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RESEARCH ARTICLE

GENETIC DIVERGENCE AMONG MAIZE (ZEA MAYS L.) INBRED LINES USING MORPHOMETRIC MARKERS

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Abstract

Genetic divergence study is imperative in breeding programmes in order to select distant parents. Forty maize inbred lines were assessed using morphometric markers to identify the potential inbred lines for yield and its component traits. The inbred lines were raised in α -RBD design replicated twice during kharif 2019. The morphological diversity analysis was done as per the standard statistical procedures using Mahalanobis D^2 -statistic. Analysis of variance revealed significant mean sum of squares due to genotypes for all the traits suggesting ample amount of genetic variability present among them. Moderate PCV, GCV and high heritability coupled with moderate genetic advance was observed for grain yield per plant, plant and cob placement height. Grain yield per plant exhibited significant positive correlation with all the traits except days to 50 per cent pollen shed and silking. Path analysis revealed high direct effects of days to 50 per cent pollen shed, harvest index, grains per row and 100 grain-weight on grain yield per plant therefore; these morphometric traits would be the best selection indices to select high yielding genotypes. D^2 -statistics grouped 40 maize genotypes into three clusters. Cluster III has the highest cluster mean values for all the traits. Seven genotypes viz., 4186-4-05-1-1, LM-14, BAJIM-08-27, BIOM 10, LQPM24 \times 1114-5, 9180-2, LDH 5(Vivek-21-1) were superior over the best check on the basis of mean performance and disease resistance and were diverse therefore, could be used in maize improvement program.

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Introduction:-

Maize (*Zea mays* L., $2n=20$) is the American Indian word for the corn which accurately means "that which sustains life". (It is, after wheat and rice, the 3rd most important cereal grain in the world, providing nutrients for humans and animals and serving as a basic staple material for the production of starch, oil and protein, alcoholic beverages, food sweeteners and, more recently, fuel. Maize contains about 70% starch, 10% protein, and 5% fat, supplying an energy density of 396 Kcal/100g, as compared to rice (384 Kcal/100g) and wheat (375 Kcal/100g). Originating in Mexico, maize has spread to all the important agro-ecologies in tropical, subtropical and temperate regions of the planet due

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to its plasticity and highest yield potential among the cereals. In recent years, this “miracle crop” is gaining popularity among the farmers mainly due to its high yield, more economic returns and versatile uses.

In order to meet up the increasing demand for maize grains and their products, hybrid breeding has been the most successful approach through the development of promising inbred lines which are the prerequisite for hybrid variety development in crop plants. Genetic improvement of any crop mainly depends upon the amount of genetic variability present within the population and germplasm which serves as a valuable source of the base population. Assessment of genetic diversity of any given crop species may be a suitable precursor for crop improvement because it provides information to guide the selection of parental lines and therefore, the design of breeding programs. The understanding of genetic variability present in a crop species for the traits under improvement is imperative for the success of any breeding program (Sankar et al. 2006). The present strategy of maize breeding lays greater emphasis on the development of single-cross hybrids (Vasal et al. 1995) for which identification of suitable parental lines and their extensive characterization is of utmost importance in hybrid breeding program. Knowledge of the genetic diversity among commercially important maize inbred lines helps hybrid maize breeding programs by planned utilization of promising source germplasm (Pushpavalli et al. 2001). Bruel et al. (2006) and Guimaraes et al. (2007) found a direct relationship between the inbred lines and the yield of the maize hybrids. Morphological traits were among the earliest markers for studying variability and diversity.

Knowledge of relationships among lines would help to identify the genotypes that possess maximum diversity at morphological levels. This will help to lead the better protection and maintenance of the genetic purity of the genotypes (Prasanna and Hoisington 2003). However, the sources of maize breeding depend upon the extent and magnitude of variability existing within the germplasm. Keeping all in view, the research has been planned with the following objectives to analyze the pattern of relationship among forty core collections including locally adapted inbred lines, CIMMYT and Indian maize inbred lines which might be helpful in distinguishing the maize germplasm and in the selection and utilization of diverse genotypes in the maize hybrid breeding programs.

Materials and Methods:-

Plant Material

The experimental material comprised of forty maize inbred lines (Table 1) viz., locally adapted inbred lines, CIMMYT and Indian maize inbred lines along with two checks CML-334 and CM-54 which were evaluated systematically. The checks were used to compare the maize inbred lines on the basis of their mean performance. Inbreds were subjected to variability and genetic diversity analysis.

Morphological Evaluation of Plant Material:

For morphological characterization the inbreds were grown in α -RBD design at the Experimental Farm of Department of Genetics and Plant Breeding, CSKHPKV Palampur (India) situated at 1290.80 m amsl having 32°6' N latitude and 76°3' E longitude and agro-climatically, represents mid-hill zone of Himachal Pradesh and is characterized by humid sub-temperate climate with high rainfall about 2500 mm; following recommended agronomic practices during kharif 2019 with a plot size of 3.0×1.2 m² with row to row and plant to plant distance of 60 cm and 20 cm, respectively (having 2 rows/plot) in 2 replications, 10 blocks/replication and 4 entries/block. The data on 12 quantitatively assessed traits including days to 50 per cent pollen shed, days to 50 per cent silking, days to 75 per cent maturity (on plot basis), plant height, cob placement height, cob length, cob girth, kernel rows per ear, grains per row, 100 grain-weight, grain yield per plant and harvest index were recorded from five randomly individual selected plants per inbred and were averaged. Morphological traits were measured based on maize descriptors developed by the Biodiversity International. The data collected on morphological traits was statistically analyzed using PROC GLM of SAS software. The genetic divergence of maize inbred lines was estimated using Mahalanobis D²-statistics which is useful tool in qualifying degree of divergence present in the inbred lines at genotypic level. Toucher's method described by Rao was used in grouping inbred lines into clusters with the aid of D² being treated as the square of the generalized distance. The Principal Component Analysis (PCA) was also done in order to find out the most relevant characters to be used as the descriptors.

