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Research Article

Hierarchical cluster analysis of genetic diversity in Maize germplasm

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Abstract

An experiment was conducted to analyze the genetic diversity among 38 maize germplasm accessions of the maize germplasm bank of Department of Millets, TNAU, Coimbatore. Observations regarding 25 morphological traits were recorded and the data matrix was used for estimation of Euclidian distance by Un-weighted Paired Group Arithmetic Average (UPGMA) method. Clustering was done by Sequential Agglomerative Hierarchical Non-overlapping (SAHN) clustering. The genotypes were grouped in to four clusters. The grouping of the genotypes was not influenced by their geographical origin. Maximum dissimilarity was observed between the genotypes UMI 551 and UMI 696. Widely divergent clusters and genotypes were identified which could be further evaluated for their breeding value as parents and could be exploited in maize crop improvement.

Key words : Maize, genetic diversity, UPGMA, SHAN, Clustering

Introduction

Maize is considered the third most important cereal crop after Rice and Wheat in the world. This cereal is referred as Miracle crop and Queen of the Cereals due to its high productivity potential compared to other Graminacea family members. On global front, maize has gained tremendous importance due to rising demand from diversified sectors like food, feed and ethanol production. As a result, since last one decade, the acreage under maize cultivation is continuously on increasing trend. India stands in fifth position in the world interms of corn production. The area under maize during 2008 was 8.12 million hectare with a production of 18.96 million tonnes and productivity of 2335 kg/ha. (http:// dacnet.nic.in).Maize facts and trends report (CIMMYT, 2000) indicated that 17 per cent of maize produced in the world is used as food for humans and 66 per cent is used as feed for animals. In India, 77 per cent of maize produced is used for human consumption, while only two per cent is used as feed for animals. This indicates the importance of maize in Indian agriculture, and the role it plays in meeting the ever-increasing demand for food and also warrants the development of new, high yielding varieties and hybrids of maize to increase production and productivity. Breeding methodologies of maize include population improvement, inter-varietal crossing, development of synthetics, composites and hybrids.

The plant breeder's choice of source germplasm determines the potential improvement for traits under selection in a breeding programme. The success of any breeding method depends on the availability of genetic diversity in the base population. Utilisation of diverse parents in hybridisation programmes has been observed to yield better hybrids. Hierarchical cluster analysis highlights the nature of relationship between any type of samples described by any type of descriptors . It could serve as a basis for selection of parental types that could result to superior hybrids. The objective of this study was to analyze the genetic diversity among 38 Maize germplasm accessions of the maize germplasm bank of Department of Millets, TNAU, Coimbatore and to classify the genotypes in to different groups based on Euclidian distance.

Materials and Methods

Seeds of 38 maize inbred lines listed in Table 1 were obtained from Maize breeding unit, Department of Millets, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU). They were raised in Randomized Block Design (RBD)with three replications. Observation

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regarding 25 morphological *viz.,* plant height, ear height, leaf number, leaf length, leaf width, tassel length, peduncle length, tassel branching space, number of primary, secondary and tertiary branches, cob number, days to anthesis, days to silking, anthesis - silking interval , number of grain rows per cob, number of grains per row, ear length, ear diameter, cob diameter, rachis diameter, grain length, grain width, grain thickness and seed yield per plant, were recorded in five random plants in each replications. The quantitative data gathered on different traits were standardized to zero mean and unit variance as per Sneath and Sokal, (1973) and Manly (1986). Squared Euclidian distance between genotypes was calculated from the standardized data matrix by Unweighted Pair Group Method using Arithmetic Averages (UPGMA) method and clustering was done by Sequential Agglomerative Hierarchical Non-overlapping (SAHN) clustering using NTSYSpc version 2.02 (Rohlf, 1998).

