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Genetic divergence studied in quality protein maize inbreds (*Zea mays* L.)

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Abstract

Thirty quality protein maize inbreds were evaluated for genetic divergence through analysis using Mahalanobis D^2 statistic for a set of 15 quantitative characters. The analysis of variance revealed significant differences among the genotypes for all the traits under study. The thirty inbred lines were grouped into six different clusters using D^2 statistic. Highest inter cluster distance was observed between cluster V and VI (3990.93) followed by cluster I and V (2946.25) and cluster III and VI (2195.13) on the basis of their genetic distances. Genotypes, Dholi QPM-2009, DMR QPM-03-103-6, DMR QPM-03-103-7, 2006-6-CML-471, POP 61-CL QPM TEYF-S4-2-2-1-2-B-2-B-B, POP-61 CL QPM TEYF-S4-2-2-2-2-B-1-B-B from these clusters may be selected as parents for hybridization programme for developing new hybrid combinations.

Keywords: Genetic divergence and Quality Protein Maize (QPM).

Introduction

Maize (*Zea mays* L.) is one of the most important cereal crop and plays a very important role for human and animal nutrition in a number of developed and developing countries worldwide. The resultant genotype with elevated lysine and tryptophan level and without the negative effect of soft endosperm was termed as Quality Protein Maize (QPM) by CIMMYT scientists (Prassanna *et al.* 2001). QPM, looks and performed like normal maize except that its nutritional value got elevated. The discovery of nutritional value of opaque-2 mutant in maize was a significant breakthrough as a recessive opaque-2 mutation which changed the amino acid profile of the endosperm protein resulting in enhanced concentration of tryptophan and lysine. This enabled the maize breeders to develop new cultivar with high lysine protein. A plant breeder is constantly engaged in making an effective choice of desirable parents for a successful hybridization programme. In this context, existence of genetic diversity among genotypes to be used as parents is very much desired. Mahalanobis D^2 statistic measuring the divergence in biological population has been applied in maize to choose diverse parents based on genetic distance. The present paper deals with divergence analysis in 30 elite inbred lines of quality protein maize.

Materials and methods

The material comprised of thirty inbred lines derived from different maize populations were grown in Randomized Block Design (RBD) with 3 replication at TCA, Dholi during *kharif* 2012. Each plot consisting of two rows of 4m length spaced at 60 cm row to row and 25 cm plant to plant. Observations were recorded on five random competitive plants for 15 quantitative characters. The data were subjected to Mahalanobis D^2 statistics and inbred lines were grouped into different clusters following the Touchers method as described by Rao (1952) [8].

Results and Discussion

The analysis of variance showed significant differences among all thirty genotype of quality protein maize for all the fifteen characters (table-1). This indicated the presence of considerable extent of inherent differences among genotypes of QPM. In the present investigation, maximum 10 genotypes were grouped in the cluster IV and minimum number i.e. single genotype was

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placed in cluster VI. The cluster I, II, III and V consist of 2, 5, 9 and 3 genotypes respectively. The relationship between different genotypes is presented in the form of ward minimum variance dendogram which was prepared using the rescaled distance (fig.-1) Reddy *et al.* (2012) [9] also reported similar findings in maize. Geographical and genetic diversity exhibited no correspondence between them as genotype from different geographical region are grouped together, which might be due to free exchange of genetic material from different regions. On the basis of cluster mean values (table-5), cluster I was found rich for number of leaves above ear. Cluster II was rich for tassel length, peduncle length, ear diameter, number of kernel rows per ear and number of kernels per row. Cluster III was rich only for yield per plot. Cluster V was rich for plant height, total number of leaves, ear height, ear length, 100 kernel weight and ear weight. Cluster VI was rich for days to 50% silking and days to 50% tasseling. Therefore, these clusters may be chosen for transferring the traits having high mean values through hybridization programme. The highest inter cluster distance was observed in between cluster V and VI (3990.93) and lowest inter cluster distance was observed in between cluster II and IV (195.63). Similar findings were reported earlier by Nehvi *et al.* (2008) [4], Patel *et al.* (2009) [5], Pradhan *et al.* (2009) [6] and Astha Gupta and Singh (2011) [1] in case of maize. On the basis of these intra and inter cluster distances it is observed that quality protein maize lines grouped together were less divergent than the inbred lines which fall into different clusters (table-3). Therefore, considering inter cluster distances and cluster mean values inbred lines from cluster V and VI, I and V & III and VI found suitable to get desirable hybrids. In terms of per cent contribution towards total genetic divergences characters such as 100 kernel weight had maximum contribution, followed by small contribution by yield per plot and days to 50% silking (table-4). Similar observations were recorded by Nehvi *et al.* (2008) [4] and Ganesan *et al.* (2010) [2]. However, plant height, leaves above ear, total number of leaves, ear height and ear length had no contribution towards genetic divergence.