Results and Discussions:-

Significant differences were observed among all the genotypes through analysis of various studies for grain yield and morphological traits viz., days to 50% pollen shed and silking, days to 75% brown husk, plant height(cm), cob placement height(cm), cob length(cm), cob girth(cm), kernel rows per ear, grains per row, grain yield per plant(g),

100-grain weight(g) and harvest index(%) justifying the presence of sufficient genetic variability in the genetic material under study. Singh et al. (2018) has also reported the similar results in which the ANOVA for all the characters viz., days to 50% pollen shed and silking, days to 70% dry husk, plant and ear height, seed yield, cob weight, shelling percentage, initial plant stand, and cob count showed significant values. Promising inbred lines were found on the basis of mean performance (Table 2) and these lines could be used in future maize breeding programmes.

Parameters of Variability:

The success of any breeding program depends on the presence of genetic variability within the population. The estimates of PCV for all the traits studied were higher than the corresponding GCV, which indicated that the apparent variation is not only due to genotypes but also due to the influence of environment on the traits. Moderate PCV and GCV was observed for plant height, cob placement height and grain yield per plant. So, these traits provide an average chance for selection as they exhibit moderate level of genetic variability for these characters. Whereas, for rest of the traits low PCV coupled with low GCV was observed indicating the need for creating the variability for these characters (Table 3). Jilo et al. (2018) observed that GCV for all the traits studied was smaller than the PCV, indicating the significant role of the environment in the expression of the traits.

Heritability and Genetic Advance

Heritability denotes the proportion of phenotypic variation due to genotypes thus helps the breeders to select the elite variety for a character. However, heritability indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance but it fails to indicate the expected genetic progress in one cycle of selection. High heritability alone is not enough to make efficient selection in segregating generations, unless information is accompanied for substantial amount of genetic advance.

Due to the selection of individual genotypes, heritability alone cannot assess genetic development; knowledge about genetic advance combined with heritability is most useful. Expected genetic advance as per cent of mean indicates the mode of gene action in the expression of a trait, which helps in choosing an appropriate breeding method. For predicting reliable estimates of additive and non-additive effects, heritability should be considered in conjugation with genetic advance (Burton and De Vane 1953 and Johnson et al. 1955). High heritability (>80%) and moderate genetic advance (25-50%) were observed for plant height, cob placement height and grain yield per plant indicating the influence of non-additive gene action and considerable influence of environment on the expression of these traits. Thus, suggesting that careful and restricted selection will be effective for the improvement of these characters. These results were supported by Rajesh et al. (2013) which indicates the improvement of traits under selection and provides better opportunities for selecting plant material for which traits in maize breeding program. High heritability (>80%) coupled with low genetic advance (<25%) was observed for days to 50% pollen shed, days to 50% silking, 75% dry husk, grains per row which also indicated the role of non-additive gene action in the inheritance of these traits, which revealed the importance of dominance and epistatic effects in the inheritance of these traits and selection would be less effective (Table 3).

Correlation, Path and Principal Component Analysis

Knowledge of the relationships among plant characters is useful while selecting traits for yield improvement. In the present study, correlation coefficient analysis measured the mutual relationship between 12 different morphological traits to determine the component character on which selection can be emphasized for yield improvement. The correlation coefficient enables the breeder in determining the direction and number of characters to be considered in improving the grain yield. The phenotypic and genotypic correlations were highly significant and positively associated for all the traits except days to 50% pollen shed and silking (Table 4 and 5). Similar results of significant positive correlation of grain yield was reported by Gazal et al. (2018) which showed highly significant positive association of grain yield with plant height, cob placement height, 100-grain weight and number of kernel rows. Genotypic correlation revealed the true genetic performance of the genes that actually control the characters. In many characters, genotypic correlations were higher than the respective phenotypic correlations. Low phenotypic correlation values can be explained due to masking or modifying effects of environment on genetic association between the characters.

At phenotypic level, when the direct and indirect contribution of correlation was estimated, the direct effects were found to be positive and high for grains per row, days to 50% pollen shed, 100-grain weight, harvest index and kernel rows per ear. High indirect effects on grain yield via cob girth, cob length, plant height, cob placement height

and days to 75% brown husk indicated that for hybrid development the improvement of these traits is essential before selecting them for high grain yield (Table 6). Similar studies were reported by Iiker (2011), Raghu et al. (2014) and Matin et al. (2017). At genotypic level, the direct effects were found positive and high for days to 50% pollen shed, harvest index, cob girth, cob length, grains per row and 100-grain weight whereas less direct effects of rest of the traits were observed (Table 7). Similar results were also reported by Amini et al. (2013), Natraj et al. (2014) and Begum et al. (2016).

