



Study of genetic diversity of maize (*Zea mays* L.) hybrids

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Abstract: The present study was under taken to find out the genetic diversity of various maize genotypes for ten metric traits. Ten parental lines, three testers and their 30F₁s were evaluated in a randomized block design in order to identify genetic divergence on the basis of non-hierarchical euclidean cluster analysis in maize (*Zea mays* L.). All the genotypes were grouped into seven clusters revealing the presence of considerable amount of genetic diversity in the material for different traits. According to results, cluster II, VI and VII each had the maximum nine genotypes. Cluster I and V had minimum genotypes with five and two genotypes, respectively. The highest intra-cluster distance value was found for cluster III (127.613) followed by cluster VII (68.551) and lowest intra-cluster distance was found in cluster V (11.517). The maximum inter-cluster distance was recorded between cluster III and VI (1945.319) followed by cluster III and VII (1279.354) whereas, minimum inter-cluster distance was observed between clusters I and II (91.049). Based on results, genotypes grouped into different clusters showed more valuable heterotic pool that could be utilized in crossing the genotypes selected from those cluster which have maximum inter-cluster and intra-cluster distance in developing the desirable segregants.

Key words: Clustering pattern, D² analysis, Genetic diversity, and Genotypes

Introduction

Maize or corn (*Zea mays*) is a plant belonging to the family of grasses (*Poaceae*). Maize is the third most important cereal of the world after wheat and rice during 2000. It is cultivated globally being one of the most important cereal crops worldwide. Maize is not only an important human nutrient, but also a basic element of animal feed and raw material for manufacture of many industrial products. The products include corn starch, maltodextrins, corn oil, corn syrup and products of fermentation and distillation industries. It is also being recently used as biofuel. "Zea" (zela) was derived from an old Greek name for a food grass. The genus *Zea* consists of four species of which *Zea mays* L. is economically important. The other *Zea* sp., referred to as teosintes, is largely wild grasses native to Mexico and Central America. The number of chromosomes in *Zea mays* is $2n = 20$. Based on study, the choice of genetically diverse parents for use in hybridization programme is based on hypothesis that "Crosses involving divergent parents offer greater possibility of obtaining desirable segregants in the segregating generation higher magnitude of heterotic effect in hybrids". Several workers emphasized need of diverse parent in optimum magnitude to obtain superior genotypes in the segregating generations as well as in crosses combinations (TingZhao, 2013, Zaman and Alam, 2013, Copandean, 2012 and Kumar *et al.*, 2013).

Materials and Methods

A field experiment was conducted in a randomized block design with three replications at oilseed research farm of during *Kharif* 2012. The experimental material comprised of maize lines including ten parental lines, three testers and their 30F₁s (Table-1). The F₁s of maize were developed through Line x tester mating design. The row to row and plant to plant spacing was kept 45 cm and 25 cm, respectively. On the basis of five randomly taken plants,

data were recorded for plant height (cm), cob weight (g), cob length (cm), cob diameter (cm), number of row cob⁻¹, number of grains row⁻¹, grain weight cob⁻¹, 100 grain weight, number of cob plant⁻¹ and grain yield plant⁻¹. Non-hierarchical Euclidean cluster analysis was used in order to classify the genotypes into different groups based on their similar and dissimilar performance for the traits. Genetic divergence among genotypes was studied through Non-hierarchical Euclidean cluster analysis (Beale, 1969 and Spark, 1973).

Results and Discussion

The table-1 represents the experimental material consisting of forty three genotypes/lines. Analysis of variance revealed that treatments /genotypes were significant for all the traits under study indicating variability among them for various characters. Then Non-hierarchical Euclidean cluster analysis was carried out in order to classify the genotypes into different groups based on their similar and dissimilar performance for the traits. All these genotypes were grouped into seven clusters which showed large amount of diversity among the genotypes of experimental material. The genotypes were grouped into seven clusters through Non-hierarchical Euclidean cluster analysis, tables-2 and cluster mean for ten traits is given in table 4, the perusal of traitsshowed clusters II, VI and VII had each the maximum but equal ninegenotypes/hybrids, respectively. Cluster I and IV had five genotypes each; cluster III had only four genotypes whereas cluster V had minimum only two genotypes results obtained confirm the finding of Hepziba *et al.* (2013), Khaldun and Sanda, (2012) for classification of genotypes into different clusters. Whereas these clusters were differ for yield traits *e.g.*, each cluster genotypes showed different effect on yield and its components. Cluster I genotypes exhibited maximum mean for plant height, cob diameter, number of row cob⁻¹ and yield plant⁻¹; cluster III genotypes showed maximum mean values for cob weight,

