

RESEARCH ARTICLE

DEVELOPMENT AND EVALUATION OF BACKCROSS PROGENIES OF IMPROVED *SACCHARUM* SPP. FOR YIELD AND QUALITY TRAITS

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Abstract

Forty one improved *Saccharum officinarum*, 29 improved *S. spontaneum*, 27 improved *S. robustum* and 37 commercial hybrid clones were utilized in this genetic base broadening programme. PIO 88-100, PIO 90-202, PIO 00845, PIO 88-100, PIO 88-110, PIR 88-3350, PIR 88-327, PIR 96-258 and PIR 96-285 were good combiners for quality and yield traits. The programme created abundant genetic variability with genetic improvement for quality and yield parameters in the nobilized populations and the derivatives showed significant differences for cane yield and quality traits. Frequency distributions for yield and quality characters tended towards normality. The correlations among the characters indicated that there was a possibility of introgressing desirable characters from the improved germplasm. Backcross progenies exhibited higher values for most of the yield-related traits analyzed in comparison with the improved parents. In the improved *S. officinarum* x improved *S. spontaneum* group, even though there was an increase in number of millable canes, cane weight also increased considerably in first generation (31.5%). This resulted in higher cane yield which ranged from 52.4 t/ha to 101.25 t/ha in the population. About 12% of the BC₁ families exhibited 23.5% higher cane yield. In the improved *S. officinarum* x improved *S. robustum* group, first stage nobilized hybrids showed an improvement of 12.25 % and 8.50% for sucrose % at 300 and 360 days over the improved *S. robustum* parents. BC₁ showed improvement for both yield and quality parameters with an improvement of 21.91% and 14.79 % for sucrose % at 300 and 360 days respectively. The study also suggested further back crossing (BC₂, BC₃ and BC₄) with commercial hybrids in this group to generate new gene pool for future breeding.

Key words: *Saccharum* spp., base broadening, back cross, gene pool

Introduction

The present day sugarcane cultivars are interspecific derivatives of two important *Saccharum* species, namely *S. officinarum* and *S. spontaneum* in the early 1900s (Price, 1967) and breeders were contented with crosses among these interspecific derivatives. Sugarcane breeding has been a success all over the world by intercrossing the original interspecific hybrids and their derived progenies but very few *Saccharum* species clones have been exploited in the breeding programme. The

exploitation of the unutilized clones of cultivated and wild species of *Saccharum* in breeding program was suggested in the early 1960's by Berding and Roach (1987) who indicated that repeated use of few parents in hybridization has resulted in narrow genetic diversity in modern sugarcane cultivars. This narrow genetic diversity in modern sugarcane varieties has been thought to be the reason for the slow progress in sugarcane breeding (Arceneaux 1965; Roach 1977; D'Hont et al. 1996). To increase this restricted genetic base, introgression of genes

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from wild species is being followed in sugarcane. Incremental efforts for cane yield and ratooning ability have been made by sugarcane breeders over the last 40 years. As hypothesized, due to the narrow genetic base, favourable alleles for high commercial cane sugar in the breeding parent pool have already been fixed in current cultivars. In this regard, concern for the overall reduction of the gene pool available for sugarcane improvement has been recognized. Introgression of new germplasm is important to improve the commercial breeding populations. In recent years, the importance of genetic base broadening by exploring unutilized clones of wild *Saccharum species* in the germplasm introgression programs has been strengthened across the globe, considering the increase in sugarcane area under adverse environments, climate change issues and multiple uses of sugarcane besides conventional sugar production. Efforts being made elsewhere to broaden the genetic base of cultivated sugarcane through wide crosses with *S. spontaneum* and other related species have been a success. Broadening the genetic base and identifying introgressed genes in commercial back ground are some of the objectives the USDA works with. Efforts to broaden the genetic base and introduce novel genes to cultivated sugarcane varieties utilizing *S. spontaneum* have been strengthened (Milligan et al. 1994; Kennedy 2001; Zhou et al. 2013). The genetic base broadening programme of West Indies is a success and through the incorporation of wild germplasm, clones with diverse genetic background were identified as promising parents or commercial varieties. In Sugarcane Breeding Institute, Coimbatore, India, an intra-population improvement programme involving wild species of *Saccharum*

was formulated and a large number of hybrid derivatives with improved quality and yield traits were developed for further introgression and utilization (Anonymous 2000, 2003). A programme to broaden the base and tap genes that exist in the wild species by introgression of these improved clones of *S. officinarum*, *S. spontaneum* and *S. robustum*, and commercials was undertaken and the programme repeats the nobilization stage as backcross and introgression on a wider genetic base which will be useful for genetic improvement in breeding programmes. The objectives of this research were to broaden the genetic base of improved parental germplasm through backcross breeding, develop and identify advanced superior back cross families for development of commercial clones with better adaptability to the prevailing changing climatic scenario and identification of prebreeding stocks for yield, quality, ratooning ability, biomass yield, fibre % and resistance to diseases like red rot.