Path coefficient analysis is presented in Table 7 and 8. The lower residual effect (0.2360 and 0.1008) at phenotypic as well as genotypic levels revealed that the characters chosen in path analysis were adequate and appropriate and indicated that most of the variation found in dependent trait was well explained by the contributing traits. Based on path analysis, it was concluded that days to 50 pollen shed, harvest index, grains per row and 100-grain weight were observed as best selection indices because of their high direct contribution towards grain yield per plant.

Principal component analysis (PCA) helps in identifying the most relevant characters that can be used as descriptors by explaining as much of total variation in the original set of variables as possible with a few components as possible and reducing the dimension of the problem. The characters contributing more to the divergence gave greater emphasis for deciding on the cluster for the purpose of further selection and the choice of parents for hybridization (Thakur et al. 2016). The first principal component (PC1) was the most important and explained 31.81 % of the total variance which was mainly contributed by grain yield per plant, cob girth, harvest index, 100-grain weight, plant height, cob length and grains per row while, the principal component (PC2) contributed 27.16 % of the total variance and was demonstrated by days to 50% pollen shed, days to 75% brown husk and days to 50% silking. While, the principal component (PC3) explained 12.40 % of the total variance which was mainly contributed by cob length, cob placement height and plant height. PC4 contributed 7.85 % of the total variance through days to 50% silking. The PC1, PC2 and PC3 showed relatively large variation (eigen values 3.82, 3.26 and 1.49, respectively) (Table 8). The eigen values were greater than one. The PC4 had small or modest variances (eigen values less than 0.5). The first three PCs with eigen values greater than one contribute 71.37% of the variability amongst the genotypes. Considering the Eigen vectors days to 50% silking, plant height, cob placement height, days to 50% pollen shed, 100-grain weight, cob length and grain yield per plant are the major sources of diversity among these maize inbred lines (Table 8 and Fig. 2). The results are in accordance with the findings of Sandeep et al. (2015); Avinash and Mishra (2016) and Shrestha (2016).

Genetic diversity studies through morphological markers

The information on genetic divergence present in the germplasm assists in selection of suitable parents and accelerates the techniques on the genetic gain. Genetic diversity present among inbred lines provides immense value in crop improvement for trait(s) of interest. For selecting the parents for hybridization, estimation of genetic distance is important. It is estimated by using an effective statistical tool; Mahalanobis D^2 -statistic provides a clear idea about the diverse nature of the population. The assessment of genetic diversity helps in reducing the number of breeding lines from large base population and the progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and dispense better scope to isolate superior recombinants.

In the present investigation with non-hierarchical Euclidean cluster analysis, 40 genotypes of maize were grouped into three clusters. All the clusters were polygenotypic based on genetic divergence. Cluster I had 10 inbred lines followed by cluster II (the largest cluster formed) with twenty two inbred lines whereas cluster III was formed by eight inbred lines (Table 9 and Fig 1). Thus, formation of cluster with different genotypes indicates diversity among the genotypes. The diverse grouping of genotypes in same cluster with different origins might be due to the unidirectional pressure practiced by the breeders in cointure the promising genotypes. Miranda et al. (2003) analyzed the genetic heterogeneity in nine tropical pop maize cultivars, and cultivars were grouped into four clusters mainly for grain yield, and cultivars showed substantial genetic diversity. Thakur et al. (2016) observed large variability and divided various test genotypes into two clusters.

Genetic diversity is generally associated with geographical diversity, but the former did not follow any specific pattern and found independent of their geographic region, the genotypes within the same clusters were originated from different geographical regions of the world; this indicated that there was no correlation between geographical distribution and genetic divergence which might be due to continuous exchange of genetic material among the countries of the world.

The average intra and inter-cluster distances are presented in (Table 10). The range of intra-cluster distance was from minimum of 2.42 for cluster I and maximum of 3.22 in the cluster III. The highest inter-cluster distance was observed between clusters II and III (3.81) and least for cluster I and II (2.90) indicating that the genotypes belonging to these clusters were comparatively less diverse. This apparently indicates that cluster III have inbred lines that are relatively distant from each other than the other clusters which have lower D^2 distances. High intra-cluster distances revealed that genotypes within the same cluster were quite diverse; hence the selection of parents within the cluster would be effective.

Among three clusters, cluster III showed the highest cluster mean values for all the traits, suggested that genotypes falling in cluster III can be selected directly on the basis of these traits and used as parent in the hybridization program (Table 11). It has been well established that more the genetically diverse parents used in the hybridization program, greater will be the chances of obtaining high heterotic hybrids.

Contribution of individual character towards divergence

The relative per cent contribution of the individual trait to the genetic divergence among maize genotypes was presented in Table 12. The maximum contribution towards the genetic divergence was exhibited by grains per row (21.67%) followed by grain yield per plant (19.36%), plant height (17.56%) and days to 50% pollen shed (14.87%). Thus, these characters may be given high emphasis while releasing the lines for hybridization programmes to generate large variability. Gazal et al. (2018) also observed that highest per cent contribution of divergence for trait 100-grain weight. Remaining traits had very little or no contribution towards genetic divergence and hence were of less importance. Chandel and Guleria (2019) reported that plant height and 1000-kernel weight had the greatest contribution to genetic divergence.

