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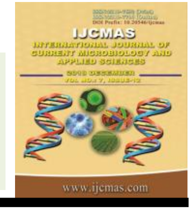

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Genetic Diversity Analysis of Maize (*Zea mays* L.) Inbred Lines on the basis of Morphological Traits

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In order to identify diversity of maize inbred lines, a trial consisting of 15 inbred lines of maize were planted in Randomized Block Design (RBD) in three replication at AICRP Maize breeding field of Dr. Rajendra Prasad Central Agricultural University, Pusa during kharif-2016. The diversity was identified on the basis of morphological data like days to 50% tasseling, days to 50% silking, plant height, ear height, number of grains per row, thousand seed weight, tassel length, tassel branch number, cob length and cob girth. Descriptive statistics and cluster analysis were done with the help of MINITAB version18 statistical software and clustering was done by ward linkage method. The inbred lines were grouped into three major clusters A, B and C. Cluster B had taller plants with maximum ear height. The cluster C was characterized with shorter plants with minimum ear height. The inbred lines categorized into cluster C had early flowering, whereas cluster B had late flowering time. The inbred lines grouped into the cluster B were characterized by higher tassel length and tassel branch. Results indicated that amongst the tested inbred lines a wide range of morphological diversity were found. It could be utilized in future Maize breeding program to develop potential hybrids and synthetic varieties.

Introduction

Maize (*Zea mays* L.) is the third important cereal crop after wheat and rice and belongs to the tribe Maydeae of the grass family Poaceae. It has a remarkable productive potential among the cereals and has wide economic importance. It shows broad genetic base and wide adaptability, adjust itself globally from temperate to tropical conditions with annual rainfall of 20 to 25 cm, to those where annual rainfall may exceed 400 cm. Maize crop is cultivated from 50° N to 40° S latitude and at altitude from sea level to 3300 meters. It is highly productive crop among cereals; hence it is called Queen of cereals.

Evaluation of genetic diversity is pre-requisite for identifying promising parents for any hybridization programme in plant breeding. In order to utilize the material for hybrid development, it is imperative to know the extent of diversity present among the lines of maize. Most of the modern inbred lines used in maize hybrid programme are second, third or fourth cycle lines which were developed from other inbred lines or from synthetic populations derived from crossing the inbred lines. The genetic diversity can be elucidated by cluster analysis. Cluster analysis is done for organizing data sets so that information can be retrieved more efficiently and can be easily understood without the need for complicated mathematical techniques. It is frequently used to classify maize accessions and can be used by breeders and geneticists to identify subsets of accessions which have potential utility for specific breeding or genetic purposes (Rincon, 1996). The main aim of using a cluster technique for analysis of data from plant breeding trials is to group the inbred lines into several homogeneous groups such that those inbred lines within a group have a similar response pattern. It is reasonable that all the inbred lines in the trials will not behave complete in depend of each other. For instance, those with similar genetic make-up would be expected to behave similarly Jiban (2014). The present investigation was carried out to know the magnitude of diversity present in fifteen inbred lines of maize for morphological and yield components to select diverse parents for its further use in heterotic crosses and wide array of combination.

Materials and Methods

The experiment was conducted during kharif, 2016 at Tirhut College of Agriculture, Dholi farm of Dr. Rajendra Prasad Central Agricultural University, Pusa, Bihar, with fifteen inbred lines (Table 1) of maize derived from different maize population. The plot had a uniform topography, fertile and well drained soil. The experiment was conducted in Randomized Block Design (RBD) with three replication having plot size of 6.0 m^2. Each plot consisted of two rows of 4 m length each spaced at 75 cm (row to row) and 25 cm (plant to plant) respectively. The observations during present investigation were recorded on five competitive plants which were randomly taken from each plot in each replication for recording data of traits. The data were recorded for days of 50% tasseling, days of 50% silking, plant height (cm), ear height (cm), tassel length (cm), tassel branch number, cob length (cm), cob girth (cm), number of grains per row, 1000 seed weight (gm). Cluster analysis of morphological data was done on the basis of ward linkage method using MINITAB ver. 18 statistical software.

Results and Discussion

Analysis of the field data showed that there were highly significant differences for all the ten characters indicating the existence of genetic diversity among the tested inbred lines. On the basis of field data, mean and range were calculated and presented in Table 2. The finding of the field study showed that the tassel branch number had maximum variation (93.27%) followed by tassel length (24%) and cob girth (17.52%). Among the traits, 50% silking showed lowest variation (4.330%). Sokolov and Guzhva (1997) also reported significant amount of variability for different morphological trait in maize inbred line populations. The morphological variations were found mainly due to interaction of genetic factors with the environmental factors. The mean value for the characters *viz*. days of 50% tasseling, days of 50% silking, plant height (cm), ear height (cm), tassel length (cm), tassel branch number, cob length (cm), cob girth (cm), number of grains per row, 1000 seed weight (gm) were 55.2, 58.47,179.57, 82.93, 31.734, 8.47, 16.67, 11.66, 30.59 and 235.01 respectively.

