7)	10.20	10.08	9.66	8.83	9.67	9.69	-0.47	1.26	0.41
8. CML 332× CML 311(E8)	11.33	10.58	10.17	9.81	9.50	10.28	0.12	1.69	0.29
9. CML 332×CML 331(E9)	6.84	6.67	7.00	8.89	5.15	6.91	-3.24	1.59	1.44
10. CML 332×CML 518(E10)	11.27	10.55	11.54	11.34	11.71	11.28	1.13	0.13	0.32
11. CML 332×CML 383(E11)	11.55	11.72	10.93	7.90	10.80	10.58	0.42	3.14	1.27
12. CML 322×CML 311(E12)	10.22	10.65	10.50	8.62	10.04	9.91	-0.25	1.25	0.06
13. CML 322×CML 331(E13)	10.92	9.30	9.61	9.37	10.26	9.89	-0.26	1.91	0.44
14. CML 322×CML 518(E14)	12.00	11.63	11.58	11.54	12.00	11.75	1.60	0.91	0.14
15. CML 322×CML 383(E15)	8.90	9.95	10.72	10.72	11.23	10.30	0.15	2.09	0.08
16. CML 311×CML 331(E16)	11.58	11.70	10.69	11.67	11.88	11.51	1.35	0.93	0.29
17. CML 311×CML 518(E17)	11.30	10.17	10.06	9.74	10.67	10.39	0.23	1.76	0.50
18. CML 311×CML 383(E18)	10.56	8.52	9.26	10.52	9.10	9.59	-0.56	0.80	0.43
19. CML 331×CML 518(E19)	10.24	10.20	10.48	9.52	10.78	10.24	0.09	0.58	0.34
20. CML 331×CML 383(E20)	11.86	11.04	11.11	11.83	11.30	11.43	1.27	0.08	0.44
21. CML 518×CML 383(E21)	11.41	10.60	9.54	10.18	10.86	10.52	0.36	1.36	0.17
22.BHM 12(E22)	11.74	11.19	10.02	11.79	10.23	10.99	0.84	0.26	0.34
23.BHM 13(E23)	11.81	10.84	9.70	10.93	10.69	10.79	0.64	1.16	0.00
24.BHM 14(E24)	8.86	8.55	9.39	7.97	7.74	8.50	-1.65	0.96	0.11
E.mean	10.67	10.01	10.18	9.79	10.11	**10.16**	-	-	-
E.index(Ij)	0.51	-0.15	0.02	-0.37	-0.05	-	-	-	-
LSD(0.05)	1.22	1.17	1.24	0.76	0.93	-	-	-	-

Plate 16. Best permorming hybrid at Barishal location

Plate 17. Best permorming hybrid at Jashore location

Plate 18. Best permorming hybrid at Dinajpur location

Plate 19. Best permorming hybrid at Hathazari location

Plate 20. Best permorming hybrid at Jamalpur location

grain yield, bi~1 and S^2di~0 indicated that CML 322×CML 518 (E14) and CML 311×CML 331 (E16) were the higher yielder and suitable across the environments. On the other hand, CML 331×CML 383 (E20) & CML 332×CML 518 (E10) were higher yielder but were responsive to favorable environments. Kaundal and Sharma (2006) and Rahman *et al.* (2010) were also recorded significant differences of adaptability and yield stability in maize genotypes. The best performing hybrids at different locations are presented in Plate 16 to Plate 20.

4.4.3 Additive main effects and multiplicative interaction method (AMMI)

The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the G x E interaction. The results can be graphed in a useful biplot that shows both main and interaction effects for both genotypes and environments.

AMMI model is a valuable approach for understanding G x E interaction and obtaining better yield estimates by combining the analysis of variance and principal components analysis. The associations between the hybrids and the environments can be seen clearly when both the hybrids and the environments on the same graph are plotted. The indication of the stability of a genotype over environments is IPCA scores in the AMMI analysis. The greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype to over all environments sampled. From the biplot, environments are distributed from lower yielding environments in quadrants I (top left) and IV (bottom left) to the high yielding environments in quadrants II (top right) and III (bottom right) (Figure 4). The IPCA1 was highly significant and explained the interaction pattern better than other interaction axes. The mean genotypes or environments in AMMI biplot located on the same parallel line, relative to the ordinate, had similar yield, while those located on the right side of the center of the axis had higher yields than those on the left hand side (Figure 4). The principal components analysis of AMMI partitions G x E interactions into several orthogonal axes, the interaction principal component analyses (IPCA).

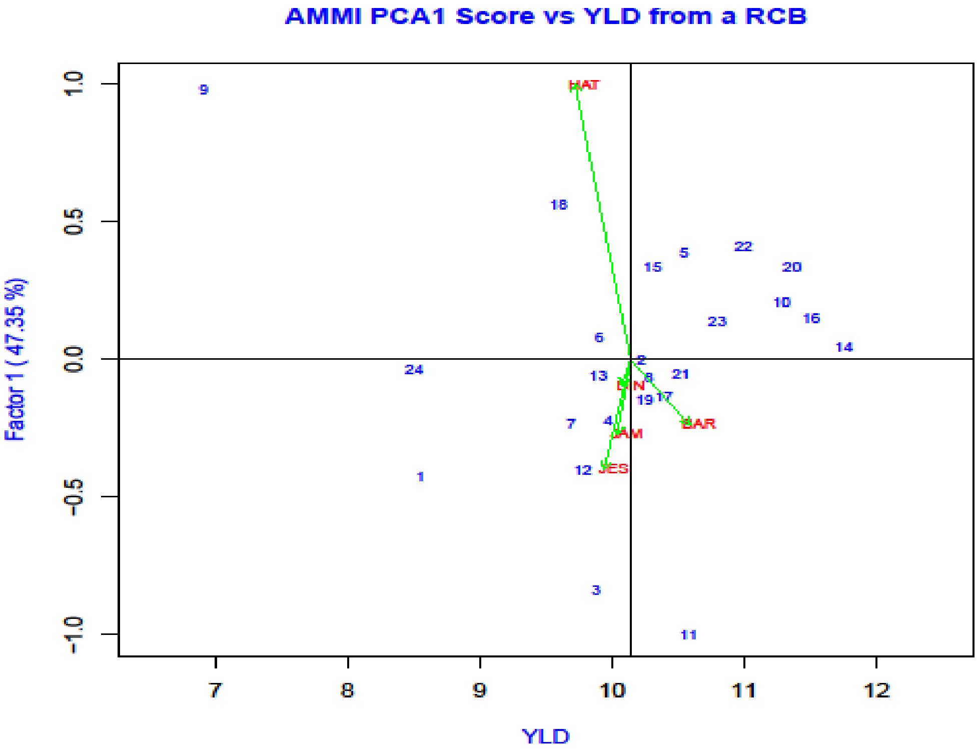

Figure 4. Biplot of the first AMMI interaction (IPCA1) score (Y –axis) plotted against mean yield (X- Axis) of twenty four maize hybrids and five environments.