Conclusions:-

Genetic diversity is the basis for survival of plants in nature and for crop improvement. Diversity in plant genetic resources provides opportunity for plant breeders to develop new and improved varieties with desirable characteristics. Sufficient genetic variability was observed for all the traits under study suggesting prevalence of wide range of genetic variability. Moderate PCV and GCV was observed for grain yield per plant (g), plant height (cm) and cob placement height (cm) so, these traits provide an average chance for selection. High heritability coupled with moderate genetic advance was observed for plant height, cob placement height and grain yield per plant. Path analysis revealed the high direct effect of days to 50 per cent pollen shed, harvest index, grains per row and 100-grain weight on grain yield per plant. Therefore, these would be the best selection indices to select high yielding genotypes. D^2 -statistics grouped 40 maize genotypes into three clusters. Cluster III has the highest cluster mean values for all the traits. Seven genotypes viz., 4186-4-05-1-1, LM-14, BAJIM-08-27, BIOM 10, LQPM24×1114-5, 9180-2, LDH 5 (Vivek-21-1) were superior over the best check on the basis of mean performance, were diverse as well as resistance to disease hence could be used in maize improvement program.

Table 1:- List of inbred lines of maize (*Zea mays*. L) evaluated under the present study.

Sr. No.	Inbred line	Source/Pedigree
1	BAJ-19-1	LDH 5 (Vivek 21)
2	BAJ-19-2	CML421×CML170
3	BAJ-19-3	LM 14
4	BAJ-19-4	CML165/CL-02839/V335
5	BAJ-19-5	4186-4
6	BAJ-19-6	6478-21-7
7	BAJ-19-7	B36-2
8	BAJ-19-8	CML161/CML165BBB8BBB
9	BAJ-19-9	CML 189
10	BAJ-19-10	BML-7
11	BAJ-19-11	P390AM/CMLC4F230-B-2-1
12	BAJ-19-12	LDH 5 (Vivek-21-1)
13	BAJ-19-13	LM 13
14	BAJ-19-14	CML465-B-B
15	BAJ-19-15	CML 335-3-4
16	BAJ-19-16	CML161-2-

17	BAJ-19-17	CML 161
18	BAJ-19-18	9366-1
19	BAJ-19-19	NB 163
20	BAJ-19-20	QPM5(MRCQPM16)
21	BAJ-19-21	CML269/BAJIM-08-26
22	BAJ-19-22	CML 360-2-
23	BAJ-19-23	BIOM 10
24	BAJ-19-24	9395-2
25	BAJ-19-25	LDH 1(Vivek-21)
26	BAJ-19-26	CML 20-5-1
27	BAJ-19-27	CML437-2-
28	BAJ-19-28	CML165×CL-02839
29	BAJ-19-29	4096-1-1-04-2
30	BAJ-19-30	LQPM24×1114-5
31	BAJ-19-31	BAJIM-08-27
32	BAJ-19-32	BML16
33	BAJ-19-33	4033-4-05-1
34	BAJ-19-34	4186-4-05-1-1
35	BAJ-19-35	9180-2
36	BAJ-19-36	CML161/CML165-BBB11BBB
37	BAJ-19-37	CML121-1-2
38	BAJ-19-38	DML-170
39	BAJ-19-39	CML-334
40	BAJ-19-40	CM-549

Sr. No.	Characters	Best checks	No. of genotypes	Genotypes
1.	Days to 50 % pollen shed	CML-334	-	-
2.	Days to 50 % silking	CML-334	-	-
3.	Days to 75 % brown husk	CML-334	1	4186-4-05-1-1
4.	Plant height(cm)	CML-334	5	LM 14, P390AM/CMLC4F230-B-2-1, CML 335-3-4, 4096-1-1-04-2, BAJIM-08-27
5.	Cob placement height(cm)	CML-334	2	CML421 'CML170, BAJIM-08-27
6.	Grain yield per plant(g)	CM-549	3	BIOM 10, LQPM24×1114-5, 9180-2
7.	100-grain weight(g)	CML-334	11	CML165/CL-02839/V335, 6478-21-7, LM 13, CML161-2-, CML 161, 9366-1, NB-163, CML269/BAJIM-08-26, 9395-2, CML161/CML165-BBB11BBB, CML121-1-2
8.	Cob length(cm)	CML-334	3	LDH 5 (Vivek-21-1), CML165×CL-02839, LQPM24×1114-5
9.	Cob girth(cm)	CML-334	1	LQPM24×1114-5
10.	Kernel rows/ear(no.)	CML-334	1	LQPM24×1114-5
11.	Grains/row(no.)	CML-334	-	-
12.	Harvest Index(%)	CM-549	-	-

Table 2:- Promising inbred lines on the basis of mean performance for yield and its component traits.

Table 3:- Estimates of parameters of variability for morphological, yield and its component traits.

