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Morphological diversity analysis for quantitative traits in Quality Protein maize (QPM)

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Abstract
Genetic divergence among parents is of paramount importance in selecting them for hybridization programme. D^2 statistics used to measure the genetic divergence among the genotypes has been successfully utilized by the breeders to analyze the morphological diversity. Hybridization is one the tools to create variability. One may create more variability through hybridization when parents are diversed. Hence, genetic diversity in the parents is a prerequisite for crop improvement programmes. The genetic divergence among 25 genotypes of QPM inbreds were estimated by using Mahalanobis D^2 statistic for eleven characters. The twenty five maize genotypes were grouped into seven different clusters based on the Inter-genetic distance. This indicates the presence of considerable diversity in the genotypes studied. Clustering pattern indicated that 15 out of 25 genotypes belongs to the same cluster that is cluster I followed by cluster IV with 4 genotypes, cluster III with 2 genotypes and cluster II, V, VI and VII having 1 genotype (mono-genotypic). The average intra cluster distance range from 3.19 to 12.11. The maximum intra cluster distance was observed in cluster IV (12.11), followed by cluster I (9.18), cluster III (3.19). Cluster II exhibited close proximity with cluster VI (9.22) and maximum divergence with cluster VII (50.23). Cluster III was nearest to cluster VII (15.32), while it was farthest from cluster II (33.02). Cluster IV showed close proximity with cluster V (19.13) and maximum divergence with cluster VI (29.47). Cluster V exhibited intimate relation with cluster VII (22.29) and wide diversity with cluster VI (57.85). Farthest clusters for Cluster VI is Cluster VII (39.07). Percent contribution of eleven quantitative characters to total divergence were found maximum for ear length (27.67 %) and minimum for No. of kernel rows per ear (0.33 %). The analysis of divergence indicated significant differences among parental lines for all the agro-morphological characters. On the basis of results obtained in the present investigation, it was concluded that the allelic diversity can be used for future breeding program. The traits under study are also major yield contributing traits and are largely associated with each other. Therefore, these traits should be taken into consideration either simultaneously or alone for selecting a high yielding maize genotype.

Keywords: Genetic diversity, D2 statistics, QPM, quantitative characters

Introduction
Maize (*Zea mays* L.) is best known as golden crop because every part of this crop is useful to man, animals and the industries. Maize is currently produced on nearly 180.64 million hectares in 125 developing countries with a production of 1033.6 million tonnes and productivity of 5.77 tonnes/ha. (Annual report maize, 2018). It is characterized by translucent, horny appearance of kernel when matures and wrinkled appearance when it dries. Maize is a low cost and rich repository of carbohydrates, fats, proteins, vitamins and minerals and therefore it is also called 'poor man's nutricereal' (Prasanna *et al.*, 2001) [20]. The nutritional qualities of maize are on par with other cereals in most of the aspects. The maize kernel contains approximately 60-70 % carbohydrates 9-11 %, crude protein 2-3.5 %, crude fiber 3-5 % lipids and 20 mg of Ca/100g of kernels. It also contains carotene which is the precursor of vitamin A. About 70-80 % of maize production is used as a feed ingredient in the world. Although normal maize contains about 8-9 % protein, the quantity of two essential amino acids, lysine and tryptophan, is below nutritional requirements for monogastric animals. Therefore, utilization of quality protein maize (QPM) can corrects this deficiency and may be advantageous in the diets of livestock, monogastric animals in particular.

Inbred lines are the prerequisite for hybrid variety development in crop plants. For developing high yielding hybrids in maize, inbred lines need to be developed and evaluated for their diverged gene pool. The genetic diversity between the genotypes is important as the genetically diverged parents are able to produce high heterotic effects (Ghaderi *et al.* 1979). The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents. D^2 analysis is a useful tool for quantifying the degree of divergence between biological population at genotypic level and in assessing relative contribution of different components to the total divergence both in intra and inter-cluster level**.** It is also helpful in assessment of relative contribution of different components to the total divergence at both intra and inter-cluster level (Sachan and Sharma, 1971). In view of above importance, 25 QPM inbred lines at Instructional farm of Tirhut College of Agricultrue, RPCAU, Pusa, Samastipur were investigated to study the extent of genetic diversity for yield and yield contributing traits.