Result and Discussion

Choice of parents for developing base population is crucial in breeding because, it largely predetermines the outcome of subsequent selection steps and affects the optimum allocation of resources in breeding programmes. The analysis of overall pattern of genetic diversity and relationships among germplasm accessions facilitates the selection of parents with diverse genetic background (Murphy *et al*., 1986 and Souza and Sorrels, 1991). In the present study, genetic diversity was analyzed among 38 maize genotypes (Table 1) on the basis of 25 quantitative traits. The summary statistics of the morphological traits over all the genotypes , presented in Table 2, indicated wide variability for all the characters studied and hence ample opportunities exists for genetic improvement of the crop through selection directly from the accessions for development of inbreds for future hybrid breeding programs.

Cluster analysis was performed by SAHN clustering using the UPGMA method. The result of clustering (Figure 1) revealed that the 38 genotypes could broadly be classified into four major groups at a truncation level of 1.0 in the coefficient scale. Cluster 1 comprised of 14 genotypes, while clusters 2 and 3 comprised of 13 and nine genotypes respectively. The genotypes UMI 458 and UMI 773 were grouped in cluster 4 (Table 3). The distribution of genotypes in the study indicated that the geographical origin did not have any bearing on clustering pattern. Similar results were reported by Hernan and Karlovski (2006) in Sesame. Coefficient of dissimilarity was minimum between the genotypes UMI 551 and UMI 696, followed by UMI 556 and UMI 842. The most plausible explanation for the comparatively low genetic distances between the inbreds is that they might have descended from a common ancestral population. The inbreds UMI 433 and UMI 773 recorded the highest diversity value of 1.36 . Among the clusters, based on the mean cluster distance, it was observed that cluster 1 and 4 are highly dissimilar and genotypes from these two groups could be evaluated for their combining ability and could be used as parents in heteriosis breeding programmes in maize as suggested by Betrán *et al***.,**2003 in maize and Firoz Mahmuda *et al* .,2008, in Brassica.

References

Betrán F. J., Ribaut J. M., Beck. D and Gonzalez de León .D. 2003.Genetic Diversity, Specific Combining Ability and Heterosis in Tropical Maize under Stress and Nonstress Environments. ***Crop Science.43***: 797 - 806

CIMMYT, 2000. World maize facts and trends report. pp. 45-57.

Firoz Mahmuda, Md. Golam Rasulb and Md. Abdur Rahima .2008.Genetic diversity analysis in some advanced lines of *Brassica napus*. ***Science Asia. 34***: 432–434

Hernán .E . Laurentin and Petr Karlovsky. 2006. Genetic relationship and diversity in a Sesame (*Sesamum indicum L.*) germplasm collection using Amplified Fragment Length Polymorphism (AFLP). ***BMC Genetics.*** *7*:10 (doi:10.1186/1471-2156-7-10)

Manly, B.F.J. 1986. Multivariate statistical methods-A primer. 2ndedn. Chapman and Hall, London.

Murphy, J.P., Cox, T.S. and D.M. Rodgers. 1986. Cluster analysis of red winter wheat cultivars based upon coefficients of parentage. ***Crop Science. 26***: 672-676.

Rohlf, F.J. 1998. Numerical taxonomy and multivariate analysis system, version 2.02 i. 100. North Country Road, Setanket, New York.

Sneath, P.H.A and Sokal. R.R. 1973. Numerical taxonomy. The principles and practice of numerical classifications. W.H. Freeman and Company, San Francisco.

Souza, E. and Sorrells ,M.E. 1991. Relationships among 70 North American oat germplasm: I. Cluster Analysis using quantitative characters. ***Crop Science. 31***:599-605.

