Research Paper

Volume : 2 | Issue : 12 | December 2013 • ISSN No 2277 - 8179

Biochemical Diversity in Maize

Agriculture

KEYWORDS : genetic divergence, biochemical characters and maize genotypes

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ABSTRACT

The present investigation was carried out using forty maize genotypes belonging to grain maize, baby corn, sweet corn, pop corn and quality protein maize, to study genetic divergence for five biochemical traits such as total sugar content, starch content, protein content, carotene content and oil content.. This study, grouped the genotypes in to six distinct clusters. Clusters III and IV recorded the maximum inter cluster distance followed by clusters IV and VI. genotypes belonging to these three clusters can be selected for future hybridization programme aiming for quality improvement.

Introduction:

Maize occupies predominant position in global agriculture. Maize is an excellent source of carbohydrate and good quality oil. It is more complete in nutrients in comparison to other cereals. It is considered to be a good source of energy for both humans and animals. The grain is also relatively easy to process because the germ can be separated from the embryo more readily than in millet or sorghum. Maize grain is primarily used in diet of low income families, animal feed rations and as a source for more number of industrial products. This indicates the importance of maize in quenching the ever-increasing demand for food and warrants the development of new high yielding varieties and hybrids of maize with improved industrial qualities.

Maize being an allogamous crop can be subjected to breeding methodologies such as population improvement, intervarietal crossing, development of synthetics and composites and heterosis breeding. The improvement of trait under selection in a breeding programme principally depends upon the selection of better genotypes. The breeder can select the better genotypes based on the variability and diversity present in the source germplasm. In maize, utilization of parents with increased genetic difference, in hybridization programme has been observed to yield better hybrids (Singh et al., 2001). Maize plays an important role in industrial sector as it is used for the manufacture of a variety of industrial products such as starch, corn oil, corn syrup, glucose, and alcoholic beverages. Hence it is essential to improve the quality of maize. Keeping in view the quality improvement in maize, the present study focussed its attention towards the diversity of genotypes based on biochemical qualities

Materials and methods:

The present investigation was carried out at Millet Breeding Station, Tamil Nadu Agricultural University, Coimbatore, with a collection of forty maize germplasm belonging to baby corn, sweet corn, popcorn, quality protein maize and grain maize lines (Table 1).

The selected genotypes were subjected to the following biochemical analyses. The total sugar content was estimated using Anthrone reagent method and expressed in milligrams per 100 grams on dry weight basis. Four to five grains selected at random per cob were ground and starch content was estimated by Anthrone reagent method (Clegg, 1956) and expressed as percentage. The total content was estimated by microkjeldhal method (Humphries, 1956). Carotene content was estimated by extraction with acetone. The oil content was estimated by solvent extraction method i.e., a known weight of plant sample was subjected to continuous extraction with petroleum ether for six hours using the Soxhlet apparatus. The oil content was calculated using the following formula

Oil content (%) = $[(X - Y) / X] \times 100$.

Where,

X = Weight of the plant sample taken for analysis (g).

Y = Weight of the sample after extraction (g).

As suggested by Mahalanobis (1936) D2 statistic was used for the genetic divergence among the genotypes taken for the study. The data were subjected to multi variate analysis (Rao, 1952). The correlated variables were transformed in to uncorrelated variables and then all possible D2 values were worked out. Transformation was done by using pivotal condensation method.

Results:

The mean values for all the forty genotypes were transformed in to uncorrelated mean values and D2 values were computed for all possible 780 combinations. The highest D 2 value of 4690.16 was observed between the genotypes USC 2 and UPC 3, and the least D2 value of 3.28 was observed between the genotypes USC 10 and USC 5.

The clustering principle suggested by Tocher was used to group the forty genotypes in to six clusters based on five biochemical characters. The distribution of the genotypes in to different clusters was given in the Table 2. A dendrogram was drawn based on this Table and was shown in the Figure 1. Cluster II had the maximum of twenty one genotypes followed by cluster I with fifteen genotypes. The remaining clusters existed as solitary clusters in having only one genotype each.

