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Genetic Variability and Diversity Studies in Maize (*Zea Mays* L.) Inbred Lines

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Abstract: *Thirty inbred lines of maize were evaluated for ten parameters to study the genetic variability and diversity in maize inbred lines. The experiment was laid out in randomized complete block design (RCBD) with three replications. Mean performance, variability, heritability, coefficient of variation and diversity analysis of yield and yield contributing characters (Cob height, plant height, cob length, cob diameter, number of kernel rows per cob, number of kernels per row, number of kernels per cob, 1000 kernels weight, yield per plant and pith weight) were performed. The highest weight of 1000 kernels (494.3g) was obtained from ML28, the lowest weight of 1000 kernels (213.96g) was recorded from ML21, 1000 kernels weight of phenotypic variation (82.24) was higher than the genotypic variation (18.65), which indicates high environmental effect was supported by narrow difference between phenotypic (23.64) and genotypic (5.36) co-efficient of difference. Weight of 1000 kernels had inherent potential among the genotype high heritability (68.83) for this trait along with high genetic advance in percentage of mean (33.51). All the genotypes were grouped into four clusters. Cluster II was the largest cluster comprising of sixteen maize genotypes followed by cluster I (9) and III (4). Cluster distance denoted by the average inter and intra cluster distance are the approximate measure of the cluster divergence. The maximum (8.34) inter-cluster divergence was observed between the clusters II and IV and it was minimum (3.94) between clusters I and III. The maximum value of inter –cluster distances indicated that the genotypes belonging to the cluster II is far diverged from those cluster IV. Genotypes of cluster II show high intra cluster distance indicating high degree of divergence among the genotypes and also mean performance of genotypes of cluster II show higher result in case of plant height and yield per plant. High degree of performances like plant height, thousand kernel weight and yield per plant with diversified genotypes of cluster II are suitable for selection as parents for future hybridization program.*

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I. Introduction

Maize, the American Indian word for corn, means literally "that which sustains life". It is, after wheat and rice, the most important cereal grain in the world, providing nutrients for humans and animals and serving as a basic raw material for the production of starch, oil and protein, alcoholic beverages, food sweeteners and, more recently, fuel. The green plant, made into silage, has been used with much success in the dairy and beef industries. After harvest of the grain, the dried leaves and upper part, including the flowers, are still used today to provide relatively good forage for ruminant animals owned by many small farmers in developing countries. The erect stalks, which in some varieties are strong, have been used as long-lasting fences and walls. Botanically, maize (Zea mays) belongs to the grass family (poaceae) and is a tall annual plant with an extensive fibrous root system. It is a cross pollinating species, with the female (ear) and male (tassel) flowers in separate places on the plant. 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. Maize provides many of the B vitamins and essential minerals along with fiber, but lacks some other nutrients, such as vitamin B12 and vitamin C, and is, in general, a poor source of calcium, folate, and iron. Iron absorption, particularly the nonheme iron present in maize, can be inhibited by some components or foods in the diet, such as vegetables, tea (e.g., oxalates), coffee (e.g., polyphenols), eggs (e.g., phosvitin), and milk (e.g., calcium). In countries where anemia and iron deficiency are considered moderate or severe public health problems, the fortification of maize flour and cornmeal with iron and other vitamins and minerals has been used to improve micronutrient intake and prevent iron deficiency. In the year 2017/2018, the United States was the largest producer of corn with a production volume amounting to about 370.96 million metric tons. China and Brazil rounded off the top corn producing countries. Total maize production in Bangladesh in the year 2013-14, 2014-15 and 2015-16 was 2123572 MT, 2271998 MT and 2445578 MT, respectively (BBS 2017). So, the production of maize in Bangladesh is continuously increasing. The most limiting factor of maize research in Bangladesh is the development, improvement and maintenance of parental/inbred lines. On the other hand, the problem of imported hybrid seed is the involvement of high price and uncontrolled quality. Moreover, the farmers cannot get the seeds timely. One important approach to improve this situation is the development of inbred lines, which can produce high yielding hybrid varieties. Before hybrid development, prospective parent (inbred line) selection is a pre-requisite. Several studies on maize have shown that inbred lines from diverse stocks tend to be more productive than crosses of inbred lines from same variety (Vasal, 1998). Saxena et al. (1998) also reported that manifestation of heterosis usually depends on the genetic divergence of the two parental lines. The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents for hybrid production. Genetic diversity is one of the useful tools to select appropriate genotypes/lines for hybridization. The genetic diversity

between the diverged parents are able to produce high heterotic effects (Falconer, 1960; Arunachalam, 1981; Ghaderi et al., 1984; Mian and Bahl, 1989). Knowledge of germplasm diversity among elite breeding materials have a significant impact on the improvement of crop plant (Hallauer et al., 1988). Maize breeders are consistently emphasizing the importance of diversity among parental genotypes as a significant factor contributing to heterotic hybrids (Ahloowalia and Dhawan, 1963). Characterization of genetic diversity of maize germplasm is of great importance in hybrid maize breeding (Xia et al., 2005). The present investigation was undertaken with a view to estimate the nature and magnitude of genetic diversity in 30 maize inbred lines.

Considering the above context, the present research work has been undertaken with the following objectives:

- To study the magnitudes of variability of inbreed lines for yield and yield contributing characters
- To analyze the genetic diversity among the genotypes in respect of yield and yield contributing characters
- To select the suitable, inbreed lines for future hybridization program

II. Materials And Methods

Geographical Location of the Experiment

The present piece of research work was conducted at the experimental plot of the Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh during the Rabi seasons, which geographically situated at 25°41' North latitude and 88°39' East latitude with an elevation of 37m from sea level.

Soil and Climatic Condition

The experimental land was medium high land. The soil belongs to the old Himalayan Piedmont Plain agro-economic zone (AEZ-1), textured by sandy loam with pH of around 6.2 during the growing period of the crop total rainfall and mean temperature for the month were recorded.

Experimental Material

In this work, maize inbred lines were used. There are thirty genotypes and each of the genotype was produced in the 2012-2013 cropping seasons, and purity and genotype percentage were around 98% and above 98%, respectively the source of all the genotypes was collected from Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh.

Layout of the Experiment

The experiment was laid out in the randomized complete block design (RCBD) with three replications. The layout of the experiment was prepared for distributing the genotypes into every line of each block. There were total of 90 lines, and 30 genotypes were assigned at random into 30 lines of each replication and each of block measuring 20m x 3.5m. The distance maintained between two lines was 0.60m and block was 0.83m. The total area of the experiment was (20 x 18) square meter.

Preparation of the Main Field

The plot selected for the experiment was opened at the second week of November 2016 with power tiller and was the exposed to the sun for a week, after one week the land was harrowed, ploughed and crossed-ploughed several times followed by laddering to obtain a good tilth. Weed and stable were removed and finally obtained a desired tilth of soil for planting of maize seed. The experiment plot was partitioned into the unit plots in accordance with experiment design mentioned in earlier. The recommended doses of well rotten cow dung as manure and chemical fertilizers as indicated in next were mixed with the soil of each unit plot.