Table 1. List of genotypes used for genetic diversity analysis

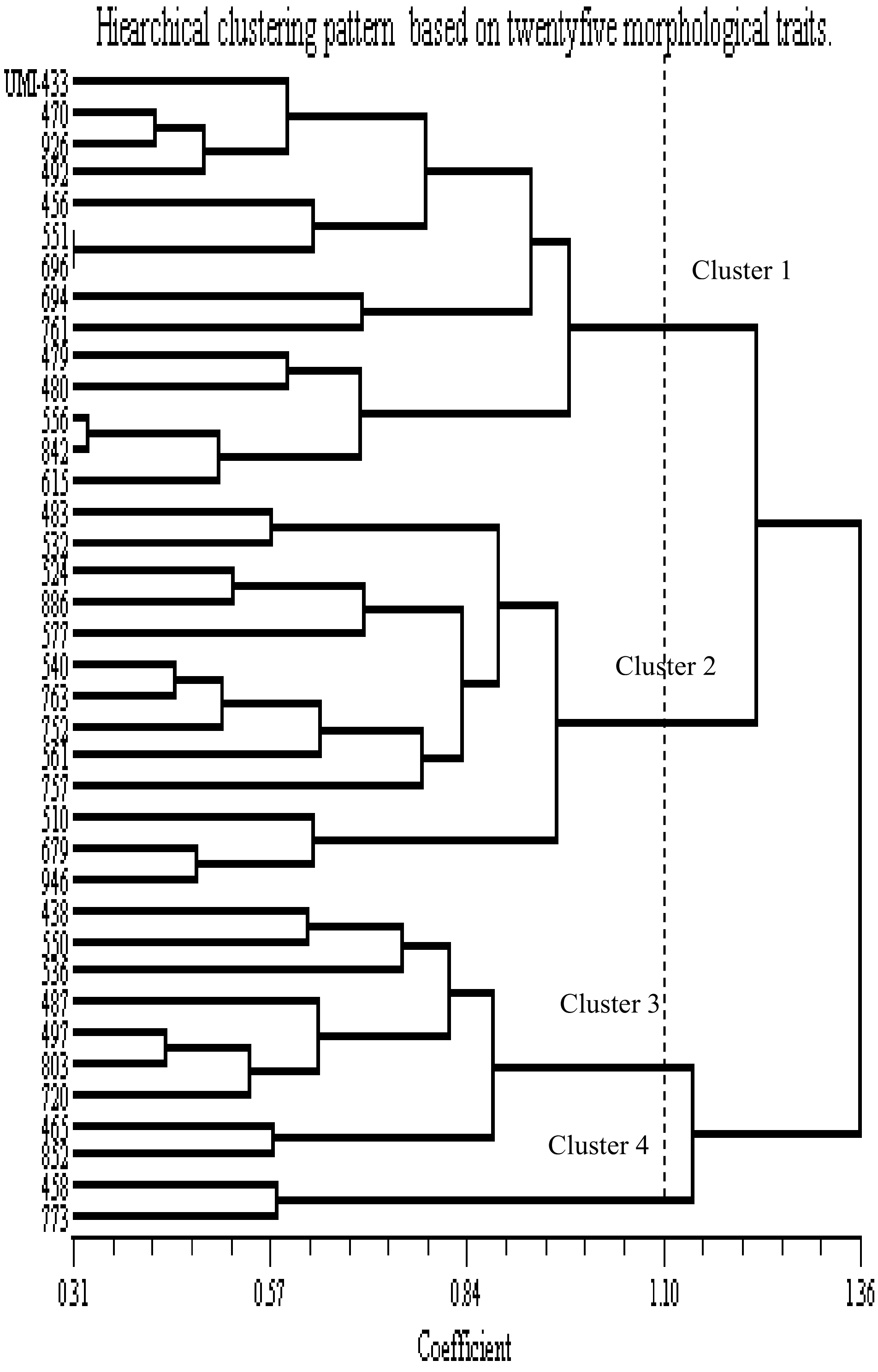
Accession No.	Parentage	Source
UMI 433	UMI-40 x UMI –101	Coimbatore
UMI 438	EH – 450879	DMR,Delhi
UMI 456	ALR –4	Coimbatore
UMI 458	ALR –6	Coimbatore
UMI 465	KLD –7	DMR, Delhi
UMI 470	K1	Kovilpatti
UMI 479	EM – 456979	DMR, Delhi
UMI 480	EH – 459379	DMR, Delhi
UMI 487	Dho –79	Bihar
UMI 492	Not known	Bihar
UMI 497	Not known	Bihar
UMI 510	T-433 / 980 K	Kanpur
UMI 524	(Sarhad x Suwan –1) x Suwan –1	Kanpur
UMI 532	UMI –79	Coimbatore
UMI 536	Hawaii Sugar	Hawaii
UMI 540	UMI – 14 x UMI –12	Coimbatore
UMI 550	UMI – 115 x UMI –3	Coimbatore
UMI 551	UMI – 126 x UMI – 80	Coimbatore
UMI 556	UMI – 140 x UMI –126	Coimbatore
UMI 561	UMI –269 x UMI – 146	Coimbatore
UMI 577	M-13	Coimbatore
UMI 615	(Sakthi x CM – 202) x C. Rattan x CM .111	Coimbatore
UMI 677	UMI – 165 x UMI –150	Coimbatore
UMI 694	Not known	Kanpur
UMI 696	Not known	Kanpur
UMI 720	7292 /2 (W)	DMR, Delhi
UMI 752	EH – 4003	DMR, Delhi
UMI 757	UMC –5	Coimbatore
UMI 761	Deccan 103	Hyderabad
UMI 763	Not known	Bihar
UMI 773	Euchan No. 5	South Korea
UMI 803	Bs 11 (FR) C6	DMR, Delhi
UMI 842	8824 ME x 2451	DMR, Delhi
UMI 852	RICA 8926 Mex x 2474	DMR, Delhi
UMI 886	Not known	DMR, Delhi
UMI 926	Not known	DMR, Delhi
UMI 946	Hyd 92 R / 1040	Hyderabad

