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Genetic variability evaluation for morphological and phenological traits of quality protein maize inbred lines

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Abstract

Present study was undertaken to examine the level of genetic variability and diversity for eleven morphological and phenological traits of eighteen quality protein maize (QPM) inbred lines evaluated in randomized block design during two seasons. The phenotypic coefficient of variation was found higher than the respective genotypic coefficient of variation for all characters during both the seasons. Relatively greater magnitude of difference in phenotypic and genotypic coefficient of variation was observed for phenological characters like days to silking, days to tasseling and days to brown husk as well as morphological characters like ear height, grain yield per plant and test weight. The data on heritability in broad sense and genetic advance as percent of mean indicated the existence of exploitable extent of genetic variability for all the characters. Ward minimum variance approach based dendrogram constructed from pooled data indicated the interrelationship among the inbred lines, which were observed to be distributed among five clusters. Six out of eighteen inbred lines were accommodated in the largest cluster, whereas the smallest cluster consisted of two inbred lines. The range of intra-cluster and inter-cluster distances revealed ample genetic differentiation and genetic diversity for morphological and phenological characters amongst inbred lines under evaluation. Experimental findings of this study provided the basis to suggest that allelic diversity among the inbred lines can be employed in future breeding programs.

Keywords: Maize, genetic variability, heritability, genetic advance, genetic diversity

Introduction

Maize is considered as the golden crop because of its importance for humans, animals, and businesses. India was a net importer of maize prior to the turn of the century, since domestic output could not keep up with rising demand from the poultry and other industries. However, hybrid adoption, particularly in nontraditional maize-growing states and to a lesser extent in traditional maize-growing states pushed maize yield and production in the country sharply higher, ensuring both self-sufficiency and export potential.

Maize is an inexpensive source of carbohydrates, fats, proteins, vitamins and minerals (Prasanna *et al.*, 2001) [22]. In most ways, its nutritional properties are comparable to those of other cereals. The maize kernel includes 60-70% carbohydrate, 9-11% crude protein, 2-3.5% crude fiber, 3-5% lipids and 20 mg of calcium per 100 g of kernels. It also includes carotene, which is a vitamin A precursor. In the world, about 70-80% of maize production is used as a feed ingredient. Despite the fact that normal maize contains about 8% to 9% protein, the amount of two essential amino acids, lysine and tryptophan, is insufficient to meet the nutritional needs of monogastric animals. Use of quality protein maize (QPM) to rectify this shortfall may be beneficial in the diets of cattle, particularly monogastric animals.

Genetic advance in economically important traits is always considered as a desired goal in maize breeding projects. Since selection and its effectiveness are dependent on the availability of larger genetic variability, genetic diversity among the parents is the most important requirement for initiation of a successful maize breeding program to ensure higher genetic gains. Therefore, assessment of genetic variability is a critical prerequisite for success in the breeding programs. Relatively higher heritability estimates combined with high genetic advance are well established to provide a lot of room for efficient selection to achieve appreciable progress. Precise information on the variability parameters and the degree of genetic divergence with inter-cluster and intra-cluster distances (Singh and Chaudhary, 1985) [28] between biological populations can aid the breeder in developing appropriate cultivars in a short period of time. With these objectives, the current study was undertaken to examine the

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genetic variance, heritability, genetic advance and genetic divergence for agronomically important morphological and phenological traits among eighteen QPM inbred lines.

Materials and Methods

The field experiments were conducted at research farm of

Tirhut College of Agriculture, Dholi, under Dr. Rajendra Prasad Central Agricultural University, Pusa, (Bihar) during May to October for Kharif season 2020 and from November to June for Rabi season 2020-21. The nucleus seed of eighteen inbred lines of quality protein maize (Table-1) were obtained from AICRP, Dholi

Table 1: List of the inbred lines evaluated in the present study along with their source