Table-1: List of parental lines, testers and their F₁s in maize

Particulars	No. of lines /genotypes	Name of genotypes	Source
Parental lines/ females inbreds	10	TSK 35, TSK 25, CIM 36, CIM 80, CIM 14, CIM 56, CIM 45, KANTI ADVANCE, TSK 22, and TSK 79.	Oilseed Research Farm, Kalyanpur at C.S.Azad University of Agriculture and Technology, Kanpur
Testers/males inbreds	3	AZAD UTTAM, BLACK DIAMOND, and AZAD KANTI.	Oilseed Research Farm, Kalyanpur at C.S.Azad University of Agriculture and Technology, Kanpur
F ₁ s/ Hybrids	30	TSK 35 x AZAD UTTAM, TSK 25 x AZAD UTTAM, CIM 36 x AZAD UTTAM, CIM 80 x AZAD UTTAM, CIM 14 x AZAD UTTAM, CIM 56 x AZAD UTTAM, CIM 45 x AZAD UTTAM, KRANTI ADVANCE x AZAD UTTAM, TSK 22 x AZAD UTTAM, TSK 79 x AZAD UTTAM, TSK 35 x BLACK DIAMOND, TSK 25 x BLACK DIAMOND, CIM 36 x BLACK DIAMOND, CIM 80 x BLACK DIAMOND, CIM 14 x BLACK DIAMOND, CIM 56 x BLACK DIAMOND, CIM 45 x BLACK DIAMOND, KRANTI ADVANCE x BLACK DIAMOND, TSK 22 x BLACK DIAMOND, TSK 79 x BLACK DIAMOND, TSK 35 x AZAD KRANTI, TSK 25 x AZAD KRANTI, CIM 36 x AZAD KRANTI, CIM 80 x AZAD KRANTI, CIM 14 x AZAD KRANTI, CIM 56 x AZAD KRANTI, CIM 45 x AZAD KRANTI, KRANTI ADVANCE x AZAD KRANTI, TSK 22 x AZAD KRANTI, and TSK 79 x AZAD KRANTI	F ₁ s were generated at Oilseed Research Farm, Kalyanpur at C.S. Azad University of Agriculture and Technology, Kanpur 208002 during Rabi 2011-12 by used of Line x Tester mating design.

Table-2: Clusters pattern of maize genotypes on the basis of D² analysis

Cluster	Name of genotype
I	TSK 35 x AZAD UTTAM, TSK22 x AZAD KANTI, TSK79 x BLACK DIAMOND, TSK35, and CIM14 xAZAD KANTI
II	CIM80 x AZAD UTTAM, KRANTI AKxAZAD KANTI, CIM 14 x BLACKDIAMOND, AZADUTTAM, CIM14 x AZAD UTTAM, TSK22, CIM45xAZAD UTTAM, CIM80 xAZAD KANTIandCIM 45
III	CIM56 xAZAD KANTI, TSK25, TSK335xAZAD KANTI, andCIM36 xAZAD KANTI
IV	TSK35 xBLACK DIAMOND, KANTIAXAZAD UTTAM, CIM 56 xBLACK DIAMOND, TSK22 xAZAD UTTAM, and CIM80 xBLACK DIAMOND
V	BLACK DIAMOND, and AZAD KANTI
VI	TSK25 xAZAD UTTAM, CIM 80, TSK 79, TSK25x BLACK DIAMOND, CIM 45 x BLACK DIAMOND, TSK25 xAZAD KANTI, TSK79 xAZAD KANTI, CIM 45xAZAD KANTIand TSK22 xBLACK DIAMOND
VII	CIM 36 xAZAD UTTAM, TSK79 xAZAD UTTAM, KANTI AK x BLACK DIAMOND, CIM 36 xBLACK DIAMOND, CIM 14, CIM56

