Evaluation and Classification of Sugarcane Germplasm using Hierarchical Cluster Analysis

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Hierarchical cluster analysis (UPGMA-method) was carried out for the classification of 50 sugarcane clones based on 14 yield and quality characters, which resulted in the formation of 5 clusters having 2 to 22 clones. Cluster II had the maximum (22) and cluster I had minimum (2) clones. It has classified germplasm accession according to their degree of similarity or dissimilarity. Dendrogram was prepared using rescaled distances.

Key Words: Hierarchical cluster analysis, Germplasm, Sugarcane.

Sugarcane is one of the important crops which produces more than 60 per cent of world sugar. India contributes around 13 per cent of the world and 41 per cent of Asian sugar production. It contributes 2 per cent to national GDP. The other byproducts of sugarcane are jaggery, *khandsari*, ethanol, paper, cattle feed, fuel, etc. For improving complex characters like yield and sugar recovery, choice of the parents is very important and it becomes easier if the germplasm is evaluated and classified properly and systematically on the basis of given set of characters. Cluster analysis is a technique which determines the degree of similarity or dissimilarity in the germplasm and is the best basis to define commonness, thereby eliminating redundancy and characterize the germplasm on the basis of degree of diversity (Peeters and Martinelli. 1989; Brown, 1991; Ordas *et al.*, 1994; Smith *et al.*, 1995). Therefore, the present study was conducted to evaluate, categorize and classify the sugarcane clones on the basis of 14 yield and quality characters.

Materials and Methods

The present study, comprising 50 clones, was conducted at CCS HAU, Regional Research Station, Uchani (Karnal) during 2001-02. Observations were recorded on 14 variables viz., number of millable canes/clump, cane height, cane thickness, number of internodes per cane, internode length, leaf length, leaf breadth, leaf area, single cane weight, cane yield/clump, Brix%, Pol%, Purity% and CCS%.

Data were recorded on five canes each from five randomly selected clumps of each genotype and average was computed. Cluster analysis was carried out on 50 clones and 14 variables using computer programme SPSS.

UPGMA (Unweighted pair-group method using arithmetic averages) with city block distances was used as it is suggested to be the best and most commonly used method (Romesburg, 1984). Dendrogram (Fig 1) was prepared using the rescaled distances. Based on the method suggested by Romesburg (1984) the dendrogram was cut to form the clusters.

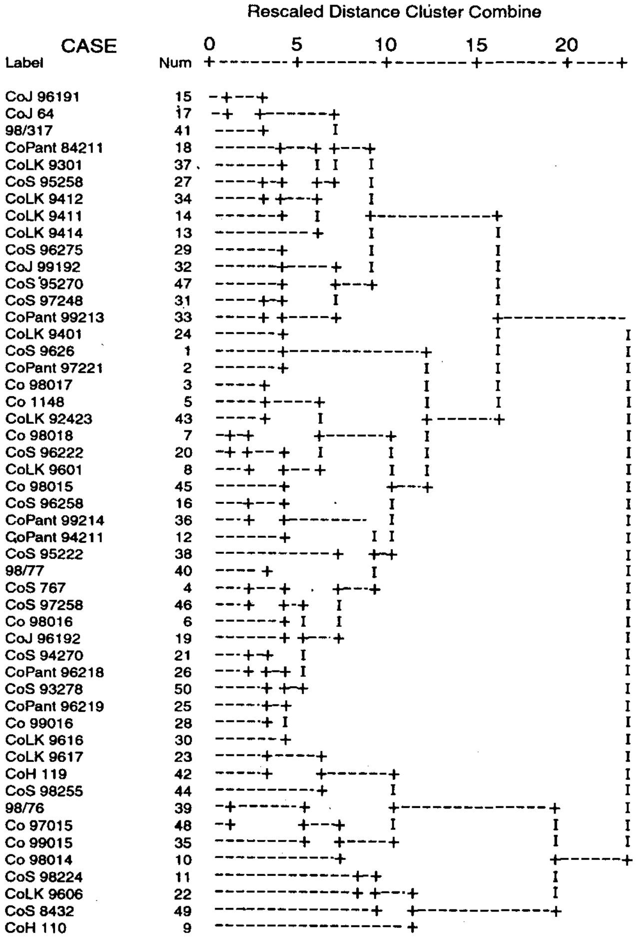

Fig. 1. Dendrogram portraying clustering pattern of different genotypes

Results and Discussion

Hierarchical cluster analysis identified five clusters (Table 1) containing two to twenty-two clones. Cluster II had twenty-two clones, cluster I had only two, cluster III had four, cluster IV had seven and cluster V had fifteen clones. Much information is not available on application of cluster analysis in sugarcane yet some of the workers viz., Nair and Sreenivasan (1992) studied 94 genotypes of sugarcane and grouped them into nine clusters with considerable diversity being observed among the clusters. White (1993) used cluster analysis to assess early line trials of *Saccharum* interspecific hybrids for resistance to sugarcane borer. Chatwachirawong and Srinives (1999) used cluster analysis to determine relationship among 26 clonal cultivars of sugarcane and pedigree of all cultivars was traced back to 11 original ancestors. Pathak *et al.* (2000) studied 22 clones of sugarcane and grouped them into five clusters, Tai and Miller (2002) used cluster analysis to classify the core collection of 75 clones of sugarcane, Cluster II and V had five clones while others had four each.