From Figure 4 it was observed that E14 (CML 322×CML 518), E16 (CML 311×CML 331), E10 (CML 332×CML 518), E20 (CML 331×CML 383), E22 (BHM 12) and E23 (BHM 13) were high yielding hybrids. E9 (CML 332×CML 331), E24 (BHM 14) and E1 (CML 330×CML 332) were low yielding and rest of hybrids are average yielder. Genotypes grouped under low yielding environments are shown at the lower left quadrant of the biplot. Among the entries, E14 (CML 322×CML 518), E2 (CML 330×CML 322), E24 (BHM 14) were more stable because they had smaller IPCA1 score that was near to zero. E21 (CML 518×CML 383), E17 (CML 311×CML 518), E19 (CML 331×CML 518) and E8 (CML 332× CML 311) were average yielder and nearly stable but E11 (CML 332×CML 383) and E3 (CML 330×CML 311) were unstable. Begum (2016) and Matin *et al.* (2017) also made similar findings using AMMI model.

Since IPCA2 scores also played a significant role in explaining the GEI; the IPCA1 scores were plotted against the IPCA2 scores for further exploring adaptation (Figure 5). Using the first two principal component scores the AMMI 2 biplot generated a clear association between genotypes and environments (Figure 5). The biplot showed that Hathazari was the most discriminating environment for the genotypes as indicated by the longest distance between its marker and the origin and gave information on the performance of the hybrids. The AMMI 2 biplot also indicated the relationship among the maize hybrids. According to Figure 5, the hybrids E11 (CML 332×CML 383), E22 (BHM 12), E9 (CML 332×CML 331), E3 (CML 330×CML 311) and E15 (CML 322×CML 383) were unstable due to their dispersed position from the other hybrids in the biplot. E24 (BHM 14), E16 (CML 311×CML 331), E13 (CML 322×CML 331), E17, (CML 311×CML 518) and E14 (CML 322×CML 518) were positioned closer to the origin of the biplot which indicated their stability in performance across environments when plotting the IPCA1 and IPCA2 scores. Ear of stable hybrid overall five locations are presented in plate 21**.** Those genotypes with IPCA1 scores near zero had little interaction across environment and clustered close to the centre tend to be stable, and those plotted far apart were unstable in performance with very high IPCA1 value (Figure 4). Gauch and Zobel (1996) showed that AMMI 1 with IPCA 1 and AMMI 2 with IPCA

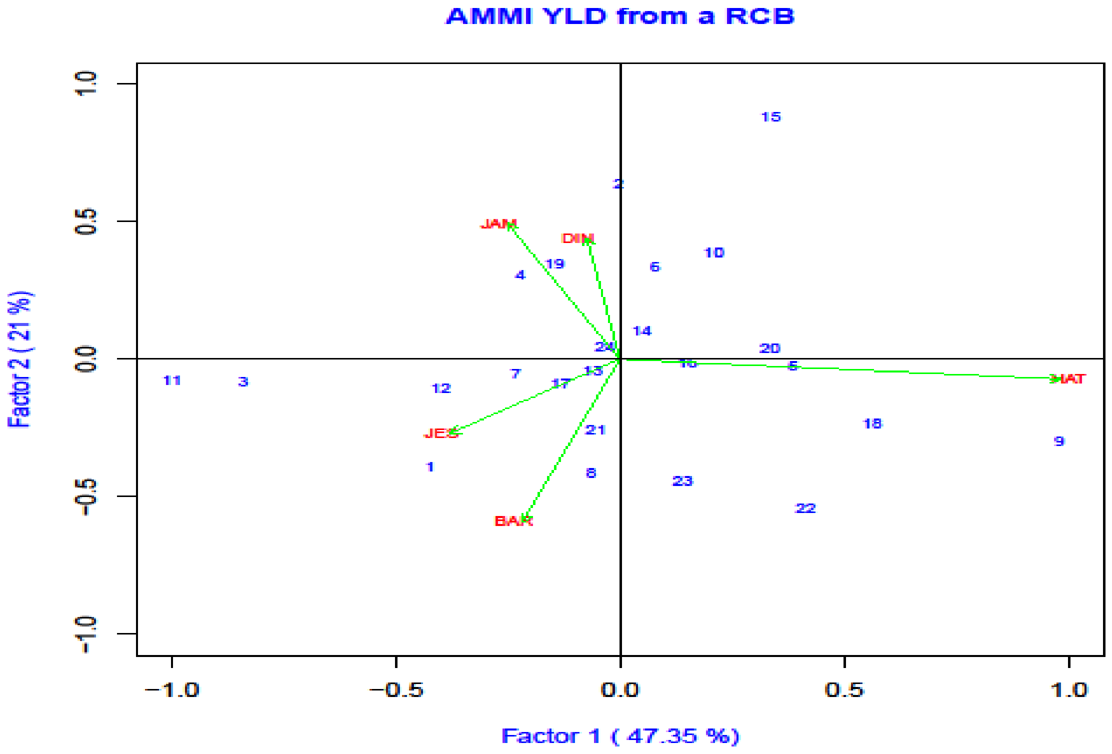

Figure 5. AMMI biplot 2 interaction (IPCA1 and IPCA2) of twenty four maize hybrids and five environments.

Plate 21. Ear of stable hybrid overall five locations

and IPCA 2 were usually selected and the graphical representation of axes either as IPCA 1or IPCA 2 against main effects or IPCA 1 against IPCA 2 is generally informative. When AMMI 3 and higher models are presented for agricultural data, the third and higher IPCA axes are dominated by noise and have no predictive value (Van Eeuwijk, 1995). Stable maize genotypes were also observed by Kaundal and Sharma (2006), Banik *et al*. (2010), Begum (2016) and Matin *et al*. (2017).

4.4.4 Comparison of genotypes with ideal genotypes

A genotype should be considered as ideal genotype which has both high mean yield performance and high stability across environments. According to Kaya *et al*. (2006) Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI, as represented by an arrow pointing to it. A genotype is more desirable if it is located closer to the ideal genotype. Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Thus, Figure 6 showed that E14 (CML 322×CML 518), E16 (CML 311×CML 331), E10 (CML 332×CML 518) and E20 (CML 331×CML 383) nearest to the ideal genotypes (the center of concentric circles) so it as more desirable than other tested genotypes. Ear of hybrids nearest to the ideal genotypes overall five locations are presented in Plate 22.

4.5 Best hybrid in each environment

For the identification of suitable or better performing hybrids in each location the “Which-Won-Where” function of GGE biplot can be used. Dehghani *et al*. (2009) also used GGE biplot method to identify superior maize genotypes for target sites. Figure 7 showed the which-won- Where view of this study. A polygon was represented by the biplot, where on the vertexes some of the testing hybrids were positioned, while rests of the hybrids were inside the polygon. Those hybrids were considered to be the most responsive due to their position on the vertex as because they had the longest distance from the biplot origin. Yan and Rajcan (2002) explained that responsive hybrids were either the best or the poorest at one or every environment.