The results of the field study (Table 3) showed that among the tested inbred lines the maximum days for 50% tasseling was found in line XI (60 days), while it was lowest *i.e.* 51 days in VI. Previously Rahman (2008) and Shrestha (2016) also reported significant amount of variability for days to tasseling among different maize genotypes. Similarly 50% silking was highest 63 days in XI and lowest 55 days in VI and XIV. This variability attributed by the inbred lines is due to differential genetic constitution. Previously Shah (2000) and Shrestha (2013) also reported similar results for days of silking traits among maize populations. Plant height ranged from 167 cm in VI to 195 cm in IV. This variation is attributed to their genetic background. These results are in conformity with those of Ihsan (2005) who also reported significant amount of variation among different maize populations for morphological traits. Ear height ranged from 99 cm in IV to lowest 71 cm in XV. These results are supported by Dijak *et al.*, (1999) who also found significant amount of variability among long and short stature maize populations for ear and plant height. Generally, medium ear height plant is preferred *i.e.* plant having ear in middle of the plant. The observed variation in the plant height and ear height is due to variability in the genetic makeup of the population. Shrestha (2013) characterized the maize inbreds in Nepal on the basis of agro-morphological traits. Abu-alrub (2006) used kernel traits as the best descriptors for classifying Peruvian high-land maize germplasm (Table 4).

Morphological variations were found on the basis of trait under consideration and these fifteen inbred lines of maize were evaluated for divergence and grouped into three major clusters A, B and C. The composition of each cluster is presented in Table 5. Cluster A consisted of 6 inbred lines namely I, III, IV, V, VIII and IX. Cluster B consisted of four inbred lines II, XI, XII and XV and cluster C consisted of five inbred lines namely VI, XIV, X, XIII and VII (Fig. 1).

Table.1 Experimental materials used to analyse morphological diversity

Sl. No.	Pedigree	Codes
1	CLQRCYQ60-B-B	I
2	CLQ2540Q-B-B-B-B	II
3	VL1110240/VL108722-B-14-1-BB	III
4	(CG18SeqC$_5$F76-2-1-2-1-2-BBB/LN/EM-46-31XCML311-2-1-3)-B-F303---B)/G18SeqC5F76-2-2-1-2BBB-D-B$_3$-B)-B-8-BBB	IV
5	WNCDMR11R4093	V
6	WNCDMR11R6429	VI
7	WNCDMR10YFWS8481	VII
8	WNCDMR10RYFWS8200	VIII
9	CML-490	IX
10	HK1-193	X
11	WLS-F$_2$ 8$_7$-1-2-1-B-1-B-B	XI
12	CLQ-RCYQ41	XII
13	G18SEQ.C5F76-2-1-1-1-B/(DT12N,EM-46-3-1XCML311-2-1-3)B-F243-1-11(DT/LN/EM-46-3-3-1XCML-311-2-1-3)-B-F243-1-1-B-1-BBB-B	XIII
14	[CML161/CML-165]-BBB-11-BBB/CML193	XIV
15	(DTPYC$_9$-F$_{46}$-3-9-1-2-2-1-3-BBB/WL-18-6-2-3-3-1-B$_5$*)-BBB-1-B	XV

Table.2 Descriptive statistics of average agro-morphological characters of 15 maize inbred lines

Items	50% tasseling (Days)	50% silking (Days)	Plant height (cm)	Ear height (cm)	Tassel length (cm)	Tassel branch (number)	Cob length (cm)	Cob girth (cm)	Grains per row (Number)	1000 seed weight (gm)
Mean	55.2	58.47	179.57	82.93	31.734	8.47	16.67	11.66	30.59	235.01
SE(±)	0.663	0.654	2.373	1.446	1.98	2.04	0.646	0.527	0.53	7.23
SD(±)	2.57	2.532	9.19	5.602	7.65	2.81	2.501	2.043	2.602	28.02
CV(%)	4.65	4.330	5.12	6.75	24	93.27	15.0	17.52	8.42	11.923
Range	9	8	28	20	25.17	8.66	10.1	6.40	9.3	83.41

SE: Standard error, SD: Standard deviation, CV: Coefficient of variation

Table.3 Characters along with their mean data of morphological traits of 15 inbred lines