Sl. No.	Pedigree	Denotation	Source
1.	[CL-G 2501×CML-170]-B-2-2-2-B-1-1-1-BBB#	QPML-01	AICRP, Dholi Centre
2.	CML-161×165-18-2-1-2-BBB-#	QPML-02	AICRP, Dholi Centre
3.	[CML-176×CLG 2501]-B55-1-5-2-BBB-#	QPML-03	AICRP, Dholi Centre
4.	[CLQ-6601×CL-0243]B-26-1-1-BB-1-B*6-#	QPML-04	AICRP, Dholi Centre
5.	CLQ-RCYQ 035-B*11-#	QPML-05	AICRP, Dholi Centre
6.	CML-161×165-3-2-3-B*4-#-B1	QPML-06	AICRP, Dholi Centre
7.	[CLQ-RCYQ 31×CLQ-RCYQ 35]-B-36-2-B*5-5	QPML07	AICRP, Dholi Centre
8.	G 33 QMH 103-3-1-5-1-B*14	QPML-08	AICRP, Dholi Centre
9.	P70CO-BBB-6-B*6#	QPML-09	AICRP, Dholi Centre
10.	CML-193-B*6#	QPML-10	AICRP, Dholi Centre
11.	[CML-161/CML-165]B-B-B-11-B-B-B/CML-193	QPML-11	AICRP, Dholi Centre
12.	POP 61 C1 QPM TEYF-51-2-1-2-2-B-1-B/CML-193	QPML-12	AICRP, Dholi Centre
13.	[CML-161×CLQ-RCYQ 31]-B-10-3-B-B	QPML-13	AICRP, Dholi Centre
14.	CML-161	QPML-14	AICRP, Dholi Centre
15.	CML-163	QPML-15	AICRP, Dholi Centre
16.	CML-165	QPML-16	AICRP, Dholi Centre
17.	Pool 34 C24 (Subtily D QPM)-B-20-BB	QPML-17	AICRP, Dholi Centre
18.	Pool- 17 QPM	QPML-18	AICRP, Dholi Centre

These inbred lines were evaluated in a randomized block design with three replications. Each plot consisted of two rows of four meters each, spaced 75 cm row to row and 20 cm plant to plant. Observations for phenological characters like days to 50% silking, days to 50% tasseling and days to 75% brown husk were recorded on plot basis. Five plants were selected randomly for recording observations on agronomically important morphological characters like plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernel in a row, number of kernels in a cob, test weight (g) and grain yield per plant. Statistical analysis of the data recorded on eleven morphological and phenological traits was carried out using the software WINDOSTAT (version 9.2).

Results and Discussion

Genetic variability for morphological and phenological characters

Many quantitative and qualitative features of plants are influenced by their environment. This influence reveals heritable as well as non-heritable variation, which can be measured on the basis of some descriptive parameters like genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance. In this study, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in the broad sense and expected genetic gain as a percentage of the mean were calculated for the observed morphological and phenological characters (Table-2). It was observed from the results that the estimate of phenotypic coefficient of variability was higher as compared to the genotypic coefficient of variability for all eleven traits during both the seasons. The possible reason could be ascribed to the presence of non-genetic cause that influenced the expression of these traits. Cob girth (cm), ear height (cm),

grain yield per plant and number of kernels in a row were observed to have relatively higher estimates of genotypic coefficient of variation as well as higher phenotypic coefficient of variation, showing the importance of these characters in manifestation of variability among the inbred lines. Plant height (cm), number of kernel in a cob, ear length (cm) and test weight were observed to exhibit moderate genotypic and phenotypic coefficient of variation. Phenological characters like days to 50% silking, days to 50% tasseling and days to 75% brown husk recorded low genotypic and phenotypic coefficient of variation. Om Prakash *et al.*, (2006) [20], Choudhari and Prodhan (2007) [6], Murugan *et al.*, (2010) [18], Shanthi *et al.*, (2011) [24], Bharathiveeramani *et al.*, (2012) [4], Hepziba *et al.*, (2013) [11], Sharma *et al.*, (2014) [27], and Umar *et al.*, (2016) [30] also obtained more or less similar results in maize.

Cob girth, ear height, grain yield per plant and number of kernels in a row exhibited relatively higher heritability. Cob girth (cm), ear height (cm), grain yield per plant and number of kernels in a row were all noted as somewhat heritable traits in maize by Aboyi *et al.*, (2004) [1], Om Prakash *et al.*, (2006) [20], Vashistha *et al.*, (2013) [31] and Kumar *et al.*, (2014) [12]. The characters like days to 50% tasseling and days to 50% silking were observed with low genetic advance as a percent of mean and moderate heritability was exhibited due to favorable environmental influence as compared to the genotypes. Selection based on these traits may not be considered as the selection procedure may not be rewarding. Kumar *et al.* (2014) [12] found similar results for these traits in maize. Days to 75% brown husk had poor estimates for heritability and genetic advance indicating that it was heavily influenced by environmental factors and therefore selection would be ineffectual as Murugan *et al.* (2010) [18] also obtained similar results in maize

