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NATURE AND PATTERN OF GENETIC DIVERGENCE OF SUGAR YIELD AND ITS COMPONENTS IN THE PROGENIES OF *SACCHARUM BARBERI*

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ABSTRACT

Thirty hybrid clones involving *Saccharum barberi* (B), *S. officinarum* (O) and Co hybrids (H) were evaluated alongwith their seven parents to study the nature and pattern of genetic divergence. Data on eleven characters of sugar yield were recorded and subjected to multivariate D^2 analysis. The clones were grouped in 15 clusters. The clustering pattern showed that grouping of progeny clones was independent of parent cross combinations, i.e. progenies of a cross and their parents were grouped in different clusters. Hybridization among clones from diverse clusters may help in isolating progenies with higher sugar yield and its traits.

Key words: *Saccharum barberi, S. officianarum*, genetic divergence, multivariate analysis, sugar yield.

The selection of diverse parents belonging to distant groups leads to a wide spectrum of gene combinations for the quantitative inherited traits. The multivariate analysis with D^2 technique measures the amount of genetic diversity in a given population in respect of the several characters considered together. In sugarcane, genetic divergence has been studied in pure species and hybrid clones, viz. foreign hybrids [1], Indian hybrids [2], *S. barberi/sinense* [3], *S. officinarum* [4] and *S. robustum* [5]. The intermating of unlikes leads to greater opportunity for crossing over which releases latent variation by breaking up the predominantly repulsion phase linkages [6]. The present study aims at understanding the nature and pattern of genetic divergence among early interspecific hybrid progenies and their parents involving clones of *S. barberi/sinense* and *S. officinarum*.

MATERIALS AND METHODS

Clones of *S. barberi/sinense* (B) were crossed with *S. officinarum* (O) to produce first nobilization stage hybrids (OB). These clones (taken at random) were crossed with Co hybrids to produce second stage hybrids (OBH). Thirty OBH hybrids from

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*Present address : Sugarcane Breeding Institute, Regional Centre, Post Box No. 52, Karnal 132 001 five crosses (six progenies of each cross) (Table 1) were evaluated alongwith their parents in a randomised block design with two replications at Sugarcane Breeding Institute, Coimbatore. The clones were planted in a row of 3m length spaced 90cm apart. Twelve three-budded setts were planted in each row at equal distance. HR brix was recorded at 300 days crop age and the trial was harvested at 360 days crop age. Data on eleven characters of sugar yield were recorded and subjected to Mahalanobis D^2 analysis. The clones were grouped in various clusters by Tocher's method as explained by Rao [7].

Table 1. Detail of materials studied

S. No.	Cross			Progenies		
1.	Co 7906	×	OB-1254	OBH-01	to	OBH-06
2.	OB-1143	×	Co 775	OBH-09	to	OBH-14
3.	OB-49	×	Co 775	OBH-17	to	OBH-22
4.	Co 7314	×	OB-70	OBH-24	to	OBH-29
5.	CoC 671	×	OB-70	OBH-32	to	OBH-37

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among clones for all characters studied indicating the potentiality of population to isolate parents which may produce better progenies. On the basis of sugar yield and its 10 components 37 clones were classified into 15 clusters (Table 2). The maximum number of clones (8) were included in cluster II, followed by 7 clones each in clusters I and III. Nine clones formed individual clusters. Of these clones, three were OB parents (OB-1143, –49, –70) and six were progenies (OBH-01, 05, 13, 29, 11, 35).

The clustering pattern of progenies was independent of parental cross combinations, i.e. progenies of a cross and their parents were grouped in different clusters. These results are contradictory to the reports of Singh and Gupta [8] and Anand and Murty [9] who reported the influence of parents on clustering pattern in cotton and linseed, respectively. This deviation in results might be due to wide genetic deviations between the two categories of parents, i.e. highly selected Co hybrids and early stage interspecific hybrids (OB). This is supported by the fact that none of the OB parents, except OB-1254, grouped with other Co hybrids as well as progenies. Grouping pattern of progenies and spatial relation between the clusters were also not in accordance with their pedigrees. The estimates of inter-cluster distance between two clusters including progenies of the same pedigree may be greater than those between clusters comprising progenies derived from two distinct

Table 2. Distribution of parents and their progenies in different clusters on the basis of sugar yield and its traits