Materials and Methods

The present investigation was carried out at the Instructional Farm, Tirhut College of Agriculture, RPCAU, Pusa, Samastipur (Bihar) during *kharif* 2018. The nucleus seed of twenty five genotypes of high quality protein maize were obtained from AICRP, Dholi (Table-1). Twenty five diverse genotypes were raised in randomized block design with three replications having plot size of 1.5 x 4.0 = 6 $m^{2.}$ Each plot consisting of two rows of 4m length spaced at 75 cm row to row and 20 cm plant to plant, respectively. All the recommended package of practices were applied to raise a good and healthy crop. The data were recorded on five randomly selected plant samples from each replication for different quantitative characters, *viz.* plant height, Ear height, Days to 75 % tasseling, Days to 75% silking, Days to 75 % Brown husk, Tassel length, Cob length, Cob diameter, No. of kernel rows per ear, No. of kernels per row, and Grain yield (kg/ha). Out of the 11 quantitative characters, days to 75% tasseling, days to 75% silking and days to 75% brown husk were recorded on plot basis. Rest of the traits were recorded on the basis of five randomly chosen plants at appropriate stage. The data recorded on different characters were statistically analyzed using software WINDOSTAT version 7.0 developed by Indostat Services Ltd., Hyderabad, India. The data were subjected to Mahalanobis D^2 analysis. Genetic diversity was estimated as per Mahalanobis D^2 statistics (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). The percent contribution of characters towards genetic divergence was calculated according to Singh &Chaudhary (1985).

Results and Discussion

The genetic divergence among 25 QPM genotypes was estimated for 11 characters, *viz.*, Plant height, Ear height, days to 75% tasseling, days to 75 % silking, days to 75 % brown husk, tassel length, ear length, ear diameter, no. of kernel rows per ear, no. of kernels per row, grain yield (kg/ha). Based on this analysis, all the genotypes were grouped into seven different clusters. The clustering pattern of genotypes is presented in table 2. Clustering pattern indicated that 15 out of 25 genotypes belongs to the same cluster that is cluster I followed by cluster IV with 4, cluster III with 2 and cluster II, V, VI and VII having 1 genotype (monogenotypic). Clustering pattern of QPM inbred lines on the basis of Tochers method dendrogram has been given in the figure 1.0. Similar approach was adopted earlier by Singh and Choudhary (2001) [25], Singh *et al*. (2003), More *et al*. (2006) [16], Bhoite and Dumbre (2007) [7], Farzana Jabeen *et al*. (2007) [8], Ganesan *et al.* (2010) [9], Astha Gupta and Singh (2011) [11], Alam and Alam (2013) [1]. Genetic diversity is generally associated with geographical diversity, but the former is not necessarily directly related with geographical distribution. The genotypes with in the same clusters were originated from different geographical regions of the world, which indicated the geographical distribution and genetic divergence did not follow the same trend which might be due to continuous exchange of genetic material among the countries of the world. The average intra cluster distance range from 3.19 to 12.11. The maximum intra cluster distance was observed in cluster IV (12.11), followed by cluster I (9.18), cluster III (3.19) presented in Table-3. The nearest and distant clusters from each of the cluster based on D values are presented in Table-3. Cluster I was nearest to cluster III (13.79) and distant from cluster V (24.62). Cluster II exhibited close proximity with cluster VI (9.22) and maximum divergence with cluster VII (50.23). Cluster III was nearest to cluster VII (15.32), while it was farthest from cluster II (33.02). Cluster IV showed close proximity with cluster V (19.13) and maximum divergence with cluster VI (29.47). Cluster V exhibited intimate relation with cluster VII (22.29) and wide diversity with cluster VI (57.85). Farthest clusters for cluster VI are cluster VII (39.07). Similar findings were reported by Farzana Jabeen *et al.* (2007) [8], Nehvi *et al.* (2008) [18], Astha Gupta and Singh (2011) [11], Haydard *et al.* (2015) and Maruthi *et al.* (2015) in case of maize. Cluster means for 11 characters were presented in Table-4. The cluster mean for plant height ranged between 93.33 and 140.00. The maximum cluster mean was observed in cluster III but minimum cluster mean was observed in cluster II. The cluster mean for ear height ranged between 32.50 to 77.50.The maximum cluster mean was observed in cluster VII but minimum cluster mean was observed in cluster II. The cluster mean for days to 75% tasseling ranged between 52.33 and 60.00. The inbreds in cluster VII appeared early in tasseling as the group had taken minimum number of days for tasseling but the inbreds grouped in cluster III had taken more number of days to 75% tasseling. The cluster mean for days to 75% silking ranged between 56.00 to 63.00. The inbreds in cluster VI and VII appeared early in silking as this group had taken minimum number of days for silk emergence. The cluster mean for days to 756% brown husk ranged between 91.33 to 95.50.The inbreds in cluster VII appeared early in brown husk stage as this group had taken minimum no. of days for brown husk but the inbreds grouped in cluster III had taken maximum no. of days to 75% brown husk. The cluster mean tassel length ranged between 24.03 to 30.72. The cluster mean tassel length ranged between 24.03 to 30.72. The maximum cluster mean was observed in cluster III and minimum cluster mean was observed in cluster VI. The cluster mean for ear length ranged between 13.43 to 22.58. The minimum cluster mean was observed in cluster II and the maximum cluster mean was observed in cluster V. The cluster mean for ear girth ranged between 11.33 to 15.78. The minimum cluster mean was observed in cluster II and the maximum cluster mean was observed in cluster V. The cluster mean for no. of kernel rows per ear ranged between 12.00 to 16.00.The minimum cluster mean was observed in cluster II but the maximum cluster mean was observed in cluster VII. The cluster mean for no. of kernels per row ranged between