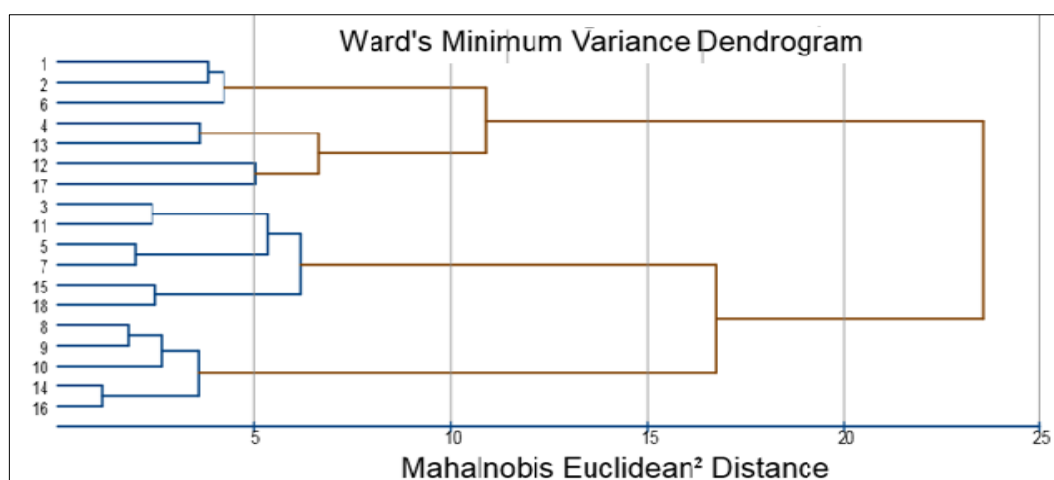
Table 2: Estimates of genetic variability related parameters for eleven morphological and phonological traits in QPM inbred lines

Genetic parameters	Cob girth	Cob length	Days to 50% silking	Days to 50% tasseling	Days to 75% brown husk	Ear height	Grain yield per plant	Number of kernels in a cob	Number of kernels in a row	Plant height	Test weight
GCV (S1)	6.13	4.58	4.77	5.04	2.00	5.46	4.29	7.03	7.19	5.75	2.34
GCV (S2)	6.79	3.15	1.46	1.55	1.59	7.76	4.58	6.14	7.50	5.97	3.33
PCV (S1)	6.86	5.06	5.73	6.04	2.85	6.75	5.36	8.66	8.72	6.21	3.36
PCV (S2)	8.44	4.59	2.25	2.39	1.97	11.31	7.27	6.74	9.99	8.66	5.00
h ² (Broad sense) % (S1)	79.6	81.7	68.5	69.7	49.3	65.5	63.9	65.5	68.1	85.7	48.6
h ² (Broad sense) % (S2)	64.6	47.3	42.3	42.0	59.1	47.0	39.7	83.0	56.3	47.1	44.4
GA as per cent of mean (S1)	11.26	8.5	8.08	8.68	2.89	9.11	7.06	11.72	12.23	10.97	3.37
GA as per cent of mean (S2)	11.25	4.47	1.96	2.07	2.40	10.96	5.94	11.53	11.60	8.44	4.58

Genetic diversity among Inbred Lines

Genetic divergence analysis is an important approach for assessing genetic diversity among genotypes and selecting parents for breeding programmes (Arunachalam, 1981) [3]. Parental selection based on genetic divergence is more likely to lead to greater success. The heterosis produced by crosses between genetically different parents is greater than that produced by crosses between closely related ones (Moll and Stuber, 1971) [16]. Accordingly, genetic divergence among eighteen QPM inbred lines was assessed in the present study using the pooled data recorded on days to 50% silking, days to 50% tasseling, days to 75% brown husk, plant height (cm), ear height (cm), cob length (cm), cob girth (cm), number of kernels in a row, number of kernels in a cob, test weight (g) and grain yield per plant. Cluster analysis revealed that all the eighteen inbred lines were categorized into five separate clusters (Table-3). Ward's minimum variance approach based

dendrogram indicated the distribution of six out of eighteen inbred lines in the same cluster, which is cluster - 04, followed by cluster - 05 with five QPM inbred lines, cluster - 01 with three QPM inbred lines, and clusters - 02 and 03 with two QPM inbred lines in each cluster (Figure 1). Carvalho *et al.* (2019) [8], Oyetunde *et al.* (2020) [21], Singh and Choudhary (2001) [28], More *et al.* (2006) [17], Bhoite and Dumbre (2007) [5], Farzana Jabeen *et al.* (2007) [7], Ganesan *et al.* (2010) [9], Astha Gupta and Singh (2011) [10], Alam and Alam (2013) [2] also used similar approach. Geographic diversity is frequently correlated with genetic diversity, but the latter is not always tied to geographic distribution. The inbred lines in the same clusters came from different parts of the world, indicating that the geographical distribution and genetic divergence did not follow the same pattern, which could be attributable to the continual exchange of genetic material among countries.