Traits	Mean±S.E (m)	Range	PCV (%)	GCV (%)	Heritability(bs) (%)	Expected GA(as % of mean)
Days to 50% pollen shed	65.24±0.94	56.00-76.50	7.66	7.39	93.00	14.68
Days to 50% silking	68.24±0.94	59.00-79.50	7.28	7.02	92.80	13.93
Days to 75% brown husk	109.50±0.92	100.00-118.00	4.25	4.08	92.20	8.08
Plant height(cm)	179.67±5.19	132.00-226.50	15.68	15.14	93.20	30.12
Cob placement height(cm)	91.26±3.70	59.50-127.00	22.52	21.78	93.50	43.39
Grain yield/plant(g)	80.34±3.54	40.18-120.25	22.30	21.41	92.20	42.18
100-grain weight(g)	24.14±1.14	16.71-29.05	13.75	12.03	76.50	21.55
Cob length(cm)	13.78±0.75	11.50-20.50	14.67	12.51	72.80	22.00
Cob girth(cm)	12.62±0.41	11.00-16.00	7.85	6.39	66.20	10.72
Kernel rows/ear(no.)	12.95±0.60	10.00-16.00	11.04	8.91	65.20	14.83
Grains/row(no.)	24.14±0.96	15.00-28.50	12.94	11.64	81.00	21.59
Harvest index(%)	25.88±1.70	19.50-33.00	13.12	9.24	49.70	13.43

Table 4:- Estimates of phenotypic correlation coefficient among various yield and morphological traits in maize.

Traits	Days to 50% silking	Days to 75% brown husk	Plant height (cm)	Cob placement height (cm)	100-grain weight (g)	Cob length (cm)	Cob girth (cm)	Kernel rows/ear (no.)	Grain s/r row (no.)	Harvest Index (%)	Grain yield per plant (g)
Days to 50% pollen shed	0.990*	0.821*	0.309*	0.289*	0.031	-0.122	-0.147	-0.007	-0.273*	-0.001	0.043
Days to 50% silking		0.793*	0.295*	0.283*	0.018	-0.143	-0.174	-0.032	-0.290*	-0.002	0.004
Days to 75% brown husk			0.269*	0.201	0.123	0.014	-0.047	0.031	-0.088	0.022	0.244*
Plant height(cm)				0.829*	0.410*	0.415*	0.259*	0.035	-0.073	0.171	0.277*
Cob					0.314	0.39	0.30	0.01	0.0	0.16	0.233*

placement height(cm)					*	3*	2*	7	02	1	
100-grain weight(g)						0.169	0.114	-0.265*	-0.269*	0.151	0.268*
Cob length(cm)							0.547*	0.311*	0.281*	0.169	0.487*
Cob girth(cm)								0.419*	0.300*	0.216	0.556*
Kernel rows/ear(no.)									0.144	0.124	0.418*
Grains/row(no.)										0.195	0.452*
Harvest Index(%)											0.543*

*Significance at $P \leq 0.05$

Table 5:- Estimates of genotypic correlation coefficient among various yield and morphological traits in maize.

Traits	Days to 50% silking	Days to 75% brown husk	Plant height (cm)	Cob placement height (cm)	100-grain weight (g)	Cob length (cm)	Cob girth (cm)	Kernel rows/ear (no.)	Grains/row (no.)	Harvest Index (%)	Grain yield per plant (g)
Days to 50% pollen shed	0.995*	0.858*	0.333*	0.289*	0.064	-0.143	-0.182	-0.038	-0.322*	-0.011	0.070
Days to 50% silking		0.833*	0.320*	0.284*	0.037	-0.168	-0.199	-0.061	-0.329*	-0.031	0.034
Days to 75% brown husk			0.299*	0.206	0.139	0.031	-0.054	0.005	-0.084	0.043	0.262*
Plant height(cm)				0.865*	0.479*	0.497*	0.348*	0.042	-0.107	0.291*	0.302*
Cob placement					0.389*	0.500*	0.386*	0.027	0.007	0.260	0.271

t height(cm)												*
100-grain weight(g)						0.251*	0.193	-0.246*	-0.269*	0.320*		0.330*
Cob length(cm)							0.715*	0.413*	0.394*	0.051		0.536*
Cob girth(cm)								0.724*	0.366*	0.527*		0.748*
Kernel rows/ear(no.)									0.375*	0.177		0.483*
Grains/row(no.)										0.427*		0.538*
Harvest Index(%)												0.726*

*Significance at $P \leq 0.05$

Table 6:- Estimates of direct and indirect effects on grain yield at phenotypic level for different traits in maize.

Traits	Days to 50% pollen shed	Days to 50% silking	Days to 75% brown husk	Plant height	Cob Placement Height	100-grain weight	Cob length	Cob girth	Kernel rows/ear	Grains /row	Harvest index	Grain yield per plant (g)
Days to 50% pollen shed	0.3623	-0.3428	0.1778	0.0030	-0.0235	0.0033	-0.0111	-0.0268	-0.0019	-0.1017	-0.0002	0.0380
Days to 50% silking	0.3587	-0.3463	0.1718	0.0029	-0.0231	0.0011	-0.0131	-0.0318	-0.0097	-0.1080	-0.0005	0.0000
Days to 75% brown husk	0.2975	-0.2747	0.2165	0.0026	-0.0164	0.0387	0.0013	-0.0086	0.0093	-0.0328	0.0074	0.2410*
Plant height	0.1119	-0.1020	0.0581	0.0098	-0.0676	0.1367	0.0378	0.0473	0.0105	-0.0272	0.0575	0.2730*
Cob Placement Height	0.1046	-0.0979	0.0435	0.0081	-0.0816	0.1021	0.0358	0.0552	0.0050	0.0007	0.0541	0.2300*
100-grain weight	0.0034	0.0011	0.0239	0.0038	-0.0238	0.3502	0.0155	0.0200	-0.0826	-0.0975	0.0485	0.2620*
Cob length	-0.0442	0.0496	0.0031	0.0041	-0.0321	0.0594	0.0911	0.0999	0.0932	0.1047	0.0567	0.4860*