Cluster	No. of clones	Parents	Progenies
I	7	OB-1254,Co 7314	(OBH-02, –06), OBH-09, (OBH-17, –20)
II	8	-	OBH-04, –12, –19, (–24, –26, –28), (–34, –37)
III	7	Co 7906,Co 775	OBH-10, (OBH-21, -22), (OBH-32, –36)
IV	3	-	OBH-03, (OBH-25, -27)
V	2	-	OBH-14, -18
VI	2	Coc 671	OBH-33
VII	1	-	OBH-01
VIII	1	-	OBH-05
IX	1	-	OBH-13
X	1	OB-1143	-
XI	1	OB-49	-
XII	1	-	OBH-29
XIII	1	OB-70	-
XIV	1	-	OBH-11
XV	1	-	OBH-35

Clones in parenthesis indicate to have originated from a cross.

parentages. This suggests that forces other than the divergence of the parents have operated in the differentiation of these progenies (Table 3). The directional selection force applied during the evolution of these hybrids is expected to result in almost parallel and similar divergence within and between clusters [8].

Cluster means (Table 4) indicated that cluster XII was the best for sugar yield followed by clusters IX, VI, II, IV, VII and XIII and all these clusters were superior to general mean of the population. The stalk yield of cluster IX was the best followed by clusters XII, XIII, II and VII. Their mean stalk yields were much higher than population mean. Of these clusters IX and XIII were very poor in quality traits. The clone OBH-29 (cluster XII) was better in both stalk yield and juice quality which resulted in highest expected sugar yield. The cluster VI (CoC 671 and OBH- 33) was the best in juice quality traits followed by clusters XII (OBH-29), IV (OBH-03, –25, –27) and XV (OBH-35) and their mean performance were better than the population mean. Cluster VII for number of millable stalks (NMS), cluster VI for single stalk weight (SSW), cluster XIII for stalk length and stalk diameter were the best.

Intracluster distance (D) varied from 0.00 to 6.05, cluster IV being the most diverse (Table 3). Intercluster distance varied from 6.36 (clusters I and II) to 36.84 (clusters VII and XIV). Clusters I, II, III, and IV were quite close to each other.

Table 3. Average intra- (in bold) and intercluster distance (D) values on the basis of sugar yield and its components in sugarcane

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV
I	**4.80**	6.36	6.98	7.57	7.11	10.31	9.85	14.95	8.54	12.50	6.44	12.86	14.29	27.00	16.20
II		**5.13**	6.40	6.87	8.72	7.54	10.81	16.96	8.35	13.13	6.81	13.07	12.09	27.13	16.10
III			**5.75**	9.18	9.14	7.61	13.48	15.80	10.79	12.87	7.89	11.58	14.71	28.63	17.55
IV				**6.05**	10.43	9.86	9.19	19.25	8.29	15.25	7.74	14.79	10.79	25.67	14.64
V					**5.52**	12.76	11.79	11.37	9.21	8.39	9.22	15.23	15.50	28.91	18.91
VI						**5.72**	14.78	19.65	12.77	15.89	10.13	14.76	13.73	29.01	17.50
VII							**0.00**	20.97	9.10	16.71	8.87	20.66	13.14	23.35	13.29
VIII								**0.00**	19.63	9.29	17.72	17.94	24.75	36.84	27.58
IX									**0.00**	15.36	8.14	16.15	10.90	23.37	14.21
X										**0.00**	13.80	18.51	18.54	32.80	23.25
XI											**0.00**	14.82	10.81	23.98	14.60
XII												**0.00**	20.49	32.65	23.27
XIII													**0.00**	25.40	16.90
XIV														**0.00**	12.51
XV															**0.00**

Table 4. Cluster means (M) and range (R) values for sugar yield and its traits in sugarcane