**Fig 1:** Ward's minimum variance approach based dendrogram showing inter-relationship and distribution pattern of eighteen QPM inbred lines

The average intra cluster distance (Figure 2) ranged from 4.605 to 10.06 (Table-4). Cluster - 03 (10.06) had the highest intra cluster distance, followed by Cluster - 01 (8.04) and Cluster - 04 (7.39). Cluster - 01 was found closest to Cluster - 02 (12.70) and farthest from Cluster - 04 (17.377). Cluster - 02 was closest to Cluster - 03 (10.95) and showed highest divergence from cluster - 05 (11.97). Cluster - 03 showed

close proximity to Cluster - 05 (14.31), whereas it showed highest divergence from Cluster - 04 (16.26). For Cluster - 04, the most divergence was observed with Cluster - 05 (11.07). Farzana Jabeen *et al.* (2007) [7], Nehvi *et al.* (2008) [19], Astha Gupta and Singh (2011) [10] and Maruthi *et al.* (2015) [15] also derived similar type of interpretation based on their studies experimental results on divergence analysis in maize.

Table 3: Clustering pattern of eighteen QPM inbred lines and composition of different clusters

Cluster No.	Number of inbred lines	Inbred lines included in cluster
Cluster-01	3	QPML-01, QPML-02, QPML-06
Cluster-02	2	QPML-04, QPML-13
Cluster-03	2	QPML-12, QPML-17
Cluster-04	6	QPML-03, QPML-05, QPML-07, QPML-11, QPML-15, QPML-18
Cluster-05	5	QPML-08, QPML-09, QPML-10, QPML-14, QPML-16

Table 4: Mean inter and intra cluster distances of five clusters among eighteen QPM inbred lines

	Cluster-01	Cluster-02	Cluster-03	Cluster-04	Cluster-05
Cluster-01	8.043	12.702	13.022	17.377	13.480
Cluster-02		7.219	10.953	11.156	11.970
Cluster-03			10.057	16.626	14.313
Cluster-04				7.386	11.074
Cluster-05					4.605

The pertinent data on cluster means for eleven morphological and phenological characters (Table-5) reveal that the cluster mean ranged from a minimum value of 4.59% in Cluster - 05 to the highest value of 5.17 in Cluster - 02 for cob girth. For cob length, this value ranged from a minimum of 6.22% in Cluster - 03 to the highest value of 6.71 in Cluster - 02. The value of cluster mean for days to 50% silking ranged from 82.00 to 83.80 days. Cluster - 02 showed early silking behavior as the cluster mean was minimum, took 82 days for the emergence of silk. The value of cluster mean for days to 50% tasseling ranged from 78.97 to 80.73 days. Cluster - 02 showed early tasseling behavior as the cluster mean was minimum, and took 78.97 days for the emergence of tassel. The value of cluster mean for days to 75% brown husk ranged from 113.61 to 116.80 days. Cluster - 01 included inbred lines that attained the brown husk stage earlier, whereas Cluster - 04 included inbred lines that had taken maximum days to attain the brown husk stage. For ear height, cluster mean

value ranged from a minimum of 56.66% in Cluster - 01 to the highest value of 66.91 in Cluster - 03. For grain yield cluster mean value ranged from a minimum of 73.63% in Cluster - 05 to the highest value of 77.11 in Cluster - 04. For number of kernels in a cob cluster mean value ranged from a minimum of 333.41% in Cluster - 04 to the highest value of 363.00 in Cluster - 03. For number of kernels in a row cluster mean value ranged from a minimum of 11.63% in Cluster - 04 to the highest value of 12.93 in Cluster - 05. For plant height cluster mean value ranged from a minimum of 135.22 present in Cluster - 01 to the highest value of 148.25 in Cluster - 03. For test weight cluster mean value ranged from a minimum of 274.16 present in Cluster - 01 to the highest value of 285.33 in Cluster - 03. As a result, these clusters could be used to transfer characteristics with high mean values via a hybridization procedure. Singh *et al.* (2005) [25], Marker and Krupakar (2009) [14] and Alam and Alam (2013) [2] also derived similar interpretations from their results.