Mean performance of different clusters calculated for different characters revealed wide variation for the characters under study (Table 2). Cluster I with only two clones was found to be better in number of millable canes, number of internodes, Brix%, Pol%, CCS% and Purity% and poor in cane height, cane thickness, leaf length, leaf breadth and leaf area. Cluster II with 22

Table 1. Cluster membership profile of different genotypes (UPGMA-City block distances)

Cluster No.	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
	CoS 96268	Co 98017	CoH 110	Co 98014	CoLK 9414
	CoPant 97221	CoS 767	CoS 98224	CoLK 9617	CoLK 9411
		Co 1148	CoLK 9606	Co 99015	CoJ 96191
		Co 98016	CoS 8432	98/76	CoJ 64
G		Co98018		CoH 119	CoPant 84211
E		CoLK 9601		CoS 98255	CoLK 9401
N		CoPant 94211		Co 97015	CoS 95258
O		CoS 96258			CoS 96275
T		CoJ 96192			CoS 97248
Y		CoS 96222			CoJ 99192
P		CoS 94270			CoPant 99213
E		CoPant 96219			CoLK 9412
S		CoPant 96218			CoLK 9301
		Co 99016			98/317
		CoLK 9616			CoS 95270
		CoPant 99214			
		CoS 95222			
		98/77			
		CoLK 92423			
		Co 98015			
		CoS 97258			
		CoS 93278			
No. of Genotypes	2	22	4	7	15

Table 2. Cluster mean for different characters in sugarcane (UPGMA-city Block)

Clusters	C1	C2	C3	C4	C5	General Mean
Characters						
No. of millable canes	3.83	3.45	3.27	3.06	3.28	3.34
Cane height (cm)	97.57	177.75	217.00	191.77	153.12	176.13
Cane thickness (cm)	1.90	2.18	2.48	2.36	2.03	2.17
No. of internodes	21.80	19.50	22.43	19.76	18.39	19.53
Inetrnode length (cm)	10.20	10.66	10.65	11.37	9.85	10.5
Leaf length (cm)	91.85	118.98	129.63	119.24	111.64	116.58
Leaf breadth (cm)	2.70	3.40	3.73	3.21	3.07	3.27
Leaf area (cm^2)	167.67	287.23	342.49	272.18	244.25	271.87
Single cane weight (g)	764.15	763.64	1326.18	1027.83	506.55	768.52
Yield/clump (kg)	2.45	2,60	3.40	3.04	1.97	2.53
Brix%	18.80	18.65	18.72	17.94	19.29	18.75
Pol%	36.33	35.55	35.75	34.48	36.91	35.85
CCS%	11.85	11.50	11.68	11.50	11.96	11.67
Purity%	91.97	90.77	91.59	91.98	91.17	91.17

Table 3. Inter and Intra (in bold)-cluster distances (UPGMA-City Block distances)

Clusters	C1	C2	C3	C4	C5
C1	**110.00**	301.90	884.50	474.73	439.36
C2		**204.33**	737.97	404.12	397.11
C3			**247.03**	493.02	1067.48
C4				**202.95**	681.35
C5					194.65

clones was found to be good for number of millable canes and leaf characters and medium in yield and quality characters. Cluster III with 4 clones was better in yielding attributes and moderate in quality characters. Cluster IV having 7 clones was better in Purity% and yield characters but poor in number of millable canes, Brix% and Pol%. Cluster V having 15 clones was better in quality characters but poor in cane yield.

The maximum inter-cluster distances was observed between cluster V and Cluster III followed by cluster III and cluster I. Minimum inter-cluster distances was observed between cluster II and cluster I followed by cluster V and cluster II (Table 3). Maximum intra-cluster distances was observed in cluster III followed by cluster II and minimum intra-cluster distances in cluster I. Cluster V had better quality attributes and cluster III had better yield attributes. The hybridization aiming diverse clones viz., clones from cluster V and III and cluster III and I are likely to produce heterotic hybrids and desirable transgressive segregants for better quality as well as yield traits in further generations. Clones with better mean values can be selected among all the clusters depending upon the objective of breeding programme. Romesburg (1984) observed that findings of similar alternatives reduce the decision problem to two stages i.e., first, to select the cluster that can best achieve the planning objectives and second to select the best alternative within the best cluster.

The association among the different clones is presented in the form of dendrogram (Fig. 1) prepared using rescaled distances. The clones lying nearer to each other in the dendrogram are similar to one another than those lying apart. The resemblance coefficient between two clones is the value at which their branches join. The dendrogram also showed the relative magnitude of resemblance among the different clusters.

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