Application of Manure and Fertilizer

Green manure and decomposed organic matter were used at the rate of 6.0 ton/ hector before final land preparation. The chemical fertilizer such as Urea, MOP, Gypsum, boric acid and zinc sulphate were applied in the plot at the rate of 50, 195, 100, 10 and 10kg/ha respectively as basal doze. The rest 1120 kg urea was applied in three equal splits (i.e. 40 kg/splits) a 25, 45 and 60 days after planting as side dressing, 3-5 cm away from the plat and the furrow of the fertilizer are hilled up immediately, At the same time third dressing of Urea, rest 35 kg of MOP was used. The doses and method of application of fertilizer are shown in the Table 1.

Table 1. Dose and methods of application of fertilizers in maize field

Manures and fertilizer	Dose/ha	Application (kg)			
		Basal Dose	25 DAP	45DAP	60 DAP
Cow dung	06 tons	6 tons	--	--	--
Urea	160 kg	40 kg	40kg	40 kg	40 kg
TSP	180 kg	180 kg	--	--	--
MOP	70 kg	35 kg	--	--	35 kg
Gypsum	100 kg	100 kg	--	--	--
Zinc Sulphate	10 kg	10 kg	--	--	--
Magnesium	10 kg	10 kg	--	--	--
Boric acid	10 kg	10 kg	--	--	--

Planting of seed in the field, their care and harvesting

The maize seed were planted in lines, plant to plant distance 0.25 m and row to row distance 0.6 m and socked seed were planted in the well-prepared plot on 24 Nov 2016. When the seedling started to emerge in beds it was kept under careful observation. After emergence of seedling, various inter-culture operations were accomplished for better growth and development of the maize seedling. Irrigation was provided knee stage, pre-flowering stage and milking stage at 35, 65 and 80 days after planting (DAP) for three times of proper growth and development of the plant. The seeding was first thinned from all of the line at 10 days after germination and 2nd thinning was carried out for maintaining proper spacing the

experimental plot. Weeding and mulching were done to keep the plots free from weeds, easy aeration of soil and to conserve soil moisture, which ultimately endured better growth and development. The newly emerged weeds were uprooted carefully after complete emergence of maize seedling as and when necessary. Breaking of crust of soil, when needed was done through mulching. After 50 days of planting, first spray of chloropyriphose was done against sucking pest such as jessid and aphid. The crops were harvested when the husk cover was completely dried and yellowish color was formed in the grain. The cobs of ten randomly selected plants of each genotype were separately harvested.

Data Collection (Quantitative Trait)

Observation on quantitatively inherited traits viz. cob height (cm), plant height (cm), cob length (cm), cob diameter (cm), number of kernel rows per cob, number of kernels per row, number of kernels per cob, thousand kernel weight (g), yield per plant (g) pith weight (g) was recorded on ten competitive randomly selected plants. the average was taken as the mean of treatment.

Statistical analysis

Analysis of variance

Mean data were statistically analyzed for each character separately. The analysis of variance for each character under study was performed by F test. The significance of the difference among the treatment means was estimated by Duncan's Multiple Range Test (DMRT) test at 5% level of probability.

Estimation of variance

Phenotypic and genotypic component of variance were computed according to the formula given by Lush (1940).

Genotypic variance (Vg) = $\frac{Tr.MSS - E.MSS}{r}$

Error variance (ve) = $E.MSS/_{r}$

Phenotypic variance (Vp) = Vg + Ve

Coefficient of variability

Phenotypic and genotypic coefficient of variability were computed according to Burton and Devane (1953)

Genotypic coefficient of variability (GCV):= $\sqrt{\frac{Vg}{x}} \times 100$

Phenotypic coefficient of variability (PCV):= $\sqrt{\frac{Vp}{x}} \times 100$

Vg = Genotypic variance
Vp = Phenotypic variance
X =General mean of the character

Estimation of Heritability

Heritability was estimated as the ratio of genotypic variance to the phenotypic variance and was expressing in percentage (Johnson et al., 1955)

Heritability (h^2): $\frac{Vg}{Vp} \times 100$

Vg = Genotypic variance
Vp = Phenotypic variance

Genetic advance

Genetic advance was computed according to the formula given by Johnson et al. (1955)

Genetic advance (GA)=$ih^2\sqrt{Vp}$

i= Selection differential (2.02) at 5% selection intensity
h2 = Broad sense heritability
Vp = Phenotypic variance

Genetic advance over mean (GAM)

GAM= $\frac{GA}{\bar{x}}$ x100

Where,
GA =Genetic advance
X = mean of the population

Multivariate analysis (D^2 statistics)

Multivariate analysis was done by computer using GENSTAT 16.2 and Microsoft Excel 2007 software through four techniques viz, principal component analysis, principal coordinate analysis, cluster analysis and canonical vector analysis.

Principal component analysis (PCA)

The technique PCA was used to examine the inter relationships among 21 quantitative characters. The principal components were computed from the correlation matrix (obtained from sum of squares and products matrix of the characters) and genotype scores (obtained from the first component and the succeeding component with latent roots greater than unity). The latent roots are called 'Eigen values'. The first component has the property of accounting for maximum variance. The PCA displays most of the original variability in a smaller number of dimensions, since it finds linear combinations of a set of variants that maximize the variation contained within them. Contributions of the different characters towards divergence are discussed from the latent vectors of the first two principal components.

Principal Coordinate Analysis (PCO)

PCO was used to calculate the inter genotype distance and it gave the minimum distance between each pair of the N points using similarity matrix through the use of all dimensions of P (Digby et al., 1989).

Cluster Analysis (CA)

Cluster analysis was performed by D^2 analysis (originally outlined by Mahalanobis 1936 and extended by Rao, 1952), which divides the genotypes based on the data set into homogeneous groups. D^2 is the sum of squares of differences between any two populations for each of the uncorrelated variables (obtained by transforming correlated variables through Pivotal condensation method). Clustering was done using non-hierarchical and hierarchical classification. D^2 statistic is defined by

$D^2x=\Sigma\Sigma(\lambda^{ij})$ di dj

Where,

X=Number of metric in point

P=Number of populations or genotypes

λ^{ij} = the matrix reciprocal to the common dispersion matrix

didj =the differences between the mean values of the two genotypes for the i^{th} and j^{th} characters respectively.

In simpler form D^2 statistic is defined by the formula

$D^2 =\Sigma d_i^2=\Sigma(y^j_i - y^k_{j)}$

Where,

Y=uncorrelated variable (character) which varies from i = to x

X=number of characters.

Superscripts j and k to y= a pair of any two genotypes.

Cluster analysis was performed by computer software Genstat 16.2, which used algorithm to search for optimal values of the chosen criterion. The algorithm did some initial classification of the genotypes into required number of groups and then repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer could be found to improve the criterion, the algorithm switched to a second stage, which examined the effect of swooping of two genotypes of different groups, and so on.

Canonical Vector Analysis (CVA)

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

Computation of average intra-cluster distances

The average intra cluster distance for each cluster was calculated by taking all possible D^2 values within the members of a cluster obtained from PCO. The formula used to measure the average intra cluster distance was:

Intra-cluster distance=$\Sigma D^2/n$

Where,

ΣD^2 is the sum of distances between all possible combinations (n) the genotypes included in a cluster.

n= Number of all possible combination.