24.17 to 33.79. The minimum cluster mean was observed in cluster II but the maximum cluster mean was observed in cluster IV. The cluster mean for grain yield ranged between 1211.75 and 3081.56. The maximum cluster mean was observed in cluster V and the minimum cluster mean was observed in cluster II. Therefore, these clusters may be chosen for transferring the traits having high mean values through hybridization programm. These findings are in accordance with Singh *et al.* (2005) [24], Marker and Krupakar (2009) [15] and Alam and Alam (2013) [1]. Percent contribution of 11 quantitative characters to total divergence were found maximum for ear length (27.67 %) followed by grain yield per plot (20.33 %),ear height (16.00 %), plant height (13.13 %), days to 75 % tasseling (10.33 %), tassel length (5.33 %), No. of kernels per row (4.00%), ear girth (1.67 %), days to 75 % silking (1.00 %) and No. of kernel rows per ear (0.33 %) and among 299 combinations, ear length ranked Ist (83 times), followed by grain yield (kg/ha) (61 times), ear height (48 times), plant height (40 times), days to 75 % tasseling (31 times), tassel length (16 times), No. of kernels per row (12 times), ear girth (5 times), days to 75 % silking (3 times) and No. of kernels row per ear (1 time). Similar observation was recorded by Anderson (1957) [3] and Rao (1952), Nehvi *et al.* (2008) [18] and Ganesan *et al.*, (2010) [9] and Rigon *et al.* (2015) [22].

It has been well established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad spectrum variability in segregating generations (Arunachalam, 1981) [5]. It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity. In maize, the traits *viz*., plant height, ear length and number of kernel rows per cob were the key component traits associated with high grain yield. Therefore, based on large inter-cluster distances, it is advisable to attempt crossing among the genotypes from cluster II, IV, VI and VII which may lead to broad spectrum of favorable genetic variability for yield improvement in maize.

Table 2: Clustering pattern of twenty five QPM inbred lines on the basis of D^2 statistics

Clusters	No. of genotypes within clusters	Genotypes in cluster
I	15	CLQ-RCYQ-41, CML76*CLG-B*4, CML*CL02843-12, CML*CLG-55, CML61-B*8, CML61*65-21, CLQ*CL-26, CML61*65-18, CLG-2501-170, POO-TEYFQM, CML61*CLQ-B*5, CML93-B*6, CML61*65-B*4, G34QC-BB-16, G33QMH-103.
II	1	CML61*65-50
III	2	CML61*65-16, CLQ-RCYQ-44
IV	4	CLQ*CL-23, P70C0-6, CLQ-RCYQ-035, CML65-B*9
V	1	CLQ-RCYQ-28
VI	1	CLQ-RCYQ-12
VII	1	CML451-B*8

Table 3: Mean inter & intra cluster distances among seven clusters in QPM inbred lines

	I	II	III	IV	V	VI	VII
Cluster I	9.18	16.86	13.79	15.37	24.62	16.42	19.20
Cluster II		0.00	33.52	25.96	48.70	9.22	50.23
Cluster III			3.19	30.07	33.02	23.69	15.32
Cluster IV				12.11	19.13	29.47	26.15
Cluster V					0.00	57.85	22.29
Cluster VI						0.00	39.07
Cluster VII							0.00