Table 5: Cluster mean for eleven morphological traits in QPM inbred lines

	Cob girth (cm)	Cob length (cm)	Days to 50% silking	Days to 50% tasseling	Days to 75% brown husk	Ear height (cm)	Grain yield per plant	Number of kernels in a cob	Number of kernels in a row	Plant height (cm)	Test weight (g)
Cluster - 01	4.89	6.40	82.94	79.83	113.61	56.67	74.88	348.27	11.66	135.22	274.16
Cluster - 02	5.17	6.71	82.00	78.91	115.75	62.50	76.33	353.25	12.08	139.58	279.16
Cluster - 03	5.02	6.22	82.67	79.58	114.67	66.91	75.41	363.00	12.50	148.25	285.33
Cluster - 04	4.69	6.67	82.19	79.16	116.80	62.36	77.11	333.41	11.63	142.41	282.94
Cluster - 05	4.59	6.33	83.80	80.73	116.67	61.50	73.63	352.56	12.93	136.40	276.66

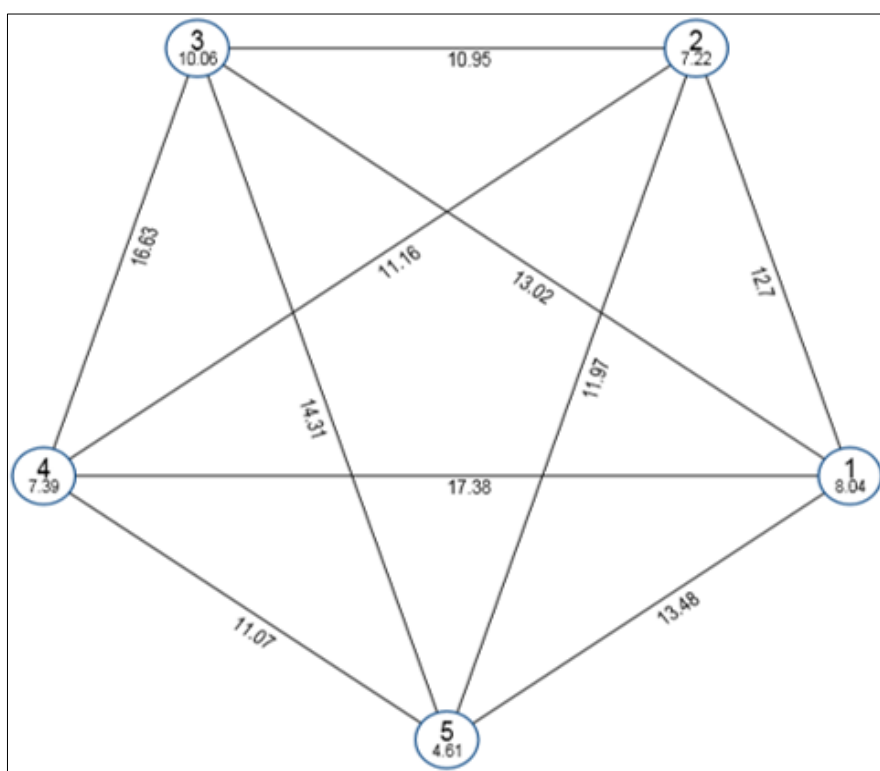


Fig 2: Euclidean cluster analysis based diagram depicting intra-cluster and inter-cluster distance

Conclusion

Variability parameters like heritability and genetic advance are considered relevant and purposeful in the utilization of the parental inbred lines. The higher heritability estimates combined with high genetic advance provide more accurate picture and scope for genetic gain and selection efficiency expected through selection based on the observed traits. When phenotypic selection is used to improve phenotypes, the higher heritability estimates are desirable. Cob girth, ear height, grain yield per plant and number of kernels in a row exhibited relatively higher heritability. Days to 50% tasseling and days to 50% silking were observed with low genetic advance as a percent of mean, indicating that selection based on these traits may not be rewarding. Days to 75% brown husk had poor estimates for heritability and genetic advance, indicating that the selection based on this trait would be ineffectual.

A quantitative evaluation of genetic diversity in the present study helped in elucidating the differentiation and divergence among eighteen QPM inbred lines, which were divided into five clusters. Ward's minimum variance approach based dendrogram indicated the hierarchical interrelationship and distribution of the eighteen inbred lines. A wide range of the average intra-cluster and inter-cluster distances was attributable to the use of several parental lines in the hybridization program as well as selection under diverse environmental conditions during the development of these inbred lines. Allelic diversity may be effectively employed in future breeding programs for further improvement by selecting genetically diverse parents from the clusters with greater inter-cluster distance.

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