III. Results and Discussion

Performance of yield and yield contributing characters

Cob height

The length between first cob to plant base varied from 42.23 cm to 87.43 cm for different genotypes under the present trial. The longest Cob height (87.43 cm) was recorded in ML26 (Table 2), which was statistically similar with ML5, ML29, ML7 ML25, ML30 and ML15 (83.33 cm, 80.83 cm, 79.47 cm, 77.9 cm, 75.97 cm and 74.77 cm). On the other hand, the shortest Cob height (42.23 cm) was observed from ML12 (Table 2) which was statistically similar with ML21, ML13, ML3, ML23, ML14. Genotype found significant at 1% and 5% level of significance (Table 3). The other genotypes showed average performance regarding Cob height. These results are similar to those from the findings of Olakojo and Olaoye, (2005); Nazir et al. (2010); Salami et al. (2007); Zahid et al. (2004); and Raghu et al. (2011).

Table 2. Mean performance of yield and yield contributing characters

Genotypes	Cob height (cm)	Plant height (cm)	Cob length (cm)	Cob diameter (cm)	Number of kernel rows per cob
ML 1	61.83 g-j	187.30 e-j	13.83 c-g	13.77 c-e	14.70 a-b
ML 2	56.43 j-l	158.97 l	14.07 c-g	14.38 b-e	15.13 a-b
ML 3	44.33 l-m	159.93 l	10.28 g	12.67 e-f	14.87 a-b
ML 4	56.87 j-l	158.90 l	14.43 b-g	13.30 d-e	14.73 a-b
ML 5	83.33 a-b	213.37 b	16.60 a-e	15.90 a-c	14.93 a-b
ML 6	73.30 b-g	174.17 k	17.73 a-d	13.78 c-e	12.73 a-b
ML 7	79.47 a-c	195.90 c-e	15.80 a-f	14.17 b-e	12.83 a-b
ML 8	66.37 d-j	167.67 k-l	14.70 b-g	13.93 c-e	13.70 a-b
ML 9	72.77 b-g	203.83 b-d	17.93 a-c	15.40 a-d	13.13 a-b

ML 10	72.53 b-g	168.17 k-l	14.40 b-g	13.77 c-e	12.33 a-b
ML 11	70.13 c-i	185.02 e-j	17.52 a-d	15.03 a-d	14.24 a-b
ML 12	42.23 m	177.17 h-k	15.07 a-f	13.52 d-e	13.43 a-b
ML 13	42.77 m	136.90 m	14.13 c-g	12.77 e-f	15.28 a-b
ML 14	47.30 k-m	188.57 e-i	17.08 a-d	14.20 b-e	13.77 a-b
ML 15	74.77 a-f	203.73 b-d	18.00 a-c	14.32 b-e	12.53 a-b
ML 16	62.59 f-j	193.60 c-f	16.87 a-e	14.80 a-e	16.53 a
ML 17	62.60 f-j	181.33 f-k	16.63 a-e	13.68 c-e	12.40 a-b
ML 18	71.35 b-h	184.47 e-j	13.20 d-g	14.75 b-e	15.50 a-b
ML 19	61.10 g-j	190.90 d-h	19.40 a	14.16 b-e	13.33 a-b
ML 20	58.88 g-k	141.83 m	11.87 f-g	10.98 f	11.73 b
ML 21	42.30 m	137.30 m	12.43 e-g	13.50 d-e	16.13 a-b
ML 22	64.77 e-j	185.73 e-j	17.63 a-d	15.07 a-d	13.73 a-b
ML 23	46.23 k-m	179.07 g-k	16.93 a-e	14.88 a-e	14.70 a-b
ML 24	57.43 i-k	175.53 i-k	15.20 a-f	14.50 b-e	13.80 a-b
ML 25	77.90 a-d	204.83 b-d	17.25 a-d	15.33 a-d	15.03 a-b
ML 26	87.43 a	230.03 a	17.43 a-d	16.28 a-b	15.00 a-b
ML 27	68.93 c-j	192.53 c-g	17.60 a-d	15.38 a-d	13.07 a-b
ML 28	68.37 c-j	191.07 d-h	18.90 a-b	17.03 a	15.23 a-b
ML 29	80.83 a-c	206.33 b-c	15.31 a-f	14.78 a-e	13.53 a-b
ML 30	75.97 a-e	189.13 e-i	14.73 b-g	16.20 a-b	16.37 a
Range	42.23-87.43	136.9-230.03	10.28-19.4	10.98-17.03	11.73-16.53
Mean	64.37	182.11	15.77	14.41	14.15

Plant height

Among the 30 maize genotypes the tallest plant (230.03 cm) was recorded in ML26 (Table 2). Again, the shortest plant (136.9 cm) was observed from ML13 which was statistically similar (137.3 cm) and (141.83 cm) with ML21 and ML20. Different genotypes produced different plant height it is genetically inherited trait. Plant height ranges from (230.03 cm-136.9 cm). Genotype found significant at 1% and 5% level of significance (Table 3). Management practices can also interfere on plant height but in the experiment 30 genotypes were cultivated in similar management practices. Ajmal et al. (2000), Grzesiak, (2001) and Ihsan et al. (2005), Kumar et al. (2006) reported similar results in plant height when working with other genotypes.

Table 2 (Continued). Mean performance of yield and yield contributing characters

Genotypes	Number of kernels per row	Number of kernels per cob	Thousand kernel weight (gm)	yield per plant (gm)	Pith weight (gm)
ML 1	17.73 b-d	291.1 a-d	349.9 a-h	77.2 d-h	28.3 k-n
ML 2	20.07 a-d	306.7 a-d	290.8 d-h	91.3 c-h	30.6 j-m
ML 3	15.10 c-d	247.5 b-d	217.1 g-h	49.7 g-h	16.4 o-p
ML 4	23.13 a-c	308.7 a-d	307.9 c-h	92.5 c-h	25.3 l-n
ML 5	22.80 a-c	337.6 a-c	380.9 a-f	129.9 a-d	51.6 b
ML 6	23.77 a-c	303.1 a-d	364.1 a-g	107.5 b-f	27.7 k-n
ML 7	22.33 a-d	285.8 a-d	394.1 a-e	118.7 a-f	29.2 k-m
ML 8	24.47 a-c	345.0 a-c	323.3 b-h	121.9 a-e	25.7 l-n
ML 9	24.23 a-c	326.2 a-c	460.7 a-b	140.7 a-c	41.2 e-g
ML 10	17.00 b-d	210.9 c-d	436.9 a-d	87.3 c-h	24.4 m-n
ML 11	24.70 a-c	353.9 a-c	313.5 b-h	105.6 b-g	49.9 b-d
ML 12	19.33 a-d	269.6 b-d	266.9 e-h	73.3 e-h	25.6 l-n
ML 13	18.12 b-d	307.5 a-d	233.2 f-h	65.2 f-h	33.3 h-k
ML 14	20.93 a-d	331.4 a-c	362.1 a-g	120.1 a-f	48.1 b-d
ML 15	24.80 a-c	315.1 a-d	450.1 a-c	131.2 a-d	40.7 e-g
ML 16	26.77 a-b	440.3 a	298.6 d-h	120.0 a-f	37.9 f-i
ML 17	20.83 a-d	251.8 b-d	415.5 a-d	102.3 b-g	33.6 h-k
ML 18	20.53 a-d	326.4 a-c	296.9 d-h	90.9 c-h	32.3 i-k
ML 19	24.37 a-c	341.8 a-c	384.4 a-e	128.3 a-e	50.6 b-c
ML 20	11.97 d	163.0 d	308.5 c-h	43.5 h	13.0 p
ML 21	16.93 b-d	282.4 a-d	213.9 h	64.6 f-h	22.1 n-o
ML 22	24.90 a-c	342.0 a-c	422.9 a-d	141.5 a-c	37.8 f-i
ML 23	23.77 a-c	352.2 a-c	323.9 b-h	117.6 a-f	49.8 b-d
ML 24	21.40 a-d	368.8 a-c	302.3 c-h	101.3 b-g	35.5 g-j
ML 25	26.13 a-b	396.0 a-b	363.2 a-g	149.2 a-b	45.1 c-e
ML 26	23.03 a-c	362.8 a-c	425.5 a-d	143.3 a-c	43.9 d-f