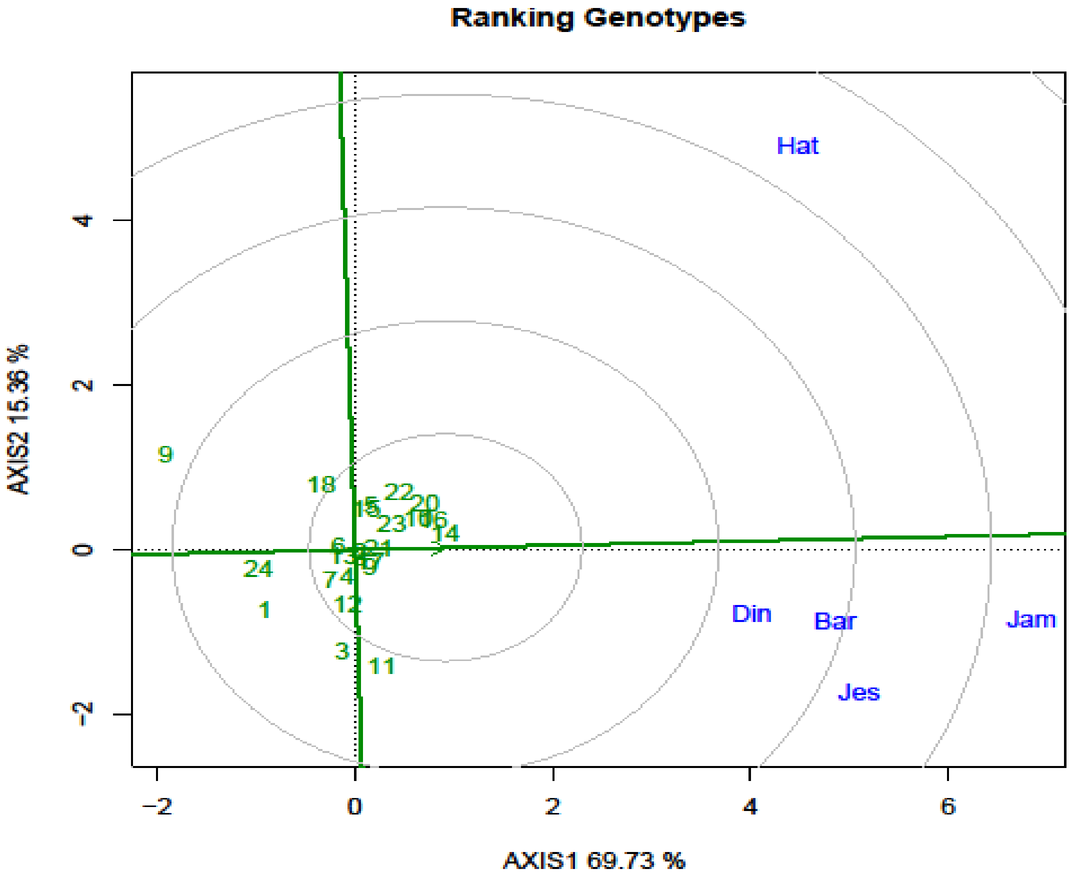

Figure 6. Comparison biplot view of yield of genotypes with the ideal genotypes

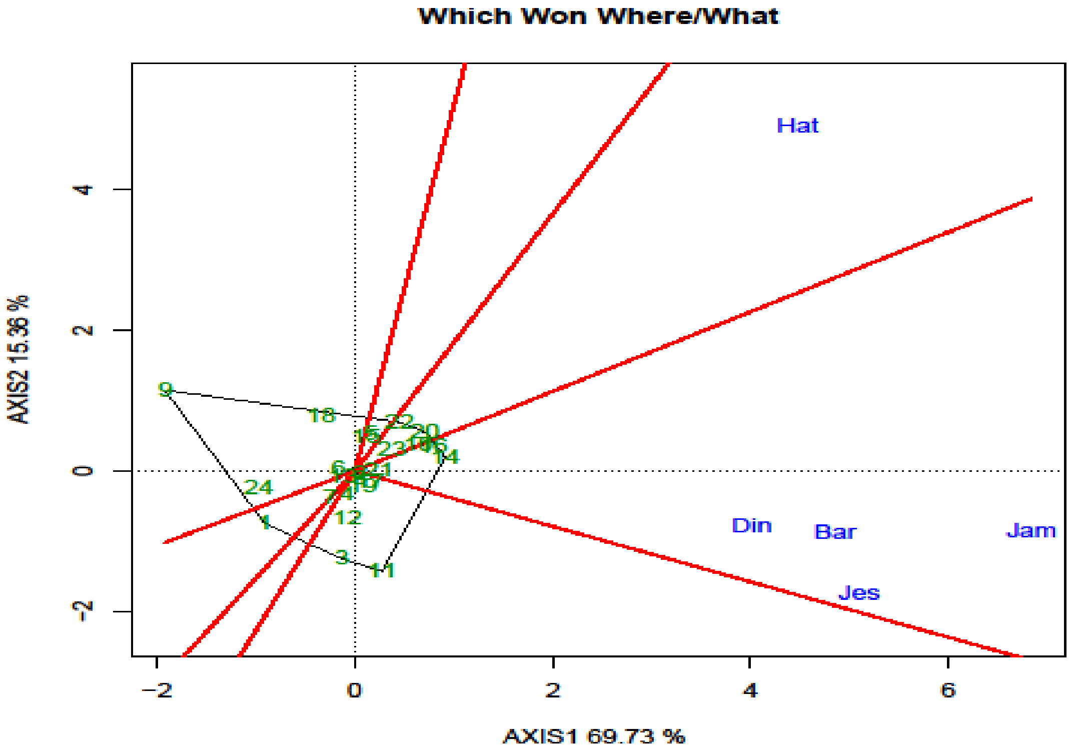

Figure 7. Genotype + Genotype x Environment interaction bi-plot showing performance in each environment

The vertex genotypes in this Figure 7 were E1 (CML 330× CML 332), E9 (CML 332×CML 331), E11 (CML 332×CML 383), E14 (CML 322×CML 518) and E20 (CML 331×CML 383) that were the most responsive one can be visually determined. The biplot was divided into seven sectors by seven rays. Out of seven sectors test environments fall in two of them. The vertex genotype for sector which encompassed environments Barishal, Jashore, Jamalpur and Dinajpur was E14 (CML 322×CML 518) and for sector content environment Hathazari was E20 (CML 331×CML 383), these implying that these genotypes were the winning genotypes for respected environments (Figure 7). In this case GE can be exploited by recommending specific genotype to specific locations (Yan *et al*., 2007). Other corner genotypes, E9 (CML 332×CML 331) was the poorest yielding among the tested genotypes and the location of this genotypes reflecting the fact that as this was poor yielded at each location so this was located far away from all of tested locations.

Plate 22. Ear of hybrids nearest to the ideal genotypes overall five locations

CHAPTER V
SUMMARY AND CONCLUSION

Inroduction of white maize in Bangladesh is a long aspiration to feed the populations. As food, maize can be consumed directly as green cob, roasted cob or popped grain. Maize grain can be used in various ways such as corn meal, fried grain and flour for human consumption**.** White maize should get priority for its various uses (porota, luchi, ruti, khichuri, khoi, moa, naru, khir, payesh, pitha, roasted cob etc.). The present research work was set up to characterize the collected inbreds and then identify potential inbred parents based on variability and genetic diversity. Then further investigation was carried out through estimating combining ability and heterosis of the tested hybrids which were obtained by making cross of selected inbreds and the performance of hybids were evaluated at different locations to determine the magnitude of GXE interaction and stability parameters.

Fifty eight inbred lines of maize collected from CIMMYT were characterized qualitatively and quantitatively and evaluated for estimating the genetic diversity in the field. This experiment was conducted at Regional Agricultural Research Station (RARS), rahmatpur, Barishal during rabi, November 2015 to April 2016. On the basis of per se performance under normal field condition, genetic diversity and association between characters, seven inbreds were selected. Then the selected inbred lines were crossed among themselves in a half diallel fashion without reciprocal and twenty one single cross hybrids were produced. The crossing program was carried out at RARS, Barishal during November 2016 to April 2017. Further the twenty one hybrids along with three checks BHM 12, BHM 13 and BHM 14 were set in five locations i.e Regional Agricultural Research Station (RARS), Rahmatpur, Barishal; Regional Agricultural Research Station (RARS), Jashore; Regional Agricultural Research Station (RARS), Jamalpur; Regional Agricultural Research Station (RARS), Hathazari, Chattogram and Wheat Research Centre (WRC), Nashipur, Dinajpur to estimate combining ability, heterosis and to identify high yielding and stable hybrids across the locations. The period of experimentation was November 2017 to April 2018.