Over all, Dholi QPM-2009, DMR QPM-03-103-6, DMR QPM-03-103-7, 2006-6-CML-471, POP 61-CL QPM TEYF-S4-2-2-1-2-B-2-B-B, POP-61 CL QPM TEYF-S4-2-2-2-2-B-1-B-B inbred lines may be selected as parents for hybridization programme for developing new hybrid combinations after testing for their combining ability.

Table 1: Analysis of variance for fifteen characters in QPM inbred lines.

Sl. No.	Characters	Mean sum of square due to		
		Replication	Treatment	Error
1.	Days to 50% Silking	1.0111	55.91**	0.6433
2.	Days to 50% tasseling	0.0778	52.3559**	0.4571
3.	Plant Height	150.20	1227.71**	65.59
4.	Leaves above Ear	0.8361	0.9235**	0.4424
5.	Total no. of leaves	0.2583	4.134**	0.8359
6.	Ear height	28.26	467.80**	28.6689
7.	Tassel length	0.2333	134.044**	6.558
8.	Ear length	0.1408	1.8745**	0.1848
9.	Peduncle length	1.104	47.3957**	1.5203
10.	Ear diameter	0.0163	0.8819**	0.0682
11.	Number of kernel row /ear	0.9590	3.1698**	0.5994
12.	Number of Kernel / row	1.5398	81.3439**	2.5316
13.	100 kernel weight	0.0254	52.5167**	0.0294
14.	Ear weight	27.5973	1363.67**	52.2377
15.	Yield per plot	0.0007	0.2784**	0.0102

Table 2: Clustering patterns of 30 genotypes of Quality Protein Maize on the basis of D^2 statistics

Cluster	No. of genotypes within clusters	Genotypes in cluster
I	2	POP 61-CL QPM TEYF-S4-2-2-1-2-B-2-B-B POP-61 CL QPM TEYF-S4-2-2-2-2-B-1-B-B
II	5	DMR-QPM-03-103-10, CML-161, DMR QPM-03-107-1, DMR QPM-03-103-12, 2006-6-CML-471
III	9	DMR QPM-03-103-9, CML-161, DMR QPM-03-103-11, DMR QPM-03-119-2, DMR QPM-17-1, DMR QPM-03-118-#-29-2, DMRO QPM-03-124, DMR QPM-03-119-4, DMR QPM-03-103-17
IV	10	2007-1-CML-469, POOL-17 QPM-S6, 69-828 K-CML-115, CML-411, CML-169, POP-61-CL QPM TEYF-S4-2-2-2-2-B-2-B-B, CML-196, CML-165, CML-163-7-2, DMR QPM-S8-26
V	3	DMR QPM-03-103-6, DMR QPM-03-103-7, 2006-6-CML-471
VI	1	Dholi QPM-2009

Table 3: Mean of inter & intra Cluster distances among six clusters of Quality Protein Maize.

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	28.27	441.78	1349.46	280.39	2946.25	215.62
2 Cluster		80.83	352.14	195.63	1257.26	1002.41
3 Cluster			109.71	670.49	447.53	2195.13
4 Cluster				209.43	1810.06	697.66
5 Cluster					128.63	3990.93
6 Cluster						0.00

Table 4: Per cent contribution of character to genetic divergence

SI. No.	Source	Rank	Contribution%
1	Days to 50% silking	21	4.83
2	Days to 50% tasseling	5	1.15
3	Plant Height (cm)	0	0.00
4	Leaves Above Ear (No.)	0	0.00
5	Total No. of leaves	0	0.00
6	Ear Height (cm)	0	0.00
7	Tassel Length (cm)	1	0.23
8	Ear Length (cm)	0	0.00
9	Peduncle length (cm)	1	0.23
10	Ear Diameter (cm)	0	0.00
11	Number of Kernel Rows/ Ear	1	0.23
12	Number of kernels/ row	10	2.30
13	100 Kernel Weight (gm)	354	81.38
14	Ear Weight (gm)	14	3.22
15	Yield per plot (Kg)	28	6.44

Table 5: Cluster mean for 15 characters of Quality Protein Maize.