ML 27	28.97 a	358.3 a-c	407.7 a-e	152.6 a-b	38.9 e-h
ML 28	22.23 a-d	338.4 a-c	494.3 a	167.2 a	65.9 a
ML 29	24.57 a-c	328.7 a-c	429.5 a-d	136.0 a-c	31.4 j-l
ML 30	19.40 a-d	297.4 a-d	388.9 a-e	130.3 a-d	49.9 b-d
Range	11.97-28.97	163.03-440.27	213.96-494.3	43.54-167.23	13.01-65.93
Mean	21.81	316.35	354.26	110.03	36.20

Cob length

The maize genotypes that were used in the present experiment among them ML19 showed the highest cob length (19.40cm) which was statistically similar with ML19, ML28, ML15, ML9, ML6, ML22, ML27 (Table 2). The lowest cob length (10.28) was recorded from the genotype ML3 which was statistically identical with different genotypes like ML20, ML21, ML18, ML1, ML2, ML13. Longest cob ensured the maximum number of grains per cob and the ultimate result of the highest grain yield per plant. Genotype found significant (Table 3) at 1% and 5% level of significance. Pavan et al. (2011) also showed significant difference in cob length.

Cob diameter

Among the 30 maize genotypes that were used in present trial the highest cob diameter 17.03cm was obtained from ML28 (Table 2), which is statistically identical with ML26 (16.28 cm), ML30 (16.2cm) and ML5 (15.9cm). Again, the lowest cob diameter 10.98cm was recorded from ML20 which was statistically similar with ML3 (12.67cm), ML13 (12.76cm). Cob diameter mainly governed by the genetically basis. Proper management practice and environmental condition also influenced cob diameter of maize genotypes. Genotype found significant at 1% and 5% level of significance (Table 3). Wolf et al. (2008) found similar result in case of cob diameter.

Number of kernel rows per cob

In this present study among 30 genotype that were used in the present trial number of kernel rows per cob varied from 16.53 to 11.73 and the highest number of kernel rows per cob (16.53) was recorded in ML16 (Table 2), which is statistically identical with ML30 (16.37). Lowest number of kernel rows per cob was recorded in ML20 (11.73) which was statistically identical with ML10 (12.33). Genotype was significant (Table 3) at 1% and 5% level of significance. Devi et al. (2001) found significant different in number of kernel rows per cob.

Number of kernels per row

In this present study among 30 genotypes that were used in the present trial highest number of kernels per row (28.97) was recorded in ML27, which is statistically identical with ML16 (26.77) and ML25 (26.13). As indicated in Table 2, lowest data was recorded in ML20 (11.97) which was statistically identical with ML3 (15.1). Genotype was found significant at 1% and 5% level of significance (Table 3), which are in conformity with the findings of number of kernels per row (Raghu et al., 2011). Sumalini (2012) found significant differences among the variety for the number of kernels per row.

Number of kernels per cob

From Table 2, it is seen that among the 30 different maize genotypes that were used in the present trial the maximum total number of kernels per cob (440.27) was found from ML16, which is statistically related with ML25 (396.0). On the other hand, the minimum number of kernels per cob (163.03) was recorded from ML20 which is statistically identical with ML10 (210.87) and ML3 (247.5). In case of number of kernels per cob genotype was found significant at 1% and 5% level of significance (Table 3).

Thousand kernel weight

Considering the different maize genotypes, the highest thousand kernel weight (494.3g) was obtained from ML28 (Table 2), which is statistically similar with ML9 (460.74g), ML15 (450.08g). On the contrary, the lowest weight of 1000 kernels (213.96g) was found from ML21 which was statistically identical with ML3 and ML13. Different genotypes produce different size of kernels because it is a genetically controlled trait. Management practices can interfere on weight of 1000 seeds, but the 30 genotypes were cultivated in similar management practices and environmental condition. Under these management and environmental condition all of the genotypes produced different weight of 1000 kernels. Genotype was found significant at 1% and 5% level of significance (Table 3). Similar results have been reported in maize by Devi et al. (2001)

Table 3. Analysis of variance (mean squares) of yield and yield contributing character of 30 maize inbred lines

Source of variation	Degrees of freedom	Mean square									
		Cob length (cm)	Plant height (cm)	Cob length (cm)	Cob diameter (cm)	Number of kernel rows per cob	Number of kernels per row	Number of kernels per cob	Thousand kernel weight (gm)	Yield per Plant (gm)	Pith weight (gm)
Genotypes	29	500.95**	1431.05*	14.1*	4.4**	4.79**	41.21**	8683.6*	16072.1**	2963.0	424.41*
Replication	2	183.55	185.93	5.11	0.43	2.51	1.18	353.2	5861.1	214.44	6.23
Error	58	16.07	18.84	2.08	0.49	2.05	11.22	2439.8	2108.2	304.49	3.71
Coefficient of variation		6.23	2.38	9.15	4.88	10.12	15.36	15.61	12.96	15.86	5.32

*** indicate 5% level of significant; ** indicate 1% level of significant**

Yield per plant

Among the 30 maize genotypes maximum yield per plant (167.23g) was recorded from ML28 (Table 2), which is statistically identical with ML27 (152.63g) and ML25 (149.15g). Lowest yield per plant was recorded from ML20 (43.54g), which is statistically identical with ML3 (49.7). In case of yield per plant the maize genotypes showed significant difference in 1% and 5% level of significance (Table 3). Although the management practices and the environmental condition can interfere on yield per plant, all the genotypes were cultivated in similar management practices and environmental condition.

Pith weight

Data of pith weight was also recorded of the maize genotypes of present study and presented in Table 2. Considering the 30 maize genotypes the highest pith weight (65.93g) was found in ML28. The lowest pith weight (13.01g) was found in ML20 which is statistically similar with ML3. Under same management practice and environmental condition genotypes considered in the study showed significant difference at 1% and 5% level of significance (Table 3) and proved that pith weight is also a genetically controlled trait.