The results of the research work have been summarized and are presented according to experiment as follows:

The inbred lines under investigation expressed considerable variations for most of the morphological traits. About 41.38% genotypes had recurved leaf attitude. Anthocyanine colour in tassel and silk were absent in 34.48% and 41.38% genotypes, respectively. A majority of genotype (56.90%) had no coloration at glume base. Among the genotypes anthocyanin in ring glume was absent for 86.21%. In case of anthocyanine coloration of node and internode maximum genotypes (77.59% and 94.83%) showed no pigmentation, respectively. Around 81.03% genotypes had no colour on leaf sheath. The angle between main axis and lateral branches was Small (32.76%) which was followed by very small (31.03%) and medium (17.24%). Among the genotypes, 37.93% produced medium number of primary branches and 36.21% had few branches. Most of the genotypes had (75.86%) flint type grain and 22.41% were semi dent.

When quantitative traits were considered for different genotypes tasseling and silking duration ranges from 70-90 and 72-92 days, respectively. The CML 243 was a good inbred line for early maturity because this inbred line required the minimum days for tasseling and silking. In this observation, plant height value was observed in 91.7 cm which was the lowest and the highest value was 186.3 cm. The highest value for plant height was recorded in inbred line CML 334 which may be good to increase fodder production but sensitive to lodging. The lowest plant height was found in inbred line CML 137 which might have increased lodging resistance. Average height of ear was 56.3 cm where the highest value was 79.8 cm in CML 319 and the lowest value was found in CML 135 (30.5 cm). Wide variations were existed among the tested materials for ear length by giving the 17.8 cm and 10.0 cm length. CML 132 had the longest length of ear and CML 381 had the shortest ear length. Ear diameter ranges from 3.3-5.3 cm in this study. Inbred line CML 535 was regarded as the best inbred for ear diameter among the genotypes tested. The maximum numbers of kernel rows (16) was observed in inbred line CML 375 and the the minimum in inbred line CML 263. Number of kernel per row ranges from 15-31 among the inbreds and the average number was 22. The highest number of kernels produced on a row was measured in the inbred CML 378. The highest thousand grain weight was recorded for inbred line CML 375 (460g) and the lowest in inbred line CML 263 (120g). Grain yield ranges from 2.05 t/ha to 6.99 t/ha. Inbred CML 331 gave the highest estimated grain yield of 6.99 t/ha followed by inbred lines CML 319, CML 384, CML 380 and CML 382.

The analysis of variance revealed the existence of sufficient amount of variability among genotypes for quantitative characters studied. So this was the indication of substantial genetic variability presence in genotypes. In this study the estimated genetic variability parameters indicated that phenotypic variance and phenotypic coefficient of variation were higher than genetic variance and genotypic coefficient of variation for all the traits. However, the estimated values of phenotypic coefficient of variation and genotypic coefficient of variation were the minimum for days to tasseling, days to silking, ear diameter and thousand seed weight suggesting that there was a minimal influence of environment on the expression of these traits. The maximum difference between phenotypic coefficient of variation and genotypic coefficient of variation estimates were observed for plant and ear height, ear length, numbers of kernel row, number of kernel per row and grain yield suggesting considerable influence of environment on these traits for expression. The traits plant height, number of kernels per row, thousand grain weight and grain yield showed high heritability estimates accompanied high genetic advance in percentage of mean. The combinations of high heritability and genetic advance in percentage of mean are important indicators of the predominant role of additive gene action in these characters. Based on high heritability and genetic advance in percentage of mean, prediction of high performance and selection of inbred would lead to successful maize breeding program. Other traits viz. days to tasseling, days to silking recorded comparatively high heritability estimates coupled with low genetic advance in percentage of mean among the character studied. This indicated that the inheritance of these characters under the large influence of environmental factors and revealed non-additive gene action and selection for these traits may not be rewarding.

For the normal approach towards the improvement of yield, selection has to be operated through associated characters. In the present investigation with the help of correlation analysis, relationship between yield and yield contributing characters were studied. Days to tasseling, days to silking, ear height, ear length, ear diameter, number of kernels per row, thousand grain weight showed significant positive correlation with grain yield both at phenotypic and genotypic levels indicating dependence of these characters on each other. Hence, for the improvement of grain yield selection criteria should be considered for these traits. In addition there was non-significant positive correlation of grain yield with plant height at genotypic level. Only number of row per ear recorded non significant negative correlation with yield, both at genotypic and phenotypic levels.

In the present study, the path coefficient analysis was performed at genotypic level which furnished a method of partitioning the correlation coefficient into direct and indirect effect and provides the information on actual contribution of a trait on the yield. Path coefficient analysis revealed that among the studied characters except silking date and plant height other characters viz., Days to tasseling, ear diameter, number of kernel per row, ear height, thousand grain weight, ear length and number of row per ear exerted positive direct effect on grain yield and correlation of these characters with grain yield was positively significant except for number of row per ear. Thus, such high positive correlation with grain yield was mainly due to the high positive direct effect and considerable indirect effects of these characters and selection for any of these independent characters will be rewarding for yield improvement.

Genetic divergence of fifty eight genotypes of maize was assessed by using principal component analysis (PCA), principal coordinate analysis (PCO), canonical variate analysis (CVA) and cluster analysis for ten characters. The principal component analysis divides the total variance into different factors and analyses revealed that eigen value above unity for first four characters of the principal component axes explaining 82.67% of the total variation towards the divergence. Seven clusters of maize were formed based on their agronomic traits with multivariate techniques. The maximum number of genotypes (13) was comprised into cluster II and cluster VII. Cluster V contained lowest number (4) of inbreds. The maximum intra-cluster distance was shown by cluster V while, minimum in cluster VI. The highest inter-cluster distance was observed between clusters V and VI, followed by the distance between cluster IV and V, cluster I and VI, cluster V and VII, It is expected that crossing of inbred lines belonging high to medium D^2 values suggesting higher probability of heterotic hybrids if selection of parents is done from these pairs of clusters. In case of days to tasseling and silking mean value was the minimum in cluster II. Second lowest value for early flowering appeared in cluster I which is desirable and cluster I ranked first for dwarf plant height and ear height. The inbred lines of cluster VI gave the highest yield and they also had the maximum value for ear diameter, number of row per ear, thousand kernel weight. The genotypes of cluster VII were performed moderately in all the cases and had highest value for ear length. Hence, for the improvement of different characters viz. days to tasseling, days to silking, plant and ear height, yield and yield contributing characters under the present study, inbred lines selected from clusters I, cluster VI and VII. The positive absolute values of the two vectors for plant height and number of row per ear revealed that these characters contributed the maximum towards divergence among the ten characters of fifty eight inbred lines.