Cob girth	-0.0531	0.0602	-0.0102	0.0025	-0.0246	0.0383	0.0498	0.1827	0.1259	0.1117	0.0726	0.5560*
Kernel rows/ear	-0.0023	0.0112	0.0067	0.0003	-0.0014	-0.0963	0.0283	0.0766	0.3002	0.0537	0.0416	0.4190*
Grains/row	-0.0989	0.1004	-0.0190	-0.0007	-0.0002	-0.0916	0.0256	0.0548	0.0432	0.3727	0.0653	0.4520*
Harvest index	-0.0002	0.0005	0.0048	0.0017	-0.0132	0.0507	0.0154	0.0395	0.0372	0.0726	0.3353	0.5440*

Residualeffect=0.2360

Table 7:- Estimates of direct and indirect effects on grain yield at genotypic level for different traits in maize.

Traits	Days to 50% pollen shed	Days to 50% silking	Days to 75% brown husk	Plant height	Cob placement height	100-grain weight	Cob length	Cob girth	Kernel rows/ear	Grain in s/row	Harvest Index	Grain yield per plant (g)
Days to 50% pollen shed	1.0406	-0.7170	0.0204	-0.0258	-0.0666	0.0078	-0.0428	-0.0604	-0.0003	-0.00846	-0.0007	0.0670
Days to 50% silking	1.0358	-0.7204	0.0198	-0.0248	-0.0654	0.0025	-0.0504	-0.0661	-0.0004	-0.00865	-0.00132	0.0310
Days to 75% brown husk	0.8932	-0.5998	0.0238	-0.0231	-0.0475	0.0252	0.0092	-0.0178	0.0000	-0.0220	0.0182	0.2590*
Plant height	0.3469	-0.2302	0.0071	-0.0774	-0.1992	0.0926	0.1491	0.1157	0.0003	-0.0281	0.1239	0.3010*
Cob placement height	0.3007	-0.2046	0.0049	-0.0670	-0.2303	0.0751	0.1500	0.1284	0.0002	0.0018	0.1106	0.2700*
100-grain weight	0.0394	-0.0087	0.0029	-0.0347	-0.0836	0.2067	0.0730	0.0640	-0.0018	-0.00680	0.1378	0.3270*
Cob length	-0.1484	0.1211	0.0007	-0.0385	-0.1152	0.0503	0.3000	0.2378	0.0028	0.01035	0.0217	0.5360*
Cob girth	-0.1889	0.1431	-0.0013	-0.0269	-0.0889	0.0398	0.2144	0.3327	0.0048	0.00962	0.2240	0.7490*
Kernel rows/ear	-0.0395	0.0436	0.0001	-0.0033	-0.0061	-0.0553	0.1239	0.2408	0.0067	0.00985	0.0751	0.4840*
Grains/r	-0.3352	0.2372	-0.0020	0.0000	-0.0016	-	0.1	0.1	0.002	0.	0.181	0.5

ow				83		0.053 5	182	218	5	26 27	6	40 0*
Harvest Index	-0.0114	0.0223	0.0010	- 0.02 26	-0.0599	0.067 0	0.0 153	0.1 753	0.001 2	0. 11 22	0.425 2	0.7 20 6*

Residual Effect = 0.1008

Table 8:- Eigen vectors for four components of different traits in 40 genotypes.

Variable	Eigenvectors			
	PC1	PC2	PC3	PC4
Eigen Value	3.82	3.26	1.49	0.94
Variation (%)	31.81	27.16	12.40	7.85
Cumulative (%)	31.81	58.97	71.37	79.23
Days to 50% pollen shed	0.05	0.50	0.06	0.05
Days to 50% silking	-0.08	0.27	0.13	0.77
Days to 75% brown husk	0.12	0.40	-0.10	-0.45
Plant height(cm)	0.34	0.19	0.43	-0.01
Cob placement height(cm)	0.31	-0.18	0.45	0.20
Grain yield per plant(g)	0.45	0.15	-0.20	0.02
100-grain weight(g)	0.35	0.13	0.16	-0.11
Cob length(cm)	0.05	-0.24	0.57	-0.30
Cob girth(cm)	0.45	0.13	-0.17	0.13
Kernel rows/ear(no.)	0.08	-0.43	0.01	0.19
Grains/row(no.)	0.30	-0.30	-0.28	-0.01
Harvest Index (%)	0.38	-0.23	-0.28	0.09

Table 9:- Grouping of maize genotypes into different clusters on the basis of Mahalanobis D²-analysis.

Cluster	Number of genotypes	Genotypes
1	10	BIOM 10, 9180-2, LDH 1(Vivek-21), LM 14, P390AM/CMLC4F230-B-2-1, CML 335-3-4, 4096-1-1-04-2, CML421'CML170, QPM51 (MRCQPM16), BAJIM-08-27
2	22	CML437-2-, CML161/CML165-BBB11BBB, CML165/CL-02839/V335, CML121-1-2, CML 20-5-1, 4186-4-05-1-1, 4186-4, CML 189, BML-7, CML 360-2-, CML 161, 6478-21-7, 9366-1, B36-2, 9395-2, DML-170, CML161/CML165BBB8BBB, 4033-4-05-1, LDH 5(Vivek 21-1), LDH 5(Vivek 21-1), BML16, CML-334
3	8	LM 13, CML161-2-, CML269/BAJIM 8-26, CML465-B-B, CML165×CL-02839, CM-549, NB 163, LQPM24×1114-5

Table 10:- Average intra and inter-cluster values of D² and √D² among clusters.

