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GENETIC DIVERGENCE IN INTERSPECIFIC HYBRIDS OF SUGARCANE

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Forty six interspecific hybrids of sugarcane derived from crosses involving various species were evaluated and grouped into eleven clusters, indicating high genetic diversity among them. Though there was no clear cut differentiation between clusters with reference to species, to some extent, dispersion of hybrids in various clusters was in accordance with their species origin. Based on inter-cluster distances and cluster means for various characters, potential parents were identified from different clusters for hybridization programme.

Breeders have constantly sought to increase the selection gains for various characters through the introduction of new genes from available germplasm. Successful exploitation of the sugarcane genetic resources in the future will require careful evaluation of interspecific hybrid (ISH) clones with reference to genetic diversity. Stevenson (1965) opined that when the nobilization from recent collections of wild forms came into general use as breeding material, seedling populations of almost unbelievable genetic complexity will be common representing a veritable treasure house of *Saccharum* forms and offering interesting possibilities of recombination. He further stated that utilization of wide range of parental material in crossing programmes leads to heterotic segregants in progenies which in turn stand as successful commercial varieties whose value depends upon balance of genes instead of getting varieties through chance. Present investigation was to test such a group of interspecific hybrids for their divergence, in order to incorporate diverse material in sugarcane breeding programmes.

MATERIALS AND METHODS

Forty six clones derived from complex crosses utilizing various *Saccharum* spp. (Table 1) were grown in randomized block design

Table 1 : Details of experimental materials

Clone	Parentage		
I. S. officinarum × S. barberi (OB)			
ISH 236	Gungera	×	Khakai
ISH 237	Gungera	×	Khakai
ISH 239	Gungera	×	Khakai
ISH 241	Gungera	×	Khakai
ISH 245	Gungera	×	Khakai
ISH 247	Keong	×	Khakai
ISH 249	Keong	×	Khakai
ISH 250	Gungera	×	Khakai
ISH 258	Keong	×	Khakai
ISH 260	Keong	×	Khakai
ISH 261	Keong	×	Khakai
ISH 264	Keong	×	Khakai
ISH 265	Keong	×	Khakai
ISH 268	Keong	×	Khakai
ISH 269	Keong	×	Khakai
ISH 270	Keong	×	Khakai
II. S. officinarum × S. robustum (OR)			
ISH 273	51 NG 131 Str.	×	57 NG 133
ISH 274	51 NG 131 Str.	×	57 NG 133
ISH 275	51 NG 134	×	NG 77-34
ISH 278	NG 77-65	×	NG 77-221
ISH 280	51 NG 131 Str.	×	57 NG 133
III. S. officinarum × Commercial Hybrid (OH)			
ISH 18	Keong	×	MS 68/47
ISH 229	57 NG 222	×	Co 62174
IV. S. officinarum × S. spontaneum (OS)			
ISH 284	Green German	×	51 NG 2
ISH 288	Orambo	×	SES 275
ISH 289	NG 77-63	×	Holes I
V. S. barberi × Commercial Hybrid (BH)			
ISH 155	Pansahi	×	Co 1307
ISH 172	Ubawhite	×	Co 775
ISH 292	Kansar	×	MS 68/47
ISH 297	Pathri (Self 3)	×	Co 62174
VI. Commercial Hybrid × S. barberi (HB)			
ISH 126	Q 68	×	Khakai

VII. Commercial Hybrid × *S. spontaneum* (HS)				
ISH 128	Co 62174	×	IMP 1532	
ISH 307	Co 62174	×	51 NG 2	
VIII. Commercial Hybrid × *S. robustum* (HR)				
ISH 282	Q 68	×	28 NG 289	
IX. Hybrids from complex Crosses				
ISH 1	CoC 671 × (57 NG 110 × NG 77-28)			H/OR
ISH 4	(Saipan G × Co 62174) × (51 NG 77 × 57 NG 45)			OH/OR
ISH 5	(Q 68 × Khakai) × (51 NG 199 × NG 77-55)			HB/OR
ISH 9	Co 7229 × (Mont 1585 × NG 77-28)			H/OR
ISH 10	(Q 68 × Khakai) × (Q 68 × 28 NG 289)			HB/HR
ISH 19	Co 7201 × (CP 61-39 × NG 77-170)			H/HR
ISH 20	Co 7201 × [Coc 671 × (57 NG 110 × NG 77-28)]			H/H/OR
ISH 23	Co 419 × [CoC 671 × (57 NG 110 × NG 77-28)]			H/H/OR
ISH 24	Co 7201 × (CP 61-39 × NG 77-170)			H/HR
ISH 25	Co 7201 × (CP 61-39 × NG 77-170)			H/HR
ISH 58	Co 7201 × [CoC 671 × (57 NG 110 × NG 77-28)]			H/H/OR
ISH 59	Co 7201 × [CoC 671 × (57 NG 110 × NG 77-28)]			H/H/OR

with three replications at Sugarcane Breeding Institute, Research Centre, Jamkhandi in 1990-91. Each clone was grown in a 3 row plot; each row was of 6 m length and spaced 90 cm apart. Twenty four three-budded setts were planted in a row at equal distance. The trial was harvested after 360 days and the data on 12 quantitative characters (Table 4) were recorded by adopting standard procedures.

The data were subjected to analysis of variance as well as D^2 analysis as suggested by Mahalanobis (1936). Test of significance of difference with regard to the pooled effect of all the characters was carried out by using Wilk's lambda criterion (Wilks, 1932).