Study of variability for yield and yield contributing characters

In the present experiment genotypic and phenotypic variance, heritability, genetic advance and genetic advance in percentage of mean was estimated for 10 yield contributing characters and yield of 30 maize genotypes and presented in Table 4 with probable interpretation under the following headings.

Cob height

Phenotypic variation (13.33) was higher than the genotypic variation (7.97) which was supported by narrow difference between phenotypic (20.98) and genotypic (12.54) co-efficient of variation. Again, high heritability (80.96) with high genetic advance in percentage of mean (39.30) was found for this trait which indicated that this trait was controlled by mainly additive genetic effect and further selection of this trait be effective. Similar results were also reported by Arha et al. (1998). Sumalini (2012) estimated Cob height showed high GCV combined with high heritability indicating improvement of these traits through simple per se selection and using them in hybrid breeding programme.

Plant height

In the context of plant height in terms of phenotypic variation (22.13) was higher than genotypic variation (3.97) indicating high environmental influence on this character. There was considerable variation between phenotypic (140.31%) and genotypic (25.18%) coefficient of variation. High heritability (96.15 %) of this trait along with high genetic advance in percentage of mean (277.91) indicating the importance of additive gene effect for the controlling of the character. Genetic improvement of this character would therefore be moderately effective. Rafique et al. (2006) reported that heritability, coefficient of variation and genetic advance value were computed for plant height. Lower difference was obtained by Satyanarayana and Saikumar (1996). Sumalini (2012) recorded high heritability for plant height (99.2%).

Cob length

Phenotypic variation (2.47) was lower than the genotypic (13.19) indicating high genetically persuade on this character along with low phenotypic (1.42%) and genotypic (7.58%) co-efficient of variation. Moderately high heritability (65.83%) for cob length attached with very low genetic advance in percentage of mean (1.92) which suggested that this trail was high heritable but there is both additive and non-additive gene effect which controls the trait cob length. Heterosis breeding may be useful for further improvement of this trait. Low values of GCV and PCV indicates the need for creation of variability either by hybridization or mutation followed by selection.

Cob diameter

In context of cob diameter in term of genotypic variation (3.80) was higher than the phenotypic (1.34) indicating low environmental persuade on this characters and high genetic effect which was supported by considerable phenotypic (9.30%) and high genotypic (26.34%) co-efficient of variation. High heritability (72.49%) for cob diameter attached with medium genetic advance in percentage of mean (13.89) which suggested that this trait was highly heritable and selection on the basis of this trait will be effective. Swamy et al. (1971), Lias et al. (1987) and Dawood and Mohamed (1997) reported high heritability for cob diameter.

Table 4. Estimation of genetic parameters for of yield and yield contributing characters of 30 maize inbred lines

Characters	Variances			Coefficients of variation		Coefficients of variation (%)		Heritability in broad sense (%)	Genetic advance	Genetic advance in (%) mean
	Genotype	Phenotype	Environmental	Genotypic	Phenotypic	Genotypic	Phenotypic			
CH	7.97	13.33	16.07	0.12	0.21	12.54	20.98	80.96	2497.70	39.30
PH	3.97	22.13	18.84	0.25	1.40	25.18	140.31	96.15	4382.63	277.91
CL	13.19	2.47	2.08	0.07	0.01	7.58	1.42	65.83	334.62	1.92
CD	3.80	1.34	0.49	0.26	0.09	26.34	9.30	72.49	200.15	13.89
NKRC	3.76	1.72	2.05	0.26	0.12	26.58	12.18	30.84	109.39	7.73
NKR	4.69	4.61	11.22	0.21	0.21	21.31	20.91	47.12	447.04	20.29
NKC	17.55	67.24	2439.8	0.06	0.22	5.70	21.83	46.03	6376.38	20.70
TKW	18.65	82.24	2108.2	0.05	0.24	5.36	23.64	68.83	11659.7	33.51
YPP	10.42	34.51	304.49	0.09	0.32	9.60	31.81	74.43	5290.47	48.77
PW	6.07	11.99	3.71	0.16	0.32	16.46	32.52	92.42	2407.81	65.25

Here, CH= Cob height, PH= Plant height, CL= Cob length, CD= Cob diameter, NKRC= Number of kernel rows per cob, NKR=Number of kernel rows, NKC=Number of kernels per cob, TKW= Thousand kernel weight, YPP= Yield per plant, PW= Pith weight

Number of kernel rows per cob

In case of number of kernel rows per cob, genotypic variation (3.76) was higher than the phenotypic (1.72) indicating high genetic persuade on this character which was supported by considerable difference between phenotypic (12.18%) and genotypic (26.58%) co-efficient of variation and high genotypic co-efficient of variation. Moderate heritability (30.84%) for number of kernel rows per cob attached with low genetic advance in percentage of mean (7.73) which suggested that this trail was moderately heritable and selection on the basis of family and progeny test will be effective. Reddy et al. (1992) reported magnitude of PCV and GCV was high for number of kernel rows per cob.

Number of kernels per row

Due to the consideration of number of kernels per row, genotypic (4.69) variation was higher than phenotypic (4.61) variation indicating high genetically effect on this character which was supported by high phenotypic (20.91%) and genotypic (21.31%) co-efficient of variation and considerable difference between them. Moderate heritability (47.12%) for number of kernels per row attached with considerably high genetic advance in percentage of mean (20.30) which suggested that this trail was moderately heritable, and few genes control this trait. As this trait possessed high variation, it has high genetic potential and selection will be effective for future genetic improvement of this trait. Sumalini (2012) observed wide difference between PCV and GCV estimates for kernels per row, Rafiq (2010) reported higher genetic advance for kernel per row depicts additive gene effects and high heritability estimates were recorded in number of kernels per row.

Number of kernels per cob

Total number of kernels per cob in respect of phenotypic variation (67.24) was higher than the corresponding genotypic variation (17.55) indicating high environmental influence. The phenotypic (21.83) co-efficient of variation was higher but genotypic (5.70) co-efficient of variation was low. The low GCV indicates that simple selection based on this trait will not be suitable. Moderate heritability (46.03%) for total number of kernels per cob along medium genetic advance in percentage of mean (20.70). The average estimate of these genetic parameter suggested that number of grains per cob was controlled joint action of genetic and non-genetic factor.

Thousand kernel weight

In term of 1000 kernel weight of phenotypic variation (82.24) was higher than the genotypic variation (18.65) indicating high environmental influence on this character which was supported by high phenotypic (23.64) and low genotypic (5.36) co-efficient of variation. The finding indicated that environment had played a big role with little genetic variation among the genotype for this trait. Therefore 1000 kernel weight had inherent potential among the genotype and moderately high heritability (68.83%) for this trait along with high genetic advance in percentage of mean (33.51) indicating the importance of additive gene effect for controlling the trait. Genetic improvement of this character would therefore be effective for the selected genotype. Similar results were also reported by Debnath (1988) for this trait. Singh (1970) evaluated low heritability for 1000 grain weight.