Results from the pooled analysis of variance over five environments revealed the significant mean squares for general and specific combining abilities for studied characters which indicated significant differences that suggested presence of notable genetic variability among the gca as well as sca effects. Significant mean square due to environments for all characters studied in this experiment which indicates the influence of differential environmental factors at different location on expression of different characters in maize. The analysis of variance also showed that genotypes differed significantly for all the characters except thousand grain weight. GCA X Environment was significant for ear length, ear diameter, number of kernel per row and yield. In addition, the interaction of SCA by environment was significant for all traits except days to silking, number of row and thousand grain weights. In the present study ratio of GCA and SCA variance was observed close to unity for number of kernel per row, thousand grain weight and grain yield indicating equal importance of both additive and non additive gene effects. The ratio of the components revealed that GCA variance was higher than SCA for for days to tasseling, days to silking, plant height, ear height, ear length, ear diameter and number of row per ear indicating the predominance of additive gene action for these traits and there was always a good chance of improving those traits by accumulation of favorable gene. Combining ability analysis also revealed that estimates of SCA variances were higher than GCA variances for the characters number of kernel per row, suggesting predominance of non-additive or dominant gene action and ratio was almost unity for thousand grain weight and grain yield indicated equal importance of both additive and non-additive gene effects.

Among the seven lines tested for their combining abilities pertaining to different characters under study indicated that none of the parent was general combiner in desired direction for all the traits. Due to importance of early maturity and lower values of days to tasseling and silking inbred lines CML 330 (P1), CML 332 (P2), and CML 311 (P4), showed significant negative GCA effects which were considered as good combiners for earliness. Three parental lines i.e CML 330 (P1), CML 332 (P2), and CML 331 (P5) showed significant negative GCA effects for short plant and low ear height, indicated good combiner for dwarfness with low ear placement of the line. Thus the parents possess high frequency of favorable genes for these characters. The estimate of GCA effects showed that the parents CML 518 (P6), was the best general combiner for grain yield along with number of row per ear and ear diameter with highly significant and positive GCA effects. The line CML 383 (P7) was also good combiner for grain yield, number of kernel per row and ear length. Result indicated that inbred line CML 322 (P3) recorded significant gca effects in desirable direction for two characters viz., grain yield (t/ha) and number of row per ear and the inbred line CML 311 (P4), for four different characters viz., grain yield (t/ha), number of row per ear, ear length and ear diameter making them good combiners for improving the traits. Thus, the inbred lines which showed good general combining ability for at least one character can be used as donor parents for the accumulation favorable genes which implied that for improvement of respective traits in hybridization program these lines can be utilized for producing better hybrid due to their good combining ability.

In the present study, crosses manifested considerable variation in SCA effects for different traits and the effects of some crosses showed significant performance in desirable directions for characters under study. CML 331×CML 383 (E20) was considered as the best combination for early maturity due to its highest negative significant SCA value for days to tasseling and silking. Among all the cross combinations CML 332×CML 331 (E9) showed desirable significant negative SCA effects both for plant and ear height indicating that the crosses had a good specific combination for shorter plant height and ear placement. Out of twenty one F_1s, eight crosses, viz. CML

311×CML 331 (E16), CML 331×CML 383 (E20), CML 332×CML 518 (E10), CML 332×CML 383 (E11), CML 332×CML 311 (E8), CML 322×CML 518 (E14), CML 330×CML 331 (E4) and CML 330×CML 322 (E2) showed significant positive SCA effects for yield. The most promising crosses for improving grain yield was CML 311×CML 331 (E16) because it gave the highest positive significant SCA for this trait along with positive significant SCA effect for ear length, ear diameter and number of kernel per row. The cross combination CML 331×CML 383 (E20) was also showed the second highest SCA effects for grain yield and positive significant sca effects for thousand grain weight, ear length and number of kernel per row. So the parents with positive gca for yield and negative GCA for plant and ear height and days to tasseling and silking may be extensively used in the hybridization program as a donor to obtain early and short statured hybrid with higher yield. The cross combinations CML 311×CML 331 (E16), CML 331×CML 383 (E20) and CML 332×CML 518 (E10) were the best specific combiner for yield which may be exploited.

The cross combinations displayed heterosis in both negative as well as positive direction for all the studied traits. The combination CML 332×CML 311 (E8) represented the maximum significant and negative heterosis over BHM 12 and BHM 13 in respect of tasseling and silking duration. For plant height, the maximum significant and negative standard heterosis was expressed by cross CML 330× CML 332 (E1) over BHM 12 and BHM 13. In case of ear height, CML 332×CML 331 (E9) produced the highest significant negative heterosis over BHM 12 and BHM 13. When BHM 14 was considered as a check all the hybrids showed the significant positive heterosis for the above mentioned traits which was not desirable for these traits. In case of grain yield the result of standard heterosis computed relative to BHM 12 and BHM 13 among tested hybrids showed that out of twenty one hybrids, only two hybrids i.e CML 322×CML 518 (E14) and CML 311×CML 331 (E16) exhibited significant positive heterosis over BHM 12 and four hybrids i.e CML 322×CML 518 (E14), CML 311×CML 331 (E16), CML 331×CML 383 (E20) and CML 332×CML 518 (E10) manifested positive heterosis over BHM 13. When BHM 14 was considered as a check, nineteen hybrids showed the significant positive heterosis which was desirable for this trait. CML 322×CML 518 (E14) produced the highest significant positive heterotic value in all the cases.

Results of combined analysis of variance showed that the mean sums of squares for the genotypes were highly significant for all the traits which revealed the presence of genetic variability in the material under investigation for all the characters studied. Environments mean sum of squares were highly significant for all the characters except number of row per ear and thousand grain weights suggesting that these traits were significantly influenced by environments. Variance for genotype x environment interactions were significant for all characters except plant height and thousand grain weight it means that in different locations or environments genotypes exhibited different performance which is due to their different genetic makeup or the variation due to the environments or both. box plot showed that genotypic variation for grain yield was more at Jashore, Hathazari and Jamalpur where genotypic variation was less at Dinajpur and Barishal and the Barishal location gave the highest grain yield. In Barishal, Dinajpur and Jamalpur locations one genotype gave remarkably lower yield than other genotypes. In case of mean yield over the environment three genotypes gave noticeable lower performance than other.

The adaptability in performance across the location for all the genotypes was indicated by the non significant regression coefficient value (bi) different from unity. The differences in bi value ranges from 0.08 to 3.75 reflected the respose of tested hybrid and indicated that these materials responded differently in different environment. The genotypic mean ranged from 6.91 t/ha to 11.75 t/ha. Among the hybrids, Hybrid CML 322×CML 518 (11.75 t/ha), CML 311×CML 331 (11.51 t/ha), CML 331×CML 383 (11.43 t/ha) CML 332×CML 518 (11.28 t/ha) produced higher yield than check BHM 12 and BHM 14. Considering higher grain yield, bi~1 and S^2di~0 indicated that CML 322×CML 518 (E10) and CML 311×CML 331 (E16) were the high yielder and suitable across the environments. On the other hand, CML 331×CML 383 (E20) & CML 332×CML 518 (E14) were high yielder but were responsive to favorable environments. The range of environmental indices for grain yield was -0.37 to 0.51 which reflects the variation in performance from one location to another. The environment of Hathazari was the poorest, where as Barishal and Dinajpur were the most favorable environmental for maize production.