RESULTS AND DISCUSSION

The dispersion between the variables was highly significant as tested by Wilk's criterion (χ^2_{540} = 881.05). The D^2 values for different pairs of genotypes ranged from 1.53 to 562.68. All the 46 genotypes were grouped into 11 clusters (Table 2). Though there was no clear cut differentiation between clusters with reference to species, all complex hybrids (H/OR,OH/OR,HB/OR, HB/HR, H/HR, H/H/OR) were distributed in few clusters viz., I, II, V and VII. Clones from OB group predominantly were distributed in clusters III, V and VI. Likewise, Gupta and Singh (1970) showed that the parentage had definite effect on clustering pattern.

Table 2 : Cluster means for various characters

Sl.No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
1. NMC/plot	34.73	39.50	50.62	68.13	33.53	42.06	56.67	40.67	28.67	36.67	110.67
2. Yield (Kg/plot)	26.89	36.82	32.11	30.83	28.49	30.19	38.27	26.00	37.20	23.23	31.00
3. Brix (%)	18.78	19.26	16.79	17.34	17.70	14.21	18.56	22.88	18.79	13.29	12.49
4. Sucrose (%)	17.05	18.11	14.53	14.26	15.19	11.17	16.09	19.84	16.42	9.40	8.79
5. Purity (%)	90.52	94.02	86.30	82.25	85.66	78.42	92.50	86.81	86.80	70.71	70.31
6. CCS (%)	11.94	12.86	10.02	9.53	10.56	7.26	12.16	13.59	11.29	5.72	5.33
7. CCS (Kg/plot)	3.16	4.76	3.19	2.96	2.88	2.15	4.72	3.50	4.15	1.38	1.65
8. Cane diameter (cm)	2.50	2.63	2.20	1.75	2.48	2.22	2.28	2.13	3.17	2.20	1.57
9. S.C. Wt (Kg)	0.86	0.93	0.65	0.48	0.92	0.78	0.66	0.62	1.37	0.71	0.31
10. Cane length (m)	1.79	1.80	1.88	1.93	1.81	1.95	1.86	1.43	1.83	2.16	2.00
11. Extract (%)	46.92	49.70	46.23	37.56	50.15	45 77	53.90	44.76	51.19	34.69	34.23
12. Internode number	16.39	16.11	18.29	6.33	19.53	19.73	15.33	13.33	19.00	19.00	16.00

TABLE 2

Intra-cluster distances ranged from 3.50 to 7.28 (Table 3). The highest intra cluster distance was recorded for cluster VI followed by cluster VIII and the lowest for clusters I, II, III, IV and V respectively. Since cluster IX, X and XI were having only one clone each, their intra-cluster distances were zero. The inter-cluster distances were higher than intra-cluster distances in all cases. The highest inter-cluster distance was recorded between IX and XI cluster (23.72) and the lowest between I and II (4.22).

Table 3 : Grouping of various clones into different clusters

Cluster	Clones
I.	ISH 9, ISH 59, ISH 4, ISH 265, ISH 245, ISH 128, ISH 289, ISH 24, ISH 172, ISH 19, ISH 126
II.	ISH 229, ISH 20, ISH 25, ISH 58, ISH 1, ISH 18
III.	ISH 269, ISH 275, ISH 250, ISH 237, ISH 239, ISH 307, ISH 264
IV.	ISH 284, ISH 273, ISH 274, ISH 280, ISH 155
V.	ISH 241, ISH 10, ISH 236, ISH 270, ISH 261
VI.	ISH 260, ISH 269, ISH 258, ISH 268, ISH 247
VII.	ISH 292, ISH 23, ISH 5
VIII.	ISH 282
IX.	ISH 297
X.	ISH 278
XI.	ISH 288

Based on inter-cluster distances (D values), the clusters XI, X, IX and VIII were found to be highly divergent from all the clusters. Hence, the types from these clusters when crossed with the types from other clusters may result in high heterosis. Murthy and Anand (1966) claimed that there was a positive relationship between the specific combining ability and the degree of genetic diversity.

Cluster mean of number of millable canes was high for cluster XI followed by cluster IV (Table 4). Cluster mean of cane yield was high for cluster II followed by cluster VII. Sucrose and brix were high for cluster VIII. Such clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various economic characters as also

Table 4 : Inter and intra-cluster genetic distance (D values)

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	3.50	4.22	5.84	9.46	8.16	7.72	5.81	6.20	6.81	11.33	19.38
II		3.89	7.08	10.97	5.37	8.66	6.28	6.71	6.11	12.16	20.75
III			3.86	6.88	12.25	6.49	5.92	9.12	10.40	10.46	16.28
IV				3.90	9.56	9.08	8.39	11.48	14.71	11.68	12.65
V					4.25	6.97	6.44	7.72	7.00	11.25	19.46
VI						7.28	8.71	10.81	10.77	7.58	16.53
VII							5.95	7.82	10.03	12.18	18.35
VIII								6.68	8.61	13.28	20.83
IX									0.00	13.51	23.72
X										0.00	15.62
XI											0.00

reported by Endany *et al.*, (1977). As series of polycrosses based on high mean values may prove to be highly fruitful.

Hybridization programme which includes complex hybrids from cluster II, F_1s of commercial hybrid x *S. robustum* from cluster VIII and F_1s of *S. officinarum* x *S. spontaneum* from cluster XI are expected to produce superior and diverse segregants.

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