Yield per plant

In case of the trait yield per plant phenotypic (34.51) variation was higher than genotypic (10.42) variation which indicates the influence of environment on the character which was supported by high phenotypic (31.81) and low genotypic (9.60) co-efficient of variation. Therefore, yield per plant had a high heritability (74.43%) coupled with high genetic advance in percentage of mean (48.77). Yield per plant showing additive gene effect and so selection based on this character may be effective.

Pith weight

Considering the character pith weight phenotypic variation (11.99) was higher than genotypic variation (6.07) indicating a moderate environmental influence. Phenotypic (32.52) variance was high with moderate genotypic (16.46) variance. The character showing high heritability (92.42) with higher genetic advance in percentage of mean (65.25). High inherent potential along with high genetic advance and medium genotypic co-efficient of variation indicate selection will be effective for this trait because the character pith weight is controlled by few genes with a little environmental effect. High heritability coupled with high genetic advance as percentage of mean observed for Cob height, plant height, thousand kernel weight, yield per plant and pith weight. Thus, the straits are predominantly under the control of additive gene action and hence, these characters can be improved by selection. Similar results were reported by Khehra et al. (1985), Reddy and Agarwal (1992), Saha and Mukherjee (1993), Kabdal et al. (2003), Abayi et al. (2004), Akbar et al. (2006), Sofi and Rather (2007), Ali et al. (2010) and Reddy et al. (2012).

Genetic Diversity

Mahalanobis'D^2 -statistics was used to measure the degree of diversification among the genotypes. Using this technique, grouping of genotypes was arranged into four clusters, where genotypes grouped together were less divergent than the ones placed in different cluster are more divergent. The cluster separated by greatest statistical distance exhibited maximum divergence. Composition of different cluster with their corresponding genotypes and their source are shown in table7. Cluster II was the largest cluster comprising 16 maize genotypes followed by cluster I and III with 9 and 4 genotypes. Cluster IV contents only 1 genotype. By application of non-hierarchical clustering using Distance matrix, 30 inbred lines of maize were grouped into four different clusters (Table 5). It was revealed that cluster II comprised maximum number (16) of genotypes, followed by cluster I and cluster III comprising 9 and 4 genotypes, respectively. The lowest (1) genotype was included in cluster IV.

Table 5. Clustering pattern of 30 maize genotypes

Cluster group	Number of genotypes	Name of the genotypes
I	9	ML 1 ML 10 ML 17 ML 18 ML 2

		ML 24 ML 4 ML 6 ML 8
II	16	ML 11 ML 14 ML 15 ML 16 ML 19 ML 22 ML 23 ML 25 ML 26 ML 27 ML 28 ML29 ML 30 ML 5 ML 7 ML 9
III	4	ML 12 ML 13 ML 21 ML 3
IV	1	ML 20

Clustering pattern of inbred lines under this study reveals that the inbred lines showed considerable genetic diversity among themselves by occupying four different clusters. Similar results were reported by Singh et al. (2005) and Liu et al. (2006) in maize and by Masud et al. (1995) in pumpkin. Another study was carried out by Chen et al. (2007) who reported that 186 maize genotypes could be classified into ten clusters. Similar results were reported by Gaur et al. (1978) in potato, Mannan et al. (1993) in Colocasia esculenta and Singh and Singh (1979) in okra.

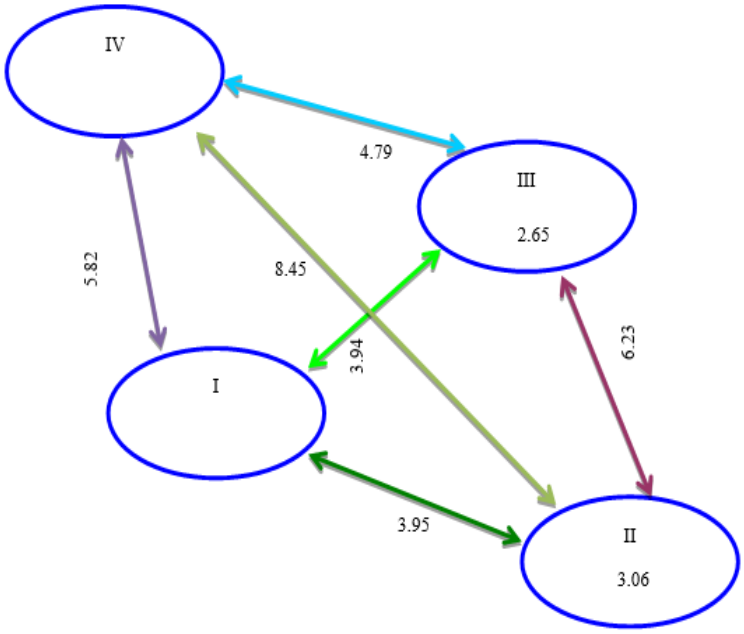

Figure 1. Cluster diagram showing intra and inter cluster distances of 30 Maize inbred lines

The inter cluster distance were always higher than intra cluster distance suggesting wider genetic diversity among the genotype of the groups. The maximum inter-cluster divergence (8.45) was observed between the clusters II and IV and it was minimum (3.94) between clusters I and III (Figure 1). Intra cluster distance was much lower than the inter cluster one, suggesting, heterogeneous and homogeneous nature between and within groups, respectively. This was further supported by an appreciable variation observed for cluster means. Clusters with comparatively less magnitude of divergence showed instability, while widely divergent clusters remained distinct in different environments (Somayajulu et al., 1970 and Singh et al., 1980). Higher inter and intra cluster distances indicate the higher genetic variability among accessions between and within clusters, respectively. The lower inter and intra cluster distance indicates closeness among the accession of two clusters and within the clusters.

Table 6. Cluster mean for ten characters of 30 maize inbred lines

Characters	I	II	III	IV
First cob length (cm)	64.30	70.12	42.91	58.88
Plant height (cm)	172.94	197.10	152.82	141.83
Cob length (cm)	14.91	17.19	12.98	11.87
Cob diameter (cm)	13.99	15.18	13.11	10.98
Number of kernel rows per cob	13.89	14.25	14.93	11.73
Number of kernels per row	20.99	24.00	17.37	11.97
Number of kernels per cob	301.39	344.25	276.74	163.03
Thousand kernel weight (gm)	343.08	393.78	232.78	308.45
yield per plant (gm)	96.94	133.26	63.22	43.54
Pith weight (gm)	29.27	44.50	24.37	13.01

The cluster II composed of sixteen genotypes (Table 5). These were ML11, ML14, ML15, ML16, ML19, ML22, ML23, ML25, ML26, ML27, ML28, ML29, ML30, ML5, ML7, ML9. It produced the highest Cob height, plant height, cob length, cob diameter, number of kernels per row, number of kernels per cob, thousand kernel weight, yield per plant and pith weight.

Cluster III contain four genotypes such as ML12, ML13, ML21, ML3 (Table 5). It produces the highest number of kernel rows per cob and low Cob height and thousand kernel weight in all other character such as plant height, cob length, cob diameter, number of kernels per row, number of kernels per cob, 1000 kernel weight, yield per plant and pith weight produce moderate value.