z	50% tasseling (Days)	50% silking (Days)	Plant height (cm)	Ear height (cm)	Tassel length (cm)	Tassel branch (number)	Cob length (cm)	Cob girth (cm)	Grains per row (Number)	1000 seed weight (gm)
I	56	59	177.5	87.5	27.33	9.33	15.7	11.6	28.14	222.51
II	57	60	187	87	17.83	6.33	17.7	14.45	31.5	274.28
III	54	57	180	83	23.33	8	16.95	9.8	29.9	228.35
IV	55	59	195	91	28.17	4.67	15.4	12	29.03	228.5
V	53	57	188.5	85	24.17	7	16.6	11.15	29.42	243.93
VI	51	55	167	84.5	37.17	6	14.5	11.9	30.11	202.82
VII	54	57	189.5	72.5	24.83	6.33	9.9	11.1	27.1	198.3
VIII	56	60	175.5	88.5	32.17	12.33	13.75	9.3	29.63	248.02
IX	53	57	178.5	84.5	38.17	7.67	16.25	8.15	32.74	251.42
X	54	56	167.5	80	33.5	5.33	14.5	8.75	36.4	216.56
XI	60	63	187.5	81	43	13.33	15.9	13.6	29.98	261.63
XII	56	58	186	81	32.17	8.33	16.25	14.1	28.32	270.25
XIII	59	62	167.5	80	41.67	13	18.85	13.05	29.82	211.93
XIV	52	55	168	87.5	30	8.33	19.5	11.4	30.98	191.65
XV	58	62	178.5	71	42.5	11.33	20	14.55	35.73	275.06

*The name of maize inbred lines were assigned as code no. in mean data table and for their clustering in dendrogram

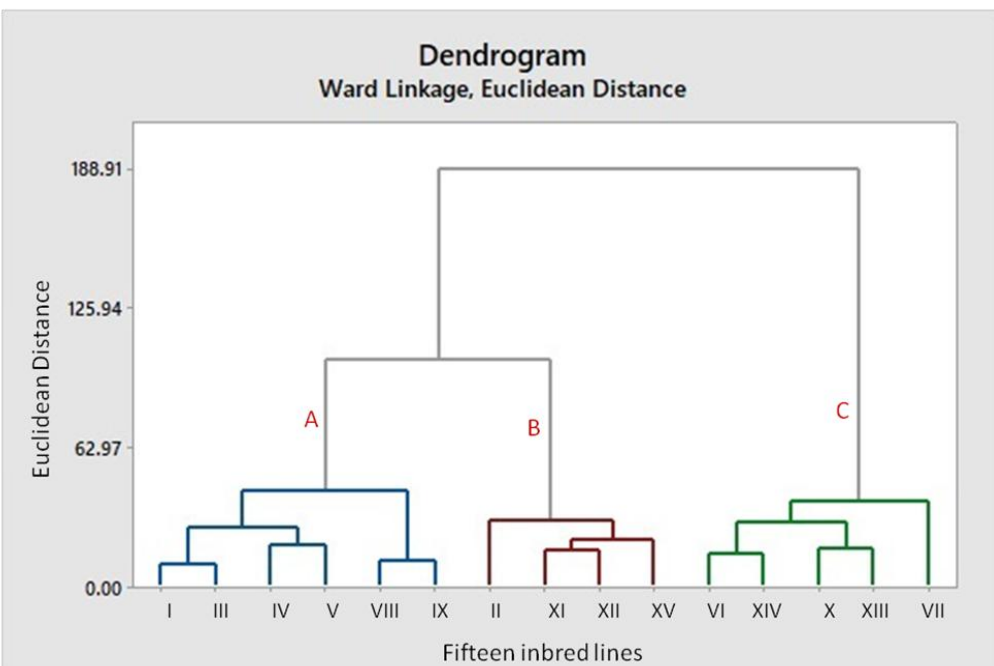
Table.4 Agro-morphological traits of 15 inbred lines within and among three clusters

Variable	Cluster A	Cluster B	Cluster C
Days to 50% tasseling	54.500	57.750	54.000
Days to 50% Silking	58.167	60.750	57.000
Plant height (cm)	182.500	184.750	171.900
Ear(height cm)	86.583	80.000	80.900
Tassel length (cm)	28.890	33.875	33.434
Number of Tassel branch	8.167	9.830	7.798
Cob length (cm)	15.775	17.462	15.450
Cob girth (cm)	10.333	14.175	11.240
Number of grains/row	29.810	31.383	30.882
1000 seed weight (gm)	237.122	270.305	204.252

Table.5 Grouping of 15 inbred lines into three clusters based on agro-morphological traits

Cluster	Number of inbred lines	Code of inbred lines
A	6	I, III, IV, V, VIII, IX
B	4	II, XI, XII, XV
C	5	VI, VII, X, XIII, XIV

Figure.1 Cluster diagram obtained on the basis of morphological data (algorithm: Ward's method and similarity measure: Euclidean distance) depicting relationship among 15 inbred lines



In conclusion the genetic diversity was observed in agromorphological traits namely days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), tassel length (cm), tassel branch number, cob length (cm), cob girth (cm), number of grains per row, 1000 seed weight (gm) in the tested maize inbred lines. The inbred lines grouped into cluster B had larger tassel length and tassel branch whereas lines in cluster A showed greater variation in anthesis-silking interval, which is a desirable agro-morphological trait for out crossing. The presence of high level of diversity among the inbred lines grouped into divergent clusters indicated their suitability for hybridization and breeding program to develop potential hybrid and synthetic varieties.

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