Clusters	1	2	3	CLUSTER II
1	5.85 (2.42)	8.37 (2.90)	13.20 (3.63)	
2	-	8.20 (2.86)	14.54 (3.81)	
3	-	-	10.35 (3.22)	

Bold values are intra-cluster distance
Data in parenthesis are √D² value

Table 11:- Cluster means of three clusters for different traits of maize genotypes.

Trait	Cluster 1	Cluster 2	Cluster 3	Mean	Min	Max
Days to 50% pollen shed	60.54 *	66.91	69.15 **	65.53	60.54	69.15
Days to 50% silking	63.46*	70.03	72.05 **	68.51	63.46	72.05
Days to 75% brown husk	105.79 *	110.38	113.30 **	109.82	105.79	113.30
Plant height(cm)	176.46	164.84 *	207.90 **	183.07	164.84	207.90
Cob placement height(cm)	88.11	81.81*	110.80**	93.57	81.81	110.80
Grain yield/plant(g)	81.28	68.18 *	98.47 **	82.64	68.18	98.47
100-grain weight(g)	25.06	22.41 *	25.63 **	24.37	22.41	25.63
Cob length(cm)	14.11	12.72 *	15.05**	13.96	12.72	15.05
Cob girth(cm)	12.93	12.06 *	13.10 **	12.70	12.06	13.10
Kernel rows/ear(no.)	12.93	12.56 *	13.60 **	13.03	12.56	13.60
Grains/row(no.)	24.79	23.06 *	24.95 **	24.27	23.06	24.95
Harvest Index(%)	26.32	24.34 *	27.75 **	26.14	24.34	27.75

*Minimum;**Maximum

Table 12:- Relative contribution (%) of the individual trait to the divergenceamong maize genotypes.

Traits	No. of times ranked first	Contribution (%)
Days to 50% pollen shed	116.00	14.87
Days to 50% silking	0.00	0.00
Days to 75% brown husk	52.00	6.67
Plant height(cm)	137.00	17.56
Cob placement height(cm)	85.00	10.90
Grain yield/plant(g)	151.00	19.36
100-grain weight(g)	31.00	3.97
Cob length(cm)	11.00	1.41
Cob girth (cm)	16.00	2.05
Kernel rows/ear(no.)	0.00	0.00
Grains/row (no.)	169.00	21.67
Harvest index (%)	12.00	1.54