	Days to 50% silking	Days to 50% tasseling	Plant Height (cm)	Leaves Above Ear (No.)	Total No. of leaves	Ear Height (cm)	Tassel Length (cm)	Ear Length (cm)	Peduncle length (cm)	Ear Diameter (cm)	No. Kernel Rows/ Ear	No. kernels/ row	100 Kernel Weight (gm)	Ear Weight (gm)	Yield/ plot (Kg)
1 Cluster	55.00	54.00	132.92	5.58	11.58	63.67	42.75	5.17	16.17	4.85	11.37	25.64	12.10	101.50	0.56
2 Cluster	54.33	52.47	144.33	5.07	11.03	65.77	46.87	6.33	18.43	5.65	12.20	30.84	16.77	93.00	0.85
3 Cluster	52.96	51.07	139.13	5.19	12.24	71.26	45.41	6.07	17.80	5.58	12.01	25.63	20.93	94.30	0.91
4 Cluster	55.40	53.77	116.47	4.67	10.88	60.63	41.00	5.44	14.67	5.05	11.49	22.75	15.42	104.22	0.74
5 Cluster	57.78	55.89	148.89	5.06	12.44	78.28	44.72	6.54	18.28	5.57	11.79	28.96	25.66	104.56	0.87

Mahalanobis Euiclidean^2 Distance

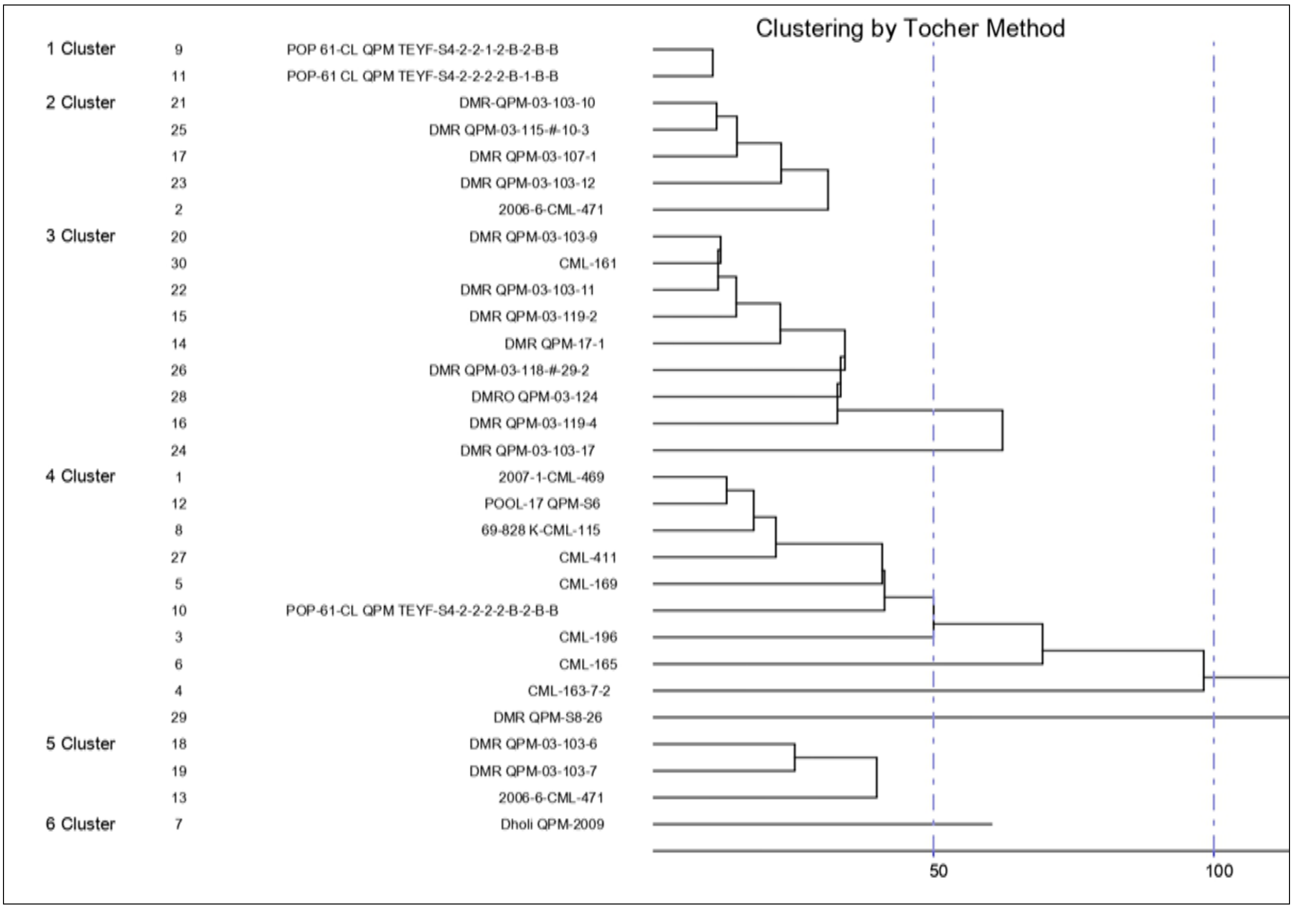

Fig 1 Clustering pattern of genotypes of QPM by wards minimum variance dendogram

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