AMMI model is a valuable approach for understanding G x E interaction and obtaining better yield estimates by combining the analysis of variance and principal components analysis. The associations between the hybrids and the environments can be seen clearly when both the hybrids and the environments on the same graph are plotted. The indication of the stability of a genotype over environments was IPCA scores in the AMMI analysis. From the biplot it was observed that among the entries, E14 (CML 322×CML 518), E16 (CML 311×CML 331), E10 (CML 332×CML 518), E20 (CML 331×CML 383), E22 (BHM-12) and E23 (BHM-13) were high yielding hybrids. The cross combinations E14 (CML 322×CML 518), E2 (CML 330×CML 322 and E24 (BHM 14) were more stable because they had smaller IPCA1 score that was near to zero. E21 (CML 518×CML 383), E17 (CML 311×CML 518), E19 (CML 331×CML 518) and E8 (CML 332× CML 311) were average yielder and nearly stable but E11 (CML 332×CML 383) and E3 (CML 330×CML 311) were unstable.

Since IPCA2 scores also played a significant role in explaining the GEI; the IPCA1 scores were plotted against the IPCA2 scores for further exploring adaptation. The AMMI 2 biplot also indicated the relationship among the maize hybrids and indicating that the hybrids E11 (CML 332×CML 383), E22 (BHM 12), E9 (CML 332×CML 331), E3 (CML 330×CML 311) and E15 (CML 322×CML 383) were unstable due to their dispersed position from the other hybrids in the biplot. E24 (BHM-14), E16 (CML 311×CML 331), E13 (CML 322×CML 331), E17 (CML 311×CML 518) and E14 (CML 322×CML 518) were positioned closer to the origin of the biplot which indicated their stability in performance across environments. When genotypes were compared with ideal genotypes it was observed that E14 (CML 322×CML 518), E16 (CML 311×CML 331), E10 (CML 332×CML 518) and E20 (CML 331×CML 383) were the nearest to the ideal genotypes (the center of concentric circles) so it was more desirable than other tested genotypes.

For the identification of better performing hybrids in each location the “Which-Won-Where” function of GGE biplot can be used. The vertex genotypes were E1 (CML 330× CML 332), E9 (CML 332×CML 331), E11 (CML 332×CML 383), E14 (CML 322×CML 518) and E20 (CML 331×CML 383) that were the most responsive one can be visually determined. The vertex genotype for sector which encompassed environments Barishal, Jashore, Jamalpur and Dinajpur was E14 (CML 322×CML 518) and for sector content environment Hathazari was E20 (CML 331×CML 383), these implying that these genotypes were the winning genotypes for respected environments.

Conclusion

Traits measured in this study revealed different levels of variability, heritability and GA estimates in inbred lines. Based on statistical analysis of the morphological traits of the inbred lines, wide variability was found for all the characters studied and thus offer scope for genetic improvement through selection. However, plant height, number of kernel per row, thousand grain weight and grain yield, to a great extent, were governed by additive gene effect, as demonstrated by high heritability and high GA in percentage of mean. Days to tasseling, days to silking, ear height, ear length, ear diameter, number of kernels per row, thousand grain weight showed significant positive correlation with grain yield both at phenotypic and genotypic levels indicating dependence of these characters on each other. From correlation coefficient and path analysis studies, it was found that days to tasseling, ear height, ear diameter, number of kernel per row and thousand grain weight were most important components for getting higher yield due to significant positive correlation with grain yield and had high direct positive effect on yield. Therefore, the present study suggested that these traits were important yield components and selection based on these traits would give better response for improving grain yield. Considering plant architecture and other traits the inbreds were clustered into seven diverged groups. It was expected that inbred lines belonging high to medium D^2 values would give high manifestation of heterosis for yield. On the basis of the findings of the present study, it could be concluded that the genotypes from cluster I, IV and VII were selected to obtain better parents and parents from these clusters would exert high heterosis for further breeding program to obtain desirable new recombinants in respect of different yield and yield contributing characters. The estimate of GCA effects showed that the parents P6 (CML 518) was the best general combiner for grain yield along with number of row per ear and ear diameter with highly significant and positive GCA effects. The parental line P7 (CML 383) was also good combiner for grain yield, number of kernel per row and ear length. Result indicated that parental line P3 (CML 322) recorded significant GCA effects in desirable direction for two characters viz., grain yield (t/ha) and number of row per ear and parental line P4 (CML 311) for four different characters viz., grain yield (t/ha), number of row per ear, ear length and ear diameter making them good combiners for improving these traits. Among all the crosses, the cross combinations CML 311×CML 331 (E16), CML 331×CML 383 (E20) and CML 332×CML 518 (E10) were best specific combiner for yield which may be exploited. In case of grain yield out of twenty one hybrids, only two hybrids i.e CML 322×CML 518 (E14) and CML 311×CML 331 (E16) exhibited significant positive heterosis over BHM 12 and four hybrids viz. CML 322×CML 518 (E14), CML 311×CML 331 (E16), CML 331×CML 383 (E20) and CML 332×CML 518 (E10) manifested significant positive heterosis and CML 322×CML 518 (E14) produced the highest significant positive heterotic value over BHM 13. When BHM 14 was considered as a check nineteen hybrids showed the significant positive heterosis. The AMMI biplot indicated E24 (BHM14), E16 (CML 311×CML 331), E13 (CML 322×CML 331), E17 (CML 311×CML 518) and E14 (CML 322×CML 518) were positioned closer to the origin of the biplot which indicated their stability in performance across environments. When genotypes were compared with ideal genotypes it was observed that E14 (CML 322×CML 518), E16 (CML 311×CML 331), E10 (CML 332×CML 518) and E20 (CML 331×CML 383) were the nearest to the ideal genotypes (the center of concentric circles) so it was more desirable than other tested genotypes.

Findings

Based on this research work, the following findings were ascertained and presented as follows

- Based on characterization, evaluation and statistical analysis of the morphological traits of the inbred lines, wide variability was found for all the characters studied and thus offer scope for selection of inbred lines .
- Inbreds are clustered into seven diverged groups on the basis of multivariate analysis.
- The genotypes from cluster I, IV and VII were selected to obtain better parents and parents from these clusters would exert high heterosis for further breeding program to obtain desirable new recombinants in respect of different yield and yield contributing characters.
- The estimate of GCA effects showed that the parents P6 (CML 518), P7 (CML 383), P3 (CML 322) and P4 (CML 311) were good general combiners for improving the yield and yield contributing traits.
- Among all the crosses the cross combinations CML 311×CML 331 (E16), CML 331×CML 383 (E20) and CML 332×CML 518 (E10) were best specific combiner for yield which may be exploited.
- The result of standard heterosis computed relative to BHM 12 and BHM 13 among the tested hybrids showed that out of twenty one hybrids, only two hybrids i.e CML 322×CML 518 (E14) and CML 311×CML 331 (E16) and four hybrids viz. CML 322×CML 518 (E14), CML 311×CML 331 (E16), CML 331×CML 383 (E20) and CML 332×CML 518 (E10) manifested significant positive heterosis over both BHM 12 and BHM 13, respectively.
- The AMMI biplot indicated that E24 (BHM 14), E16 (CML 311×CML 331), E13 (CML 322×CML 331), E17 (CML 311×CML 518) and E14 (CML 322×CML 518) were positioned closer to the origin of the biplot which indicates their stability in performance across environments.
- When hybrids were compared with ideal genotypes it was observed that E14 (CML 322×CML 518), E16 (CML 311×CML 331), E10 (CML 332×CML 518) and E20 (CML 331×CML 383) were nearest to the ideal genotypes.