Table 4: Cluster mean for eleven characters in QPM inbred lines

	Plant Height (cm)	Ear Height (cm)	Days to 75% Tasseling	Days to 75% silking	Days to 75% Brown husk	Tassel length (cm)	Ear length (cm)	Ear girth (cm)	No. of kernels row/Ear	No. of kernels/ Row	Grain yield (kg/ha)
Cluster I	120.51	54.50	56.64	59.71	94.04	28.97	16.99	12.50	13.57	28.77	1981.61
Cluster II	93.33	32.50	55.67	59.33	93.33	28.67	13.78	11.33	12.00	24.17	1211.75
Cluster III	140.00	72.08	60.00	63.00	95.50	30.72	16.52	14.16	13.43	28.25	1768.26
Cluster IV	113.54	50.50	54.00	57.17	93.00	28.68	18.30	12.85	13.90	33.79	2799.76
Cluster V	118.53	52.27	58.00	61.67	94.33	27.48	22.58	15.78	13.07	27.33	3081.56
Cluster VI	122.10	53.33	52.67	56.00	91.67	24.03	13.43	11.27	13.07	28.17	1534.51
Cluster VII	139.03	77.50	52.33	56.00	91.33	29.62	20.60	12.38	16.00	29.50	2347.11

Table 5: Percent contribution of character towards genetic divergence

S. No.	Source	Time Ranked 1st	Contribution %
1	Plant Height (cm)	40	13.13%
2	Ear Height (cm)	48	16.00%
3	Days to 75 % tasseling	31	10.33%
4	Days to 75 % silking	3	1.00%
5	Days to 75 % Brown husk	0	0.00%
6	Tassel length (cm)	16	5.33%
7	Ear length(cm)	83	27.67%
8	Ear girth (cm)	5	1.67%
9	No. of kernel rows per ear	1	0.33%

10	No. of kernels per row	12	4.00%
11	Grain yield (kg/ha)	61	20.33%

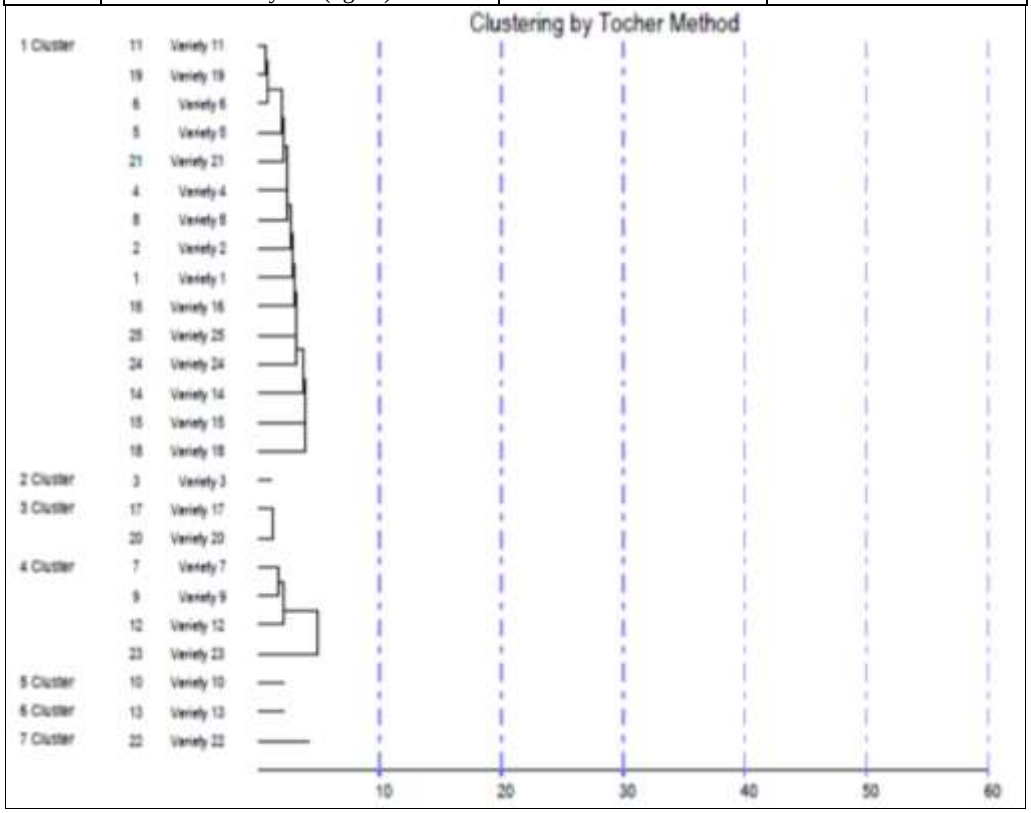

Fig 1: Ward Minimum Variance Dendrogram for distribution of twenty five QPM inbred lines in seven clusters based on non-hierarchical Euclidean Cluster analysis

