

## GENETIC DIVERSITY IN QUALITY PROTEIN MAIZE QPM INBREED LINES

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### Abstract

The experimental material consisting of 18 lines and four standard checks were raised in RBD in three replications. Significant differences between the test entries were observed for all the traits. Twenty-two genotypes were grouped into VII clusters on the basis of observed distance among genotypes within a cluster as compared to genotypes in another cluster. Cluster III contains maximum number (seven) of genotypes. Cluster I had highest grain yield per plant, 100-grain weight, harvest index and tryptophan content while cluster VII had lowest anthesis silking interval and highest oil and lysine content and cluster V had maximum starch content. The better performing genotypes from clusters I, II and III were identified for all the traits. Therefore, F<sub>1</sub> derived from such diverse crosses is expected to show high yield.

### Introduction

Four types of prolamines (zeins), namely  $\alpha$ ,  $\beta$ ,  $\gamma$  and  $\delta$  are found in maize and they are distributed in a distinctive pattern, but it lacks in two essential amino acids viz., lysine and tryptophan. Effort was initiated with the discovery of mutant alleles, opaque-2 gene (Mertz *et al.* 1964) at Purdue University, which was found to alter the amino acid profile and composition of maize endosperm protein and result in twice increase in the levels of lysine and tryptophan compared to proportion in normal maize genotypes (Kumar *et al.* 2017a).

Because of very wide utilization of maize, the main goal of all maize breeding programs is to obtain new inbred and hybrids that will outperform the existing hybrids with respect to a number of traits (Kumar *et al.* 2017b). In working towards this goal, particular attention was paid to find out the diversity among the quality protein maize (QPM) lines for important agronomic characteristic, which can be useful for development of superior hybrids. The genetic diversity between the genotypes is important as the genetically diverged parents can produce high heterotic effects (Mian and Bahl 1989). Knowledge of germplasm diversity among elite breeding materials has a significant impact on the improvement of crop plant (Hallauer *et al.* 1988). Maize breeders are consistently emphasizing the importance of diversity among parental genotypes as a significant factor contributing to heterotic hybrids (Azad *et al.* 2012). Estimation of genetic diversity among maize lines is of great importance in hybrid maize breeding. D<sup>2</sup> analysis is a useful tool for quantifying the degree of divergence among biological population at genotypic level and in assessing relative contribution of different components to the total divergence both intra and inter-cluster level (Sachan and Sharma 1971).

### Materials and Methods

The study was conducted during *Kharif* 2014 at Instructional farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, India. The experimental material consisted of 22 genotypes, which were obtained from different sources. In this experiment, 18 inbred lines and 4 checks viz., Pratap QPM hybrid-1, Vivek QPM-9, HQPM-1 and HQPM-5 were used.

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Twenty-two QPM genotypes were grown in randomized block design with three replications during *Kharif* 2014. The seeds of each entry were sown in four-meter-long one row maintaining crop geometry of 60 × 25 cm. between rows and hills, respectively. One plant was kept per hill after proper thinning. Recommended doses of fertilizers were applied. The other intercultural operations were done timely and properly to raise the crop uniformly. Observations for all traits (Anthesis silking interval, plant height, ear height, ear length, 100-grain weight, grain yield per plant, harvest index, oil content, starch content, protein content, tryptophan content and lysine content) were recorded on five randomly selected competitive plants of each entry in each replication except for days to 50 per cent tasseling, days to 50 per cent silking and days to 75 per cent brown husk where observations were recorded on plot basis.

Estimation of oil content, starch content and protein content was done as per method suggested by Soxhlet's ether extraction method developed by A.O.A.C. (1965), Anthrone reagent method and micro Kjeldahl's method used by Lindner (1944), respectively. Tryptophan was estimated through calorimetric method designed by Hernandez and Bates (1969). Lysine was estimated according to the calorimetric method designed by Tsai *et al.* (1972) and modified by Villegas and Mertz (1971). Genetic divergence was calculated for 15 characters by Mahalanobis  $D^2$  statistics (1936).

### Results and Discussion

Significant differences between the test entries were observed for all the yield and yield contributing traits and quality parameters. Twenty-two genotypes were grouped into VII clusters on the basis of observed distance among genotypes within a cluster as compared to genotypes in another cluster (Table 1). Cluster III was found to have maximum number of genotypes i.e. 7 followed by 6 in cluster II, 5 in cluster I, 1 in each cluster IV, V, VI and VII. The clustering pattern revealed that, in general, genotypes from same origin showed no tendency to be in same cluster.