Intra and inter cluster distances

The intra and inter cluster average distances are presented in the Table 3. Cluster I showed the maximum intra cluster distance of 12.54 followed by cluster II with intra cluster distance of 12.20. All the other clusters showed no intra cluster distance due to the presence of single genotypes in each of them.

The inter cluster distance ranged from 68.48 (between cluster III and cluster VI) and 7.80 (between cluster III and cluster IV).

Cluster mean values of the characters

The cluster mean values for the biochemical characters under investigation with respect to six clusters are furnished in the Table 4. The behavior of individual cluster is as follows.

Cluster I

This cluster included baby corn and sweet corn accessions and this cluster showed moderate mean values for all the five characters.

Cluster II

This cluster also exhibited moderate mean values for all the characters similar to that of the previous cluster.

Cluster III

Among all the clusters, this cluster showed the maximum mean values for maximum number of characters (two).

This cluster also exhibited maximum mean values of 78.40 per cent and 0.96 mg per 100 g for starch content and carotene content, respectively. This cluster is also characterized by low protein content of 10.80 per cent. This cluster included most of the popcorn, quality protein maize and grain maize accessions.

Cluster IV

This cluster recorded the maximum mean value for protein content (11.93 per cent) and lowest mean value for oil content (2.12 per cent).

Cluster V

The cluster recorded maximum mean value for oil content (5.05 per cent) and lowest mean value of 2.10 for total sugars.

Cluster VI

Among all the clusters, this cluster showed minimum mean values for maximum number of characters viz., starch content (65.45 per cent) and carotene content (0.30 mg per 100 g). This cluster also exhibited maximum mean value for total sugar content (8.30 per cent).

Discussion:

D2 analysis based on biochemical characters revealed that the selected maize genotypes were grouped into six clusters. Among the six clusters, two clusters namely clusters II and I had more than one genotype and exhibited genetic similarity within them. Genotypes USC 5 and USC 4 were obtained by selection from Bajaura sweet corn and so found to be in the same cluster (clusterI). In the same way genotypes UMH26, and UMH4, which come under the cluster II, are having UMI 90 as their common parent.

Based on the intra and inter cluster average distances given in the Table 17 the clusters III and VI can be selected because of the presence of maximum inter cluster distance. Cluster IV and VI can also be selected for the same reason. So the genotypes belonging to these three clusters can be selected for future hybridization programmes aimed at quality improvement.

Among all, the selected clusters III and VI exhibited maximum mean value for maximum characters (two) viz, starch and carotene content. Starch content in maize is having high heritability along with moderate genetic advance as per cent of mean. Similarly cluster IV recorded maximum mean value for sugar content that exhibited high heritability and genetic advance as per cent of mean.

All the selected clusters have only one genotype namely UPC 3, QPM 9120 and USC 2 in cluster III, cluster IV and cluster VI, respectively. The genotype UPC3 recorded maximum mean value for carotene content, which is the precursor of vitamin A. USC2 had exhibited highest mean value for total sugar content. Keeping in view the ever increasing demands of industrial sectors and nutritional aspects, the genotypes namely UPC3, QPM9120 and USC2 can be selected for future hybridization programmes to improve the quality.