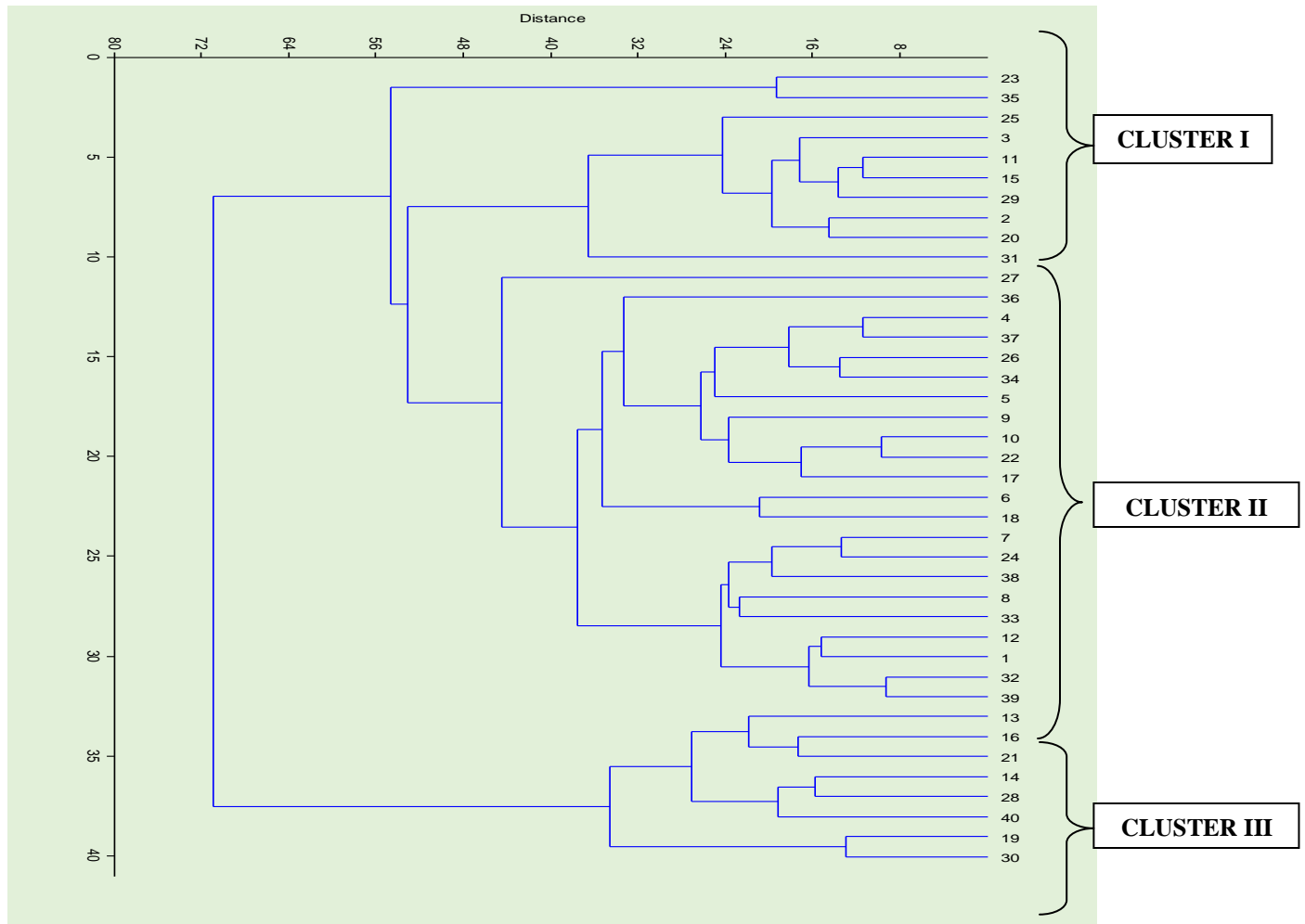


Fig 1:- Dendrogram of maize genotypes generated using MahalanobisD²-analysis.

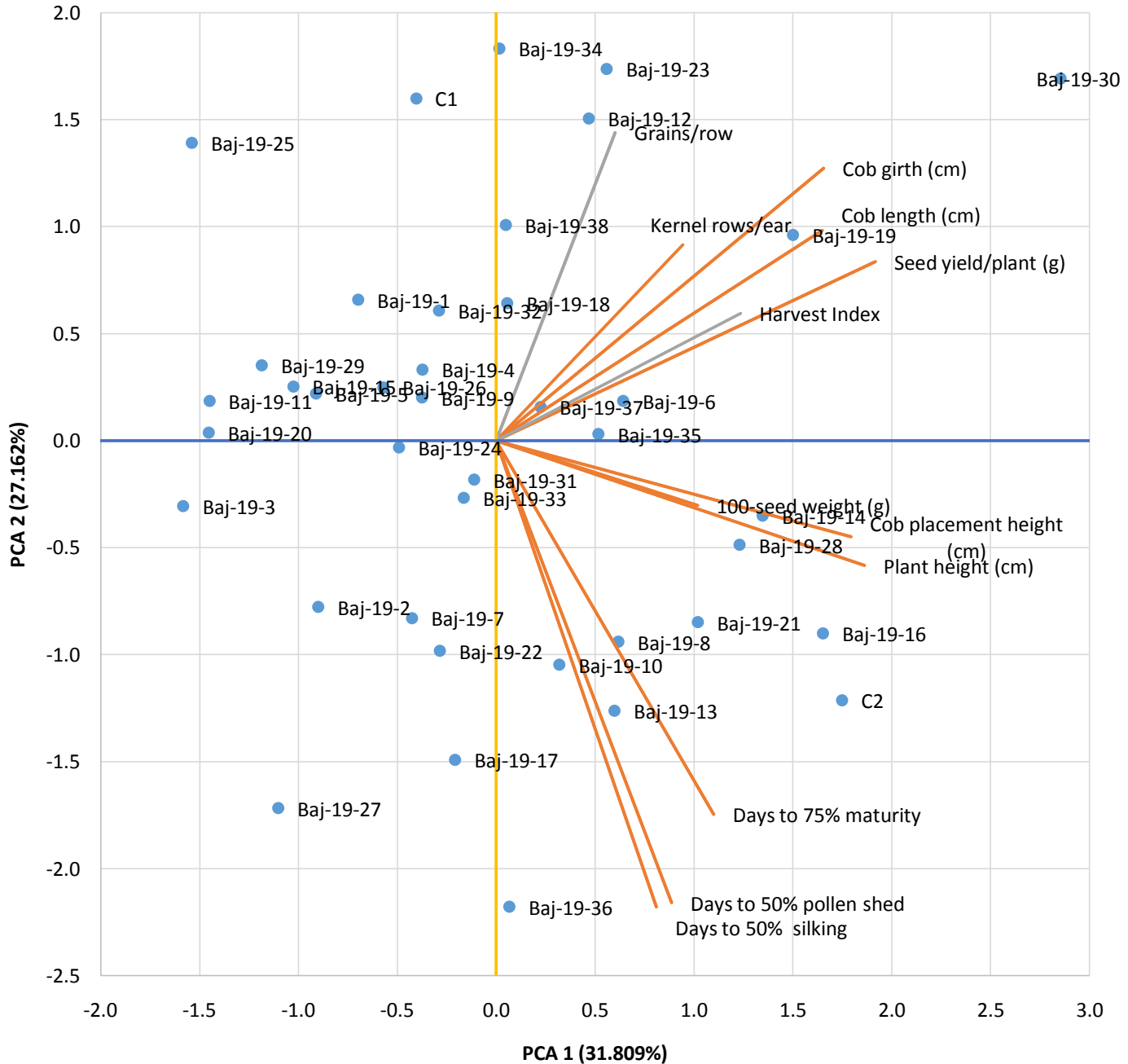


Fig 2:- Biplot of different variables and genotypes on PC1 and PC2.

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