Cluster		Sugar yield per plot (kg)	St. yield per plot (kg)	CCS % (12m)	Sucrose % (12m)	Brix % (12m)	Purity % (12m)	HR brix (10m)	NMS/ plot	SSW (kg)	Stalk length (cm)	St. diam. (cm)
I	M	2.21	19.51	11.22	16.41	19.03	86.20	18.11	33.3	0.60	172.1	2.15
	R	1.61-3.26	14.05-26.85	10.52-12.10	15.27-17.70	17.41-20.51	83.78-88.20	13.2-20.6	29-38	0.40-0.92	130-200	1.90- 2.40
II	M	3.52	29.43	11.92	17.32	19.83	87.21	19.40	31.3	0.98	203.4	2.49
	R	2.02-4.22	18.05-36.90	10.84-13.20	16.07-18.99	18.80-21.29	82.52-90.95	18.2-21.0	24-44	0.62-1.30	163-230	2.15- 2.70
III	M	2.62	22.35	11.67	17.07	19.87	86.12	18.96	23.6	0.95	175.1	2.61
	R	1.72-4.24	13.90-31.85	8.90013.31	13.20-19.32	15.91-22.11	81.71-89.77	16.6-21.2	13-29	0.68-1.18	148-215	2.15- 2.85
IV	M	3.4	27.75	12.51	18.64	22.37	83.29	20.27	38.3	0.71	217.7	2.22
	R	2.60-4.93	18.95-39.15	10.98-13.72	17.02-19.94	21.95-22.73	77.67-87.65	19.2-22.1	27-51	0.68-0.76	213-225	2.15- 2.30
V	M	1.66	21.20	7.92	12.39	16.26	76.05	15.65	32.0	0.68	169.0	2.20
	R	1.63-1.68	19.05-23.35	7.03-8.80	11.10-13.68	14.79-17.73	74.54-77.15	14.0-17.3	30-34	0.66-0.70	163-175	2.10-2.30
VI	M	3.53	25.68	13.94	20.03	22.36	89.59	20.35	19.0	1.37	225.0	2.73
	R	3.18-3.88	21.05-30.30	12.72-15.09	18.75-21.31	21.82-22.89	86.16-93.02	19.7-21.0	17-21	1.26-1.48	220-230	2.65- 2.80
VII*		3.38	29.25	11.56	16.84	19.36	86.94	18.50	61.0	0.48	170.0	2.00
VIII		0.42	5.90	7.01	11.31	15.57	72.71	12.09	16.5	0.36	148.0	1.70
IX		3.61	39.80	8.95	13.62	16.43	81.88	16.60	41.5	0.94	197.5	2.45
X		0.73	12.20	5.97	10.22	15.32	66.73	16.13	23.5	0.61	153.5	2.75
XI		2.53	23.85	10.63	15.56	18.05	86.18	15.98	37.5	0.74	167.5	2.95
XII		4.11	32.40	12.74	18.56	21.34	87.04	20.09	16.5	0.72	180.0	2.35
XIII		3.09	31.25	9.92	14.96	18.37	81.43	17.72	33.0	1.06	267.0	3.75
XIV		2.45	26.50	9.25	16.39	18.61	88.20	13.53	39.0	0.68	158.0	2.40
XV		2.53	20.85	12.19	19.32	22.06	87.60	18.42	37.0	0.74	165.0	2.20
Population		2.75	24.34	11.17	16.57	19.46	84.84	18.36	30.5	0.84	189.0	2.22

*Clusters VII to XV have single clone.

Whereas clusters XIV (OBH-11) from all clusters except cluster XV; VII (OBH-01) from VIII (OBH-05) and XII (OBH-29); VIII '(OBH- 05) from XIII (OB-70) and XV (OBH-35); X (OB-1143) from XV (OBH- 35); XII (OBH-29) from XIII (OB-70) and XV (OBH–35) were widely placed and hybridization among clones from these cluster combinations will yield the maximum variability for sugar yield and its components.

Direct relationship between progeny mean and number of superior clones to the best check has been reported by Bakshi Ram *et al.* [10]. Therefore, the mean of progenies is very important in deciding which of the crosses should be repeated or not in order to get better recombinants. The mean sugar yields of diverse cluster combinations, indicated that means of cluster combinations XIV and I, III, V, VIII, X, XI, XV; VIII and VII, XIII, XV; and X and XV were lower than population mean. Hence the hybridization among clones from these cluster combinations might result in enhancement in variability towards negative side. Hybridization among the clones from these clusters may not improve the population mean but the variance and the range of the frequency distribution are expected to increase [11] due to crossing over which releases latent variation by breaking up the predominantly repulsion phase linkages [6]. Whereas mean of cluster combination VII (OBH-01) and XII (OBH-29) was the maximum (3.75 kg) followed by cluster combinations XII (OBH-29) and XIII (3.60 kg), XV (3.32 kg), XIV (3.28 kg); XIV (OBH-11) and IX (3.03 kg), II (2.99 kg), VI (2.99), IV (2.94 kg) and VII (2.92 kg) and were better than the population mean (2.75 kg). Therefore, hybridization among clones of these cluster combinations is expected to enhance variability in the progeny populations with better means. Utilization of clones in breeding from different clusters with the maximum diversity among themselves had been suggested by many workers in sugarcane [1-5 and 12]. This will provide an opportunity to select better recombinations for various characters and utilization of such improved clones of these early interspecific hybrids in breeding would be appropriate in achieving better and quicker gains.

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