Table 1. List of genotypes used for the study

Sl. No	Genotype	Type	Sl. No	Genotype	Type
1.	CO 1	Grain maize	21.	USC-5	Sweet corn
2.	UMC-12	Grain maize	22.	USC-7	Sweet corn
3.	UMC-13	Grain maize	23.	USC-9	Sweet corn
4.	UMH-15	Grain maize	24.	USC-10	Sweet corn
5.	UMH-26	Grain maize	25.	QPM-9114	QPM
6.	UMH-40	Grain maize	26.	QPM-9120	QPM
7.	UMH-42	Grain maize	27.	QPM-9122	QPM
8.	COH (M)-4	Grain maize	28.	QPM-9127	QPM
9.	COBC-1	Baby corn	29.	QPM-3	QPM
10.	BC-Local	Baby corn	30.	QPM-4	QPM
11.	BC-5	Baby corn	31.	QPM-5	QPM
12.	BC-7	Baby corn	32.	QPM-8	QPM
13.	BC-8	Baby corn	33.	9101 PC	Popcorn
14.	2KBC-6	Baby corn	34.	9102 PC	Popcorn
15.	2KBC-7	Baby corn	35.	9103 PC	Popcorn
16.	2KBC-8	Baby corn	36.	UPC-1	Popcorn
17.	USC-1	Sweet corn	37.	UPC-2	Popcorn
18.	USC-2	Sweet corn	38.	UPC-3	Popcorn
19.	USC-3	Sweet corn	39.	Bangalore Popcorn	Popcorn
20.	USC-4	Sweet corn	40.	Amber Popcorn	Popcorn

Table 2. Distribution of 40 maize genotypes in to different clusters based on five biochemical characters

Cluster number	Number of genotypes	Name of the genotypes
I	15	USC5, USC10, USC7, USC4, BC7, 2KBC7, USC1, BC8, COBC1, BC5, USC9, 2KBC8, 2KBC6, BC Local, USC3.
II	21	QPM 4, 9102 PC, 9101 PC, 9127 QPM, COH (M) 4, QPM3, Amber Pop Corn, UMC12, UMH42, UPC2, QPM9114, QPM5, QPM9122, UMH26, CO1, Pop Corn, UPC1, UMH40, 9103 PC, UMH15, QPM8.
III	1	UPC3
IV	1	QPM 9120
V	1	UMC13
VI	1	USC2

Table 3. Intra cluster and inter cluster average distances among six clusters for five biochemical characters

Clusters	I	II	III	IV	V	VI
I	**12.54**	44.56	48.41	41.17	49.99	28.56
II		**12.20**	21.71	20.71	19.68	57.31
III			**0.00**	7.80	36.02	68.48
IV				**0.00**	35.54	61.82
V					**0.00**	54.99
VI						**0.00**

Table 4. Cluster means for the five biochemical characters

Clusters	Characters				
	Sug	Sta	Car	Pro	Oil
I	7.52	69.01	0.70	11.60	2.18
II	2.45	77.28	0.64	11.29	2.41
III	2.50	**78.40**	**0.96**	**10.80**	2.62
IV	3.30	75.90	0.93	**11.93**	**2.12**
V	**2.10**	78.00	0.42	10.94	**5.05**
VI	**8.30**	**65.45**	**0.30**	11.71	2.71

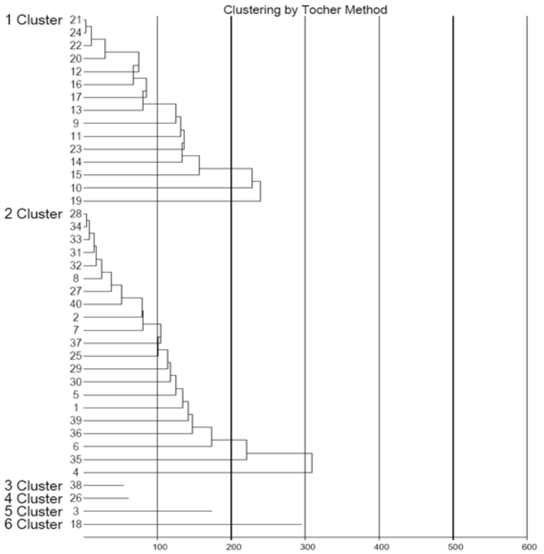

Fig 1. Dendrogram based on the D2 values for five biochemical characters

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