**Table 1. QPM lines included in each cluster.**

Clusters	No. of varieties	Varieties/genotypes
I	5	EIQ-130, Pratap QPM hybrid-1, Vivek QPM-9, HQPM-1, HQPM-5
II	6	EIQ-104, EIQ-103, EIQ-118, EIQ-119, EIQ-121, EIQ-125
III	7	EIQ-115, EIQ-120, EIQ-123, EIQ-126, EIQ-127, EIQ-128, EIQ-129
IV	1	EIQ-116
V	1	EIQ-117
VI	1	EIQ-122
VII	1	EIQ-124

Looking to the pattern of genotypes distribution into different clusters in the present study, it appeared that geographical distance between the genotypes had no relation with the genetic divergence as the genotypes from same source had fallen into different clusters as well as the same cluster contained genotypes from different sources. Similar results were reported by Azad *et al.* (2012) in maize.

As evident from Table 2, average inter cluster values were maximum between cluster I and VI followed by clusters VI and VII, clusters V and VI and clusters IV and VI on the basis of analysis. At intra cluster level, maximum values were recorded for cluster III followed by cluster II and

cluster I. Out of seven, three clusters have only one genotype in each cluster so intra cluster distance in these clusters was zero. The intercluster distances were greater than intracluster distances revealing considerable amount of genetic diversity among the genotypes. Therefore, the genotypes falling in these clusters appeared to be divergent and might have different geographical/genetic origin. Hence this technique could be gainfully utilized in maize improvement programme.

**Table 2. Average intra- and intercluster Euclidian distances in genotypes of QPM.**

Clusters	I	II	III	IV	V	VI	VII
I	<b>294.38</b>	2173.39	2470.74	907.45	935.43	4467.82	997.85
II		<b>584.80</b>	1325.61	1164.24	1202.80	2647.77	1117.69
III			<b>683.75</b>	1290.11	1666.39	1121.78	1820.02
IV				<b>0.00</b>	475.41	2538.96	1395.51
V					<b>0.00</b>	3380.05	880.07
VI						<b>0.00</b>	4038.67
VII							<b>0.00</b>

The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table 3). Cluster I had highest cluster mean for grain yield per plant, 100-grain weight, harvest index and tryptophan content while cluster VII had lowest anthesis silking interval and highest oil and lysine content and cluster V had maximum starch content. Similar results were also reported by Chen *et al.* (2007).

**Table 3. Cluster means for different characters in QPM.**

Characters	I	II	III	IV	V	VI	VII
Days to 50% tasseling	52.87	51.89	53.38	51.33	54.67	51.67	51.33
Days to 50% silking	55.27	54.61	56.10	53.67	56.67	54.00	54.33
Anthesis silking interval	2.40	2.72	2.76	2.33	2.33	2.33	3.00
Days to 75% brown husk	84.20	85.28	85.90	90.67	90.33	85.00	83.33
Plant height (cm)	190.67	188.06	185.29	196.67	186.33	178.67	211.33
Ear height (cm)	91.00	77.56	70.76	89.00	83.33	61.67	115.00
Ear length (cm)	14.61	13.62	13.76	13.93	14.38	10.16	15.23
100-grain weight (g)	29.86	19.94	21.62	27.20	29.73	18.70	27.94
Grain yield per plant (g)	89.99	40.43	47.02	82.01	67.23	36.23	48.40
Harvest index (%)	31.34	27.86	28.98	29.19	25.18	25.70	31.27
Oil content (%)	4.55	4.57	4.23	3.49	3.22	4.60	4.76
Starch content (%)	61.51	57.14	56.86	61.19	62.02	60.78	57.61
Protein (%)	8.95	8.16	9.26	8.61	8.35	9.93	8.60
Tryptophan content (%)	0.75	0.60	0.61	0.57	0.63	0.61	0.73
Lysine content (%)	3.13	2.70	2.58	2.42	2.73	2.31	3.15

The parents for hybridization could be selected on the basis of their large intercluster distance for isolating useful recombinants in the segregating generations. The better performing genotypes from clusters I, II and III were identified for all the traits. Therefore, F<sub>1</sub> derived from such diverse

crosses are expected to show high yield. Hence, these genotypes might be used in a multiple crossing programmer to recover high yielding hybrids.

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