Table 2 Summary statistics of the morphological traits.

Character	Mean	Median	Range	SD
Plant height (cm)	93.10	91.27	57.49 - 135.83	19.53
Ear height (cm)	43.22	44.75	24.08 - 64.83	10.52
Leaf number	5.09	5.10	3.88 - 6.33	0.65
Leaf length (cm)	60.68	59.75	36.4 - 85.71	10.80
Leaf width (cm)	6.96	6.95	4.1 - 9.99	1.42
Tassel length (cm)	33.55	32.69	16.67 - 47.33	6.61
Peduncle length (cm)	11.99	10.97	6.7 - 21.17	3.47
Tassel branching space (cm)	9.92	9.60	5.29 - 16.23	2.77
Number of Primary branches	11.68	11.68	2.2 - 20.5	4.02
Number of secondary branches	1.45	1.54	0 - 3.42	0.96
Number of tertiary branches	0.62	0.17	0 - 2.73	0.85
Cob no.	1.36	1.35	0.83 - 2.17	0.37
Days to tasseling	53.62	52.84	44.33 - 62.67	4.71
Days to silking	56.98	56.84	48 - 65.33	4.63
Tassel silking interval (days)	3.39	3.33	1.67 - 5.33	0.93
No. of grain rows	12.48	13.18	6.03 - 15.5	2.03
Grains/ row (no)	10.54	10.50	5.27 - 15.77	2.78
Ear length (cm)	12.09	12.57	7.37 - 15.9	2.07
Ear diameter (cm)	2.90	2.97	1.53 - 4.3	0.61
Cob diameter (cm)	2.37	2.43	1.23 - 3.63	0.51
Rachis diameter (cm)	1.16	1.12	0.63 - 2.27	0.35
Grain length (cm)	0.50	0.51	0.38 - 0.64	0.06
Grain width (cm)	0.53	0.51	0.41 - 1.49	0.17
Grain thickness (cm)	0.35	0.34	0.24 - 0.53	0.06
Seed yield per plant (gm)	25.16	19.29	10.43 - 62.23	12.75

Table 3 Distribution of genotypes in clusters

Cluster No.	No. genotypes	Genotypes
1	14	UMI 433, UMI 470, UMI 926, UMI 492, UMI 456, UMI 551, UMI 696, UMI 694, UMI761, UMI 479, UMI 480, UMI 556, UMI 842, UMI 615
2	13	UMI 483, UMI 532, UMI 524, UMI 886, UMI 577, UMI 540, UMI 763, UMI 752, UMI 561, UMI 757, UMI 510, UMI 679, UMI 946
3	9	UMI 438, UMI 550, UMI 536, UMI 487, UMI 497, UMI 803, UMI 720, UMI 465, UMI 852
4	2	UMI 458, UMI 773



Hiearchical clustering pattern based on twentyfive morphological traits.