Recommendations

Following recommendations could be considered to develop and promote white maize production

- The findings of distinct groupings of germplasm would be a potential source and can be used for further studies in developing improved varieties.
- Breeders need to evaluate germplasm with appropriate tools i.e molecular marker with better genetic base to explore and measure the genetic diversity.
- Further study may be carried out to support and confirm the present findings of stable superior white maize hybrids.
- Considering overall performance on yield, yield contributing characters, combining ability and stability, E14 (CML 322×CML 518) and E16 (CML 311×CML 331) cross combination were found superior. These two hybrids could be released to make available at farmers level for cultivation after further round of evaluation with existing superior variety.

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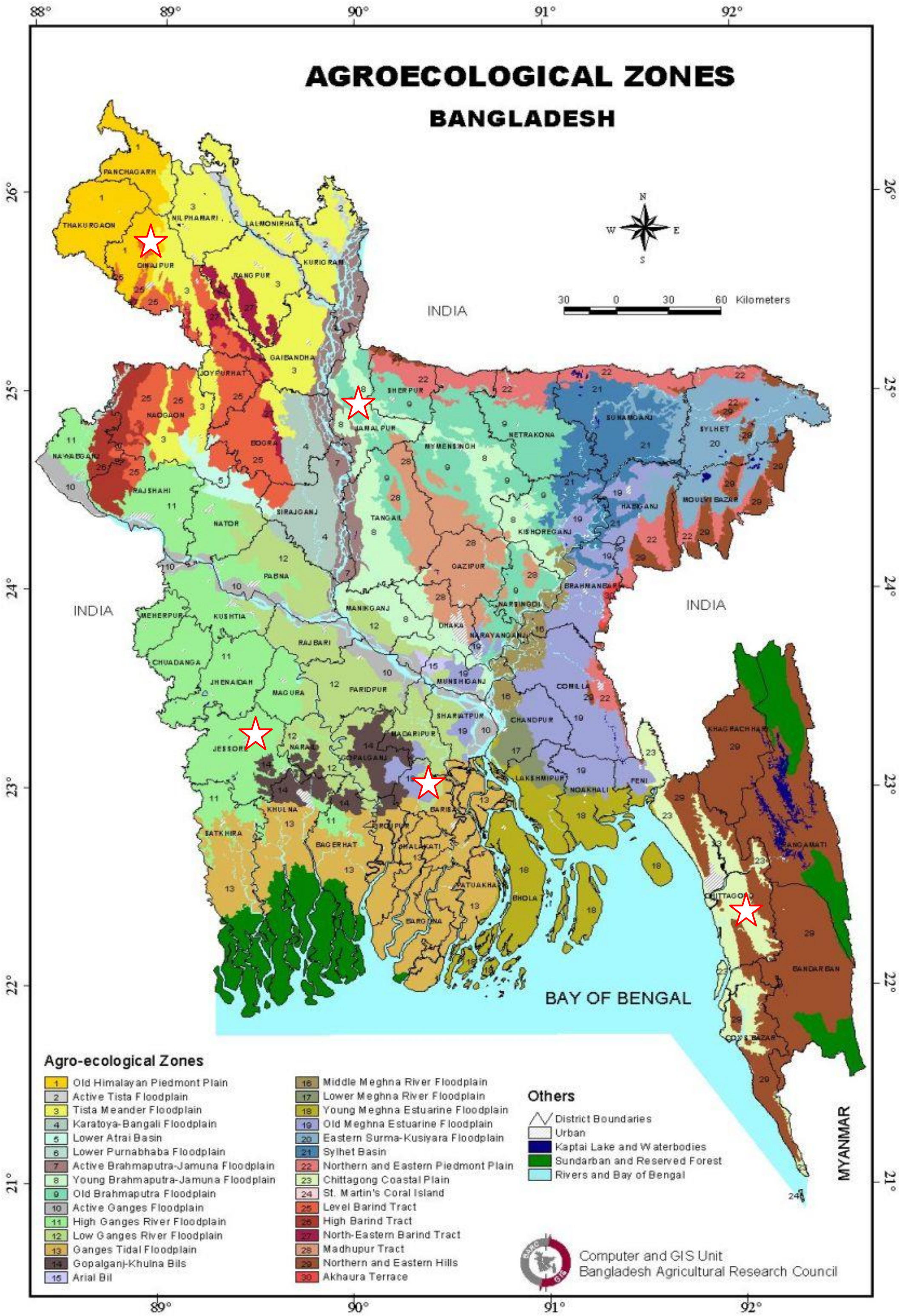
Appendix I. Map showing the experiment site under the study



☆ **The experimental site under study**

Appendix II. Maximum and minimum air temperature, total rainfall and relative humidity at Regional Agricultural Research Station, Rahmatpur, Barishal during the period from November, 2015 to May, 2016

Month	*Air temperatute (^0C)		*Relative humidity(%)	*Total rainfall (mm)
	Maximum	Minimum		
November, 2015	33	15	77	0.6
December, 2015	30	9	77	0
January, 2016	29	8	77	0
February, 2016	34	10	73	0
March, 2016	35	16	71	0
April, 2016	36	20	78	15
May, 2016	37	21	81	4

* Monthly average

Source : The Metrological Department, Agargaon, Dhaka.

Appendix III. The Physical and Chemical characteristics of initial soil (0-15 cm depth) in the experimental field at RARS, Rahmatpur, Barishal

A. Physical composition of the soil

Sl. No.	Soil separates	%	Methods employed
1	Sand	30.00	Hydrometer method (Bouyoucos, 1962)
2	Silt	38.00	Do
3	Clay	32.00	Do
4	Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.88	Walkley and Black, 1935
2	Total N (%)	0.50	Bremmer and Mulvancy, 1982
3	Available P (mg/kg)	20.00	Bray and Kurtz, 1945
4	Available S (mg/kg)	31.7	Page *et al*., 1982
5	Exchangeable K (meq/g)	0.10	Thomas, 1982
6	Exchangeable Ca (meq/g)	6.21	Thomas, 1982
7	Exchangeable Mg (meq/g)	4.55	Thomas, 1982
8	Exchangeable Na (meq/g)	0.48	Thomas, 1982
9	P^H (H_20)	7.10	Page *et al*., 1982
10	P^H (KCl)	6.00	Page *et al*., 1982
11	CEC (cmol/kg)	14.00	Schollenberger ,1980

Appendix IV. Maximum and minimum air temperature, total rainfall and relative humidity at Regional Agricultural Research Station, Rahmatpur, Barishal during the period from November, 2016 to May, 2017

Month	*Air temperatute (^{0}C)		*Relative humidity(%)	*Total rainfall (mm)
	Maximum	Minimum		
November, 2016	29	19	59	3
December, 2016	26	15	77	0
January, 2017	26	12	74	0
February, 2017	27	14	67	0
March, 2017	31	20	73	2
April, 2017	33	24	81	12
May, 2017	34	23	82	5

* Monthly average

Source : The Metrological Department, Agargaon, Dhaka.

Appendix V. Maximum and minimum air temperature, total rainfall and relative humidity at Regional Agricultural Research Station, Rahmatpur, Barishal during the period from November, 2017 to May, 2018

Month	*Air temperatute (^{0}C)		*Relative humidity(%)	*Total rainfall (mm)
	Maximum	Minimum		
November, 2017	23	23	73	0.01
December, 2017	20	20	76	0.03
January, 2018	16	16	75	0.00
February, 2018	22	22	64	0.00
March, 2018	27	26	62	0.01
April, 2018	28	27	53	0.02
May, 2018	29	28	20	0.03

* Monthly average

Source : The Metrological Department, Agargaon, Dhaka.