Cluster IV consists of one genotype namely ML20 (Table 5). This group produce lowest plant height, Cob length, Cob diameter, number of kernel rows per cob, No. of kernel rows per cob, number of kernels per row, number of kernels per cob, yield per plant and pith weight. It produced moderate value of Cob height and thousand kernel weight.

Genetically distant parents usually able to produce higher heterosis (Falconer, 1960; Moll et al., 1962 and Mian and Bhal 1989). Endang et al. (1971) stated that the clustering pattern could be utilized in choosing parents for cross combinations which likely to generate the highest possible variability for effective selection of various economic traits. It was observed that the cluster mean value that in group II contain the tallest plant with high yield per plant and in cluster IV had dwarf plant. Genotypes of cluster II show high intra cluster distance indicating high degree of divergence among the genotypes and mean performance of genotypes of cluster II show higher result in case of plant height and yield per plant. So, the genotypes of cluster II can be selected as parents for future hybridization program.

IV. Summary and Conclusion

The present study was conducted to study the genetic variability and diversity in maize. The genotypes which had been studied in this present experiment were named as ML1, ML2, ML3, ML4, ML5, ML6, ML7, ML8, ML9, ML10, ML11, ML12, ML13, ML14, ML15, ML16, ML18, ML19, ML20, ML21, ML22, ML23, ML24, ML25, ML26, ML27, ML28, ML30, ML30.This experiment was laid out in randomize complete block design (RCBD) with three replications. Mean performance, Variability, coefficient of variation and diversity analysis were done by using yield and yield contributing character viz., Cob height, plant height, cob length, cob diameter, number of kernel rows per cob, number of kernels per row, number of kernels per cob, thousand kernel weight, yield per plant and pith weight. All the genotypes were clustered in 4 groups. Cluster II was the largest cluster comprising 16 maize genotypes followed by cluster I and III with 9 and 4 genotypes, cluster IV contain 1 genotype. It was observed that the cluster mean value that in group II (ML5, ML9, ML15, ML19, ML25, ML26, ML28, ML29 and ML 30) contain the tallest plants with high yield per plant, while genotype including cluster IV was dwarf type.

References

[1]. Abayi, I. K., Ojo, A. A., Kalu, B. A. and Adeyemo, M. O. 2004.Genetic variability, heritability and genetic advance in S_1 progenies of extra-early and early maize (Zea mays L.) populations. Journal of Sustainable Agriculture and the Environment.6(2): 179-184

[2]. Ahloowalia, B. S. and Dhawan, N. I. 1963. Effect of genetic diversity in combining ability of inbred lines of maize. Indian Journal of Genetics, 23: 158-162.

[3]. Ajmal, S. U., Sohail, K., Saleem, M. and Haq, M. I. 2000. Association analysis for grain yield and yield components in maize. Pakistan Journal Plant Science, 6: 12-17.

[4]. Akbar, M., Shabbir, M., Hussain, A. and Sarwar, M. 2006. Evaluation of maize three-way crosses through genetic variability, broad sense heritability, character association and path analysis. Journal of Agriculture Research. 46(1): 39-45.

[5]. Ali, A. W., Hasan, K.A. and Samir, A. 2010. Genetic variances, heritability, correlation and path coefficient analysis in yellow maize crosses (Zea mays L.). Agriculture and Biology Journal of North America. 1(4):630-637.

[6]. Arha, M.D., Sarda, R.P., and Agarwal, K.N. 1998. Studies on maize gene pools II: Heritability and expected genetic advance. Acta Agron Hung, 39:121-125.

[7]. Arunachalam, V. 1981. Genetic distance in plant breeding. Indian Journal of Genetics, 41: 226-236.

[8]. Bangladesh Bureau of Statistics (BBS), 2017. Yearbook of Agricultural Statistics-2016. 28th Series. Statistics and Informatics Division (SID). Ministry of Planning Government of the People's Republic of Bangladesh.

[9]. Burton, G.W. and Devane 1953. Quantitative inheritance in grass pea. Proceed of the 6-int. grassland. Cong, 1:277-283.

[10]. Chen FaBo, Yang KeCheng, Rong Ting Zhao and Pan Guang Tang 2007. Analysis of genetic diversity of maize hybrids in the regional tests of Sichuan and Southwest China. Acta Agronomica Sinica, 33(6): 991-998.

[11]. Dawood, K.M. and Mohammad, A.S.A. 1997. Estimate of heritability and path coefficient analysis for some characters in maize. Mesopotamia journal Agriculture. 21:243-254.

[12]. Debnath, S.C.1988. Genotypic and phenotypic variability in quantitative character in maize. Bangladesh Journal of Agriculture Science.14:7-10.