Table-3: Average intra and inter clusters distance in maize lines

Cluster	I	II	III	IV	V	VI	VII
I	35.162	91.049	167.88	284.157	322.453	1226.243	711.768
II		45.689	319.329	152.196	134.335	841.485	426.599
III			127.613	681.256	661.45	1945.319	1279.354
IV				65.483	143.267	479.104	191.245
V					11.517	448.905	195.820
VI						46.450	144.903
VII							68.551

Note: Bold digit show the intra cluster distance and other digit show the inter cluster distance

Table-4: Cluster means for ten characters in maize genotypes

Cluster	Plant height (cm)	Cob weight (g)	Cob length (cm)	Cob diameter (cm)	Rows cob ⁻¹	Grains row ⁻¹	Grain weight cob ⁻¹ (g)	100 Grain weight (g)	Cobs plant ⁻¹	Yield plant ⁻¹ (g)
I	167.882**	112.029	17.769	15.069**	13.380**	34.905	90.887	19.685	1.400	127.128**
II	160.163	94.893	14.476	13.022	12.419	27.815	76.406	22.501	1.148	87.674
III	156.546	139.440**	18.407**	12.710	12.572	38.539**	109.625**	23.080	1.083	120.057
IV	174.142	72.284	14.911	12.740	12.740	30.750	56.357	14.822	1.533**	84.819
V	137.883	87.395	13.942	11.230*	11.893*	20.210	62.882	26.477**	1.167	73.217
VI	128.701*	39.733*	12.081*	11.795	12.379	20.804*	28.400*	11.366*	1.037*	29.159*
VII	149.492	53.784	12.170	11.900	12.024	23.672	37.752	14.584	1.111	42.435

Note- *indicate lower and ** indicate higher value

cob length, number of grains row⁻¹, and grain weight cob⁻¹; cluster IV and V genotypes exhibited maximum mean value for cob plant⁻¹ and 100 grain weight, respectively. Cluster VI genotypes showed minimum mean value for all the attributes except cob diameter and number of rows cob⁻¹ while cluster V exhibited lowest values for cob diameter and number of rows cob⁻¹. Cluster I had tall type genotypes with desirable and higher magnitude for some yield attributing traits can be used in crossing programme for development of high yielding cultivars as well as cultivars for animal feed on the base of high bio mass. According to table 3, the maximum intra cluster distance was found in cluster III and maximum inter cluster distance was found between cluster III and cluster VI. The minimum intra cluster distance was observed in cluster V and lowest inter cluster distance was exhibited by cluster I and cluster II. Crossing between genotypes from the cluster III and VI may produce maximum diversity in the segregating population and may be useful to develop high yielding cultivars. It is clear from the study of Non-hierarchical Euclidean cluster analysis, that the genotypes of the same cluster had less or no divergence from each other with respect to the aggregate effect of the character studied. This finding was also supported by earlier findings of Solanke *et al.*, (2013) and Alam *et al.*, (2013) and Zaman and Alam, (2013).

The parental lines (females) and testers (males) had much genetic diversity on the basis of analysis as lines were put into different clusters. Hence these are important lines to develop hybrids as well as composite lines because crossing between desirable diverse female lines and testers are capable to produce vigorous hybrids or progenies. The F₁s progenies may also be directly utilized as commercial purpose in the form of three-way cross hybrid, double cross hybrid, quadrilateral cross hybrids. These combinations might be growing in advanced generation under control pollination to obtain nearly homozygous lines or inbreds for various breeding purpose. These inbreds would have good potential and could be utilized in development of hybrid cultivars in future for enhancement of financial condition of farmers/country/ society. The crosses may

be attempted between the genotypes of the clusters separated by large inter cluster distance to obtain desirable segregants and ultimately for the development of inbreds. The crossing among genetically diverse lines for specific traits may be helpful in bringing the new gene pool or heterotic pool in the population.

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