Appendix VI. Maximum and minimum air temperature, total rainfall and relative humidity at Regional Agricultural Research Station, Jashore during the period from November, 2017 to May, 2018

Month	*Air temperatute (^0C)		*Relative humidity(%)	*Total rainfall (mm)
	Maximum	Minimum		
November, 2017	33	18	69	1
November, 2018	31	10	68	0
January, 2018	32	11	65	0
February, 2018	34	11	49	0
March, 2018	37	15	41	0
April, 2018	40	21	41	7
May, 2018	38	21	62	3

* Monthly average

Source : The Metrological Department, Agargaon, Dhaka.

Appendix VII. Maximum and minimum air temperature, total rainfall and relative humidity at Regional Agricultural Research Station, Jamalpur during the period from November, 2017 to May, 2018

Month	*Air temperatute (^0C)		*Relative humidity (%)	*Total rainfall (mm)
	Maximum	Minimum		
November, 2017	34	15	74	2
November, 2018	29	13	79	0
January, 2018	27	7	75	0
February, 2018	34	13	66	0
March, 2018	35	15	63	0
April, 2018	36	19	68	8
May, 2018	36	21	80	3

* Monthly average

Source : The Metrological Department, Agargaon, Dhaka.

Appendix VIII. Maximum and minimum air temperature, total rainfall and relative humidity at Regional Agricultural Research Station, Hathazari, Chattogram during the period from November, 2017 to May, 2018

Month	*Air temperatute (^{0}C)		*Relative humidity(%)	*Total rainfall (mm)
	Maximum	Minimum		
November, 2017	33	15	80	1
November, 2018	29	11	84	0
January, 2018	27	7	81	0
February, 2018	34	13	75	2
March, 2018	34	15	70	0
April, 2018	36	19	75	9
May, 2018	36	20	84	4

* Monthly average

Source : The Metrological Department, Agargaon, Dhaka.

Appendix IX. Maximum and minimum air temperature, total rainfall and relative humidity at Wheat Research Centre, Dinajpur, during the period from November, 2017 to May, 2018

Month	*Air temperatute (^{0}C)		*Relative humidity(%)	*Total rainfall (mm)
	Maximum	Minimum		
November, 2017	28	14	79	2
November, 2018	22	14	85	0
January, 2018	20	8	90	0
February, 2018	26	14	78	2
March, 2018	30	20	65	0
April, 2018	31	21	71	11
May, 2018	32	20	76	4

* Monthly average

Source : The Metrological Department, Agargaon, Dhaka

Appendix X . Analysis of variance (ANOVA) of the data on yield attributes and yield of fifty eight inbred lines of maize

Source of variation	df	Mean sum of squares									
		Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	Number of row/ear	Number of kernel/row	Thousand grain weight (g)	Grain yield (t/ha)
Genotype	57	33.61**	25.65**	1206.08**	310.07**	5.28**	0.28**	2.93**	23.75**	10168.4**	3.85**
Replication	1	1.24	0.22	793.13	201.85	0.20	0.06	0.12	0.02	116.0	0.43
Residuals	57	2.54	2.71	123.40	69.21	1.01	0.05	0.92	2.97	982.3	0.35

Appendix 11. Mean performance data on yield attributes and yield of twenty four maize hybrids

Crosses	Days to tasseling	Days to silking	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear diameter (cm)	No. of row per ear	No. of kernel per row	Thousand grain weight (g)	Grain yield (t/ha)
1. CML 330× CML 332(E1)	92.07	95.00	163.1	75.31	17.94	5.33	14.03	34.29	440.47	8.55
2. CML 330× CML 322(E2)	95.40	98.20	176.4	98.81	17.59	5.43	14.48	33.96	463.60	10.22
3. CML 330× CML 311(E3)	92.60	95.13	194.0	85.97	18.66	5.49	14.61	32.87	454.00	9.88
4. CML 330× CML 331(E4)	95.73	98.80	167.5	81.68	18.05	5.35	13.47	34.19	451.27	9.97
5. CML 330× CML 518(E5)	93.00	95.80	192.0	92.66	17.34	5.54	15.07	32.64	462.40	10.54
6. CML 330× CML 383(E6)	93.80	96.87	187.1	94.67	19.12	5.14	13.10	36.33	448.93	9.90
7. CML 332× CML 322(E7)	94.27	97.80	196.1	100.28	16.93	5.41	14.51	33.11	455.20	9.69
8. CML 332× CML 311(E8)	91.73	94.60	189.9	96.79	17.93	5.42	14.65	35.40	429.20	10.28
9. CML 332×CML 331(E9)	96.33	100.00	165.0	68.53	15.05	5.08	13.67	31.25	404.40	6.91
10. CML 332×CML 518(E10)	94.40	97.60	184.3	95.22	17.03	5.74	14.82	34.75	448.13	11.28
11. CML 332×CML 383(E11)	93.80	96.53	194.4	98.76	17.98	5.11	12.71	35.72	453.93	10.58
12. CML 322×CML 311(E12)	93.53	96.87	196.1	97.01	18.02	5.40	14.65	35.28	427.27	9.91
13. CML 322×CML 331(E13)	97.20	100.00	191.7	98.37	17.58	5.26	13.98	32.11	439.20	9.89
14. CML 322×CML 518(E14)	95.27	97.60	208.5	107.05	17.29	5.40	14.27	34.41	440.27	11.75
15. CML 322×CML 383(E15)	96.33	99.27	206.5	110.27	18.59	5.20	13.99	35.06	446.27	10.30
16. CML 311×CML 331(E16)	94.53	97.33	196.6	93.25	18.99	5.53	13.82	36.59	433.80	11.51
17. CML 311×CML 518(E17)	93.47	97.07	196.8	97.83	17.96	5.40	14.09	34.53	437.73	10.39
18. CML 311×CML 383(E18)	95.20	98.20	199.5	101.03	17.99	5.11	14.01	32.89	426.93	9.59
19. CML 331×CML 518(E19)	94.67	97.80	197.2	89.85	18.73	5.58	14.92	35.61	460.80	10.24
20. CML 331×CML 383(E20)	95.60	97.67	204.6	95.53	19.62	5.12	13.17	36.41	464.73	11.43
21. CML 518×CML 383(E21)	96.13	100.07	199.3	103.51	18.73	5.11	13.86	35.70	440.93	10.52
22.BHM 12(E22)	94.87	98.53	211.0	104.23	20.93	5.02	13.76	39.02	407.00	10.99
23.BHM 13(E23)	97.07	99.93	205.2	107.91	18.27	5.05	13.44	35.90	444.60	10.79
24.BHM 14(E24)	87.80	90.33	160.7	53.62	16.96	5.06	14.32	31.75	418.27	8.50
Mean	94.37	97.38	190.98	93.67	18.05	5.30	14.06	34.57	441.64	10.15
Maximum	97.2	100.07	211	110.27	20.93	5.74	15.07	39.02	464.73	11.75
Minimum	87.8	90.33	160.7	53.62	15.05	5.02	12.71	31.25	404.4	6.91
SD	2.03	2.17	14.52	12.98	1.11	0.20	0.61	1.80	16.57	1.06