[13]. Devi, I. S., Muhammad S. and S. Muhammad. 2001. Character association and path co-efficient analysis of grain yield and yield components in double crosses of maize. Crop Research Hisar.21: 355-359.
[14]. Digby, P.N., Galway and P. Lane. 1989. Gentat 5: A Second course. Oxford Sci. Publication, Oxford. pp. 103-108.
[15]. Endang, S., S. Andani, and H. Nasoetion. 1971. Multivariate classification of some rice (Oryzae sativa L.) varieties and strain on yield components. Int. Rice comm. Newst.20: 26-34.
[16]. Falconer, D. S. 1960. Introduction to quantitative genetics. Oliver & Boid, London. 304 p.
[17]. Gaur, P.C., P.K. Gupta and H. Kishore. 1978. Studies on genetic divergence of potato. Euphytica.27: 361-368.
[18]. Ghaderi, A., Shishegar, M., Regai, A. and Ehdaie, B. 1984. Multivariate analysis of genetic diversity for yield and its components in mung bean. Journal of American Society of Horticultural Science, 104: 728-731.
[19]. Ghosal, S., Biswas, P.L., Khatun, M. and Khatun S. 2010.Genetics variability and character associations in irrigated rice (Oryzae sativa L.). Bangladesh Journal of Plant Breeding and Genetics., 23(2): 23-27
[20]. Grzesiak, S. 2001. Genotypic variation between maize (Zea mays L.) single-cross hybrids in response to drought stress. Acta Physiology of Plant.23(4): 443-456.
[21]. Hallauer, A.R., Filho, J.B., 1988. Quantitative genetics in maize breeding, 2nd edn. Iowa State University Press.
[22]. Ihsan, H., Khalil, I. H., Rehman H. and Iqbal.M.2005.Genotypic Variability for morphological traits among exotic maize hybrids. Sarhad Journal Agriculture.21(4):599-602.
[23]. Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimation of genetic and environmental variability in soybeans. Agronomy.1(3):314-418.
[24]. Kabdal, M. K., Verma, S. S., Ahmad, N. and Panwar, U. B. S. 2003. Genetic variability and correlation studies of yield and its attributing characters in maize (Zea mays L.). Agricultural Science Digest. 23(2): 137–139.
[25]. Khehra, A. S., Malhi, N. S. and Pal, S. S. 1985. Estimation of genetic parameters in an open pollinated variety of maize. Crop Improvement.12: 137-140.
[26]. Kumar, S., Shahi, J.P., Singh, J and Singh, S.P. 2006.Correlation and path analysis in early generation inbreds of maize (Zea mays L.). Crop improvement. 33(2): 156-160.
[27]. Lias, S.J., Xu Z.B. and Wen S.P. 1987. Analysis of combining ability for major quantative character in maize in some maize inbred lines. Ningxia Agriculture and Forestry Science and Technology.5: 10-12.
[28]. Liu Yu Ai, Hou Jian Hua, Gao Zhi Jun and Zhou Wei 2006. Principal component analysis and cluster analysis of introduced maize varieties. Journal of Maize Science. 14(2):16-18.
[29]. Lush, J.L., 1940. Animal Breeding plans. Third Edition. The collegiate press, Ames, Iowa.
[30]. Mahalanobis, P.C., 1936. On the generalized distance in statistics. Proceedings of the National Institute of Science, India. 2(1): 49-55
[31]. Mannan, M.A., M.S. Ahmed, M.M. Rashid, M.K.R. Bhuiyan and R. Gomes. 1993. Genetic diversity of Colocasia esculenta (L.) Schott. Indian J. Root Crops 19(2): 95-99.
[32]. Masud, M. A. T., Chowdhury, M. A., Hossain. M. A. and Hossain, S. M. M. 1995. Multivariate analysis in pumpkin (Cucurbita moschata Duch ex. Poir). Bangladesh Journal of Plant Breeding and Genetics. 8(1&2): 45-50.
[33]. Mian, M. A. K. and Bahl, P. N. 1989. Genetic divergence and hybrid performance in chickpea. Indian Journal of Genetics, 49: 119-124.
[34]. Moll, R. H., W. S. Salhwana and H. R. Robinson. 1962. Heterosis and genetic diversity in variety crosses in crop maize. Crop Sci. 2:197-198.
[35]. Nazir, H., Zaman, Q., Amjad, M., Nadeeman A., and Aziz. 2010. Response of maize varieties under agro-ecological conditions of Dera Ismail khan Journal of Agriculture Research. 48(1): 59-63.
[36]. Olakojo, S. A. and. Olaoye G. 2005. Combining ability for grain yield, agronomic traits and strigalutea tolerance of maize hybrids under artificial Striga infestation. African Journal Biotechnology. 4(9): 984-988.
[37]. Pavan, R., Lohithaswa, H.C., Wali, M.C., Prakash. G. and Shekara, B.G. 2011. Correlation and path analysis of grain yield and yield contributing traits in single cross hybrids of maize (Zea mays L.). Electronic Journal of Plant Breeding. 2(2): 253-257.
[38]. Rafiq, M., Rafique M, Hussain A and Altaf M., 2010. Studies on heritability, correlation and path analysis in maize (Zea mays). Journal of Agriculture Research. 48(1).
[39]. Rafique, M.R., Amer, H., Tariq, M. and Abdul, W.A. 2006. Heritability and Interrelation among grain yield and yield component in maize (Zea maize). International Journal of Agriculture and biology. pp. 1560-8530.
[40]. Raghu, B., Suresh, J., Sudheer Kumar, S. and Saidaiah, P. 2011. Character association and path analysis in maize (Zea mays L.). Madras Agricultural Journal. 98(1-3): 7-9.
[41]. Rao P.K. 1952. Error variance and covariance matrix obtained from analysis of variance and covariance were inverted by pivotal condensation method. Element of Biometrical genetics. Concept publishing Company. New Delhi, India.p.44.
[42]. Reddy V.R., Jabeen F., Sudarshan M.R. and Rao A.S. 2012. Studies on genetic variability, heritability, correlation and path analysis in maize over location. www.ijabpt.com.4(1).
[43]. Reddy, K.H. P. and Agarwal, B.D. 1992. Estimation of genetic variation in an improved population of maize (Zea mays L.). Madras Agricultural Journal. 79(12): 714-719.
[44]. Saha, B. C. and Mukherjee, B. K. 1993. Grain yield of maize in relation to grain forming potential and other traits. Journal of Research, Birsa Agricultural University.5: 27-31.
[45]. Salami, A. E., Adegoke S. A. O. and Adegbite. O. A. 2007. Genetic variability among maize cultivars grown in Ekiti-State, Nigeria. Middle-East Journal Science and Research.2(1): 09-13.
[46]. Satyanarayan, E. and Sai Kumar, R. 1996. Genetic variability of yield and maturity components in maize hybrids. Current Research. 25: 10- 16.
[47]. Saxena, V.K., Mathi, N.S., Singh, N.N. and Vasal, S.K. 1998. Heterosis in maize: Grouping and patterns. Proc. of 7th Asian Regional Maize Workshop. Los Banos, Philippines. February 23-27, 124-133.
[48]. Singh K and Sharma D. 1970. Genetic variability in a germplasm complex of maize and genetic advance through selection of full sib families. Indian Journal of Agriculture Science.40:366.
[49]. Singh, D., P. Kumar and B.P.S. Chandan. 1980. Genetic diversity for some quantitative characters in barley. Indian Journal Genetics. 40(2): 391-395.
[50]. Singh, P., Sain, D., Dwivedi, V. K., Kumar, Y. and Sangwan, O. 2005. Genetic divergence studies in maize (Zea mays L.). Annals of Agricultural and Biological Research. 10(1): 43-46.
[51]. Singh, S.P. and H.N. Singh. 1979. Genetic divergence in okra (Abelmoschus esculentus L. Moech) Indian Journal of Horticulture. 36(2): 166-170.
[52]. Sofi, P. and Rather, A.G. 2007. Studies on genetic variability, correlation and path analysis in maize (Zea mays L.). International Journal of Agricultural Sciences. 3(2): 300-303.
[53]. Somayajulu, P.L.N., A.B. Joshi and B.R. Murty. 1970. Genetic divergence in wheat. Indian Journal of Genetics. 30(1): 47-58.
[54]. Sumalini K. and Manjulatha G. 2012. Heritability, correlation and path coefficient analysis in maize. Maize Journal. 1(2): 97 –101.
[55]. Swamy R.T., Ramamurty A., Patil S.J., Aradhya R.S. and Mahadevappa M. 1971. Genetic variability and heterosis in maize. Maderas agricultural Journal. 58:620-623.
[56]. Vasal, S. K. 1998. Hybrid maize technology: Challenges and expanding possibilities for research in the next century. Proc. of 7th Asian Regional Maize Workshop. Los Banos, Philippines. February 23-27, 58-62 pp.
[57]. Wolf, D.P., Peternell, i L.A. and Hallauer, A.R. 2008. Estimates of genetic variance in an F2 maize population. Maize Journal. 91(5): 384-91.
[58]. Xia, X. C., Reif, J. C., Melchinger, A. E., Frisch, M., Hoisington, D. A., Beck, D., Pixley, K. and Warburton, M. L. 2005. Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers. Crop Science, 45; 2573-2582.
[59]. Zahid, M., S. Ajmal, G. Jilani, M. Irfan and M. Ashraf. 2004. Genetic studies for high yield of maize in Chitral Valley. International Journal Agriculture Biology. 6(5): 788-789.

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