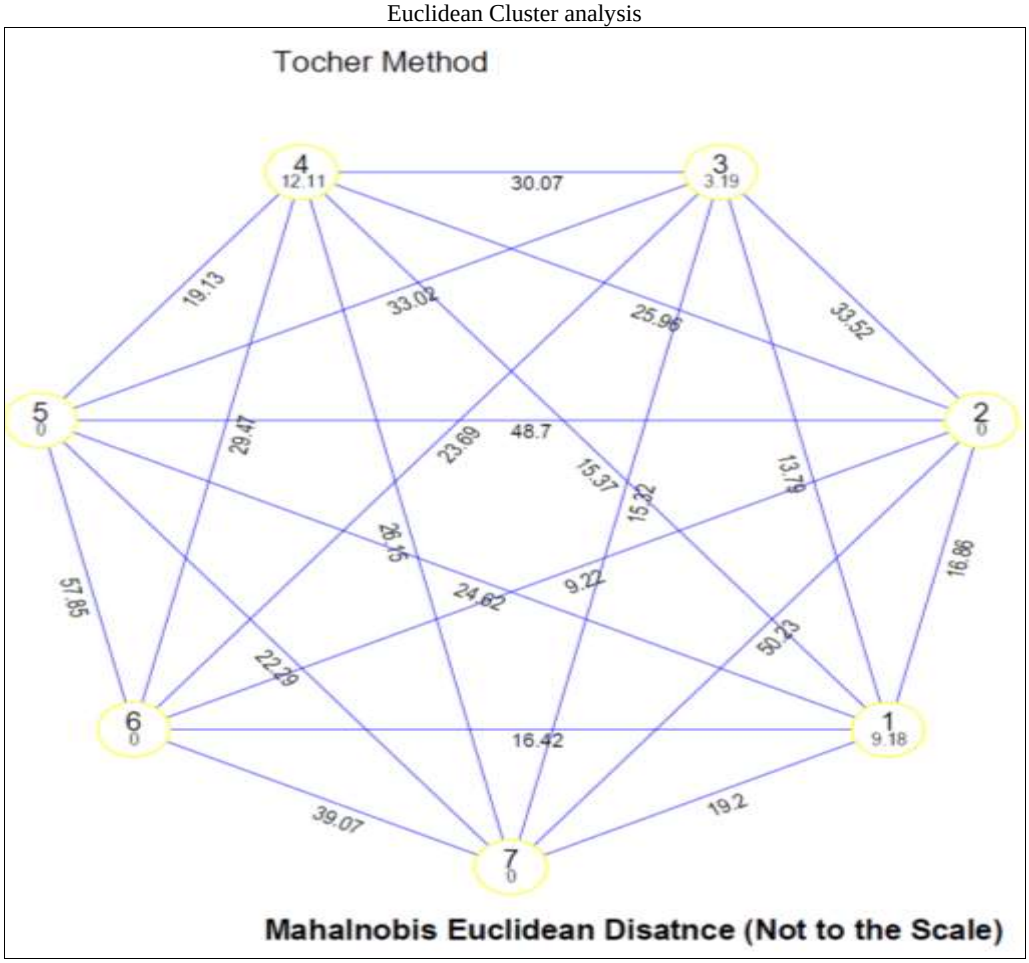

Fig 2: Inter cluster mean distance of D^2 by Toucher methods

Conclusion

The study on Quality Protein Maize (QPM) genotypes' morphological diversity concludes that significant genetic diversity exists among the 25 QPM inbreds analyzed, offering valuable insights for future breeding programs aimed at yield improvement. Through Mahalanobis D2 statistic analysis, the genotypes were classified into seven distinct clusters, indicating substantial variability. The diversity is critical for selecting genetically diverse parents capable of producing high heterotic effects in hybrids, a key strategy for enhancing maize yields. The study found that traits such as ear length, grain yield per plot, and ear height were major contributors to genetic divergence, suggesting their importance in selecting high-yielding maize genotypes. It emphasizes the potential of using allelic diversity for breeding programs and the importance of considering these major yield-contributing traits, either alone or simultaneously, in the selection process. The findings underscore the utility of genetic diversity analyses in identifying diverse and promising genotypes for hybridization, ultimately contributing to the advancement of maize breeding efforts.

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