Materials and methods

Development of breeding material

Improved *S. officinarum* and *S. robustum* clones developed through intra-population strategy were selected based on the sucrose content, morphological stand, flowering synchrony and pollen fertility and used as parents in this investigation (Table 1). The breeding stock on which this study was based has been derived from several nobilized populations of improved *S. officinarum* x improved *S. spontaneum* hybrids. Hybridization was initiated in 1994 and first batch of seedlings was evaluated in 1995. Five hundred and eighty six crosses were effected from 1995-2007 and 45,000 seedlings were

Table 1. Breeding material utilized in introgression studies

Improved <i>S. officinarum</i>				
PIO 88-81	PIO 88-96	PIO 88-101	PIO 88-100	PIO 88-110
PIO 88-1703	PIO 88-1704	PIO 88-1715	PIO 88-1809	PIO 88-1819
PIO 90-64	PIO 90-102	PIO 90-104	PIO 90-162	PIO 90-188
PIO 90-202	PIO 90-227	PIO 91-178	PIO 91-190	PIO 91-272
PIO 91-488	PIO 91-500	PIO 91-630	PIO 91- 651	PIO 91-740
PIO 91-829	PIO 93-65	PIO 93-144	PIO 94-214	PIO 94-232
PIO 94-271	PIO 94-352	PIO 2000-1058	PIO 2000-548	PIO 2000-845
PIO 2000-851	PIO 2000-891	PIO 2000-847	PIO 2000-875	
Improved <i>S. robustum</i>				
PIR 88-86	PIR 00-1122	PIR 88-400	PIR 88-2307	PIR 88-3350
PIR 88-4025	PIR 89-2	PIR 89-327	PIR 89-96	PIR 90-326
PIR 93-319	PIR 93-336	PIR 93-343	PIR 93-344	PIR 94-258
PIR 96-258	PIR 96-285	PIR 96-325	PIR 96-326	PIR 96-475
PIR 96-788	PIR 00-1002	PIR 00-1054	PIR 00-1124	PIR 00-1174
Improved <i>S. spontaneum</i>				
IND 82-319	IS 76-173	PIS 93-54	PIS 15	PIS 38
PIS 44	PIS 90	PIS 91-472	PIS 92-201	PIS 92-240
PIS 92-4	PIS 92-7	PIS 93-18	PIS 93-190	PIS 93-24
PIS 93-315	PIS 93-32	PIS 93-380	PIS 93-397	PIS 93-434
PIS 93-467	PIS 93-587	PIS 93-8	SES 90	
Commercials				
Co 62387	Co 7201	Co 775	Co 8347	Co 86010
Co 86249	Co 87002	Co 88028	Co 90019	Co 91004
Co 92013	Co 93009	Co 95021	Co 98003	Co 98007
Co 86011	CoT 8201	ISH 100	NS 450	

raised. Clonal evaluations were conducted in the experimental fields of Sugarcane Breeding Institute, Coimbatore. The F_1 progenies were back crossed

with the recurrent female parent. Fifty seven BC_1 lines were nobilized further with either one of the parents to develop BC_2 families.

Seedling evaluation was conducted with a spacing of 90 cm between seedlings and row-to-row spacing of 90 cm. At 10 and 12 months age, data on number of millable canes, cane diameter, cane length, single cane weight and H.R. brix were recorded. H.R brix was recorded from a composite sample of three canes at random in each seedling. The selected clones were evaluated in RBD with two replications. Normal package of practices were followed. Yield and quality traits were recorded for all the progenies and mean values of the traits in a family were computed. Plot yield was expressed in kg.

The back cross families and parents were evaluated for number of millable canes, cane yield, single cane weight, cane diameter, cane length, Brix %, sucrose% and CCS%. Analysis of variance was performed on yield and yield-related traits using the standard RBD analysis procedure. Descriptive statistics were calculated using means for each type (parental or progeny) and family separately. Normal distributions and histograms of various traits were determined using Minitab programme. Broad-sense heritability was estimated as the ratio of the estimate of the genetic variance to the phenotypic variance of a family mean. Coefficient of variation and standard deviation for each cross combination and each generation were calculated for all the economic traits.

Results and Discussion

Improved *S. officinarum* x improved *S. spontaneum* group

The analysis of F₁ and back cross families showed significant differences among the genotypes and families and between families for yield and yield-

related traits studied. Histograms showing frequency distribution of various agronomic traits in the F₁ hybrids showed continuous distribution for the traits studied and skewness ranged from -0.40 to 0.79. BC₁ families demonstrated near normal distribution and skewness ranged from -0.48 to 0.79. BC₂ families had normal distribution for all traits with skewness range of -1.03 to 0.73. For most of the crosses frequency distribution for quality characters tended towards normality. Tai et al. (1992) observed that distribution of brix %, sucrose and juice purity were continuous in commercial x *S. spontaneum* crosses. Regression of cane yield on cane length, cane diameter and single cane weight resulted in a good model fit (P < 0.002).

Mean values of number of millable canes, brix%, single cane weight and cane thickness were used to screen the first generation and back cross families in comparison with the parents. F₁ families showed mean values ranging from 32.12-91.96 kg cane yield and 5.40-13.38% sucrose. The other yield traits, viz. cane diameter ranged 1.47-2.21 cm and single cane weight ranged 0.27-1.01 kg. Number of millable canes was high and ranged 30-180 /row. The family PIO 88-1819 x PIS 44 recorded the maximum cane yield of 91.96 kg (Table 2) and PIO 88-1715 x PIS 93-24, the maximum sucrose of 13.38 %. In the BC₁ generation, 25 superior families (9.81%) were identified as best and the short listed families showed cane yield of 66.84-83.95 kg, sucrose of 17.67-21.40% and number of millable canes of 47.50-88.36. In BC₂ generation, there was an increase for quality and yield traits. Best families recorded cane yield in the range of 60-80 kg/row. Wide variability coupled with high heritability and genetic advance (GA) for two important yield

Table 2. Mean values of agronomic and quality traits in selected families

Improved <i>S. officinarum</i> and improved <i>S. spontaneum</i>								
Cross	Brix	Sucrose (%)	CCS (%)	NMC row	Cane ht (cm)	Cane dia (cm)	SCW (kg)	Yield / row (kg)
F₁ families								
PIO 88-96 x PIS 54	14.95	11.71	7.60	79.12	250	1.86	0.89	70.42
PIO 88-100 x 93-8	15.20	12.26	8.09	140.00	234	2.20	0.67	59.63
PIO 88-1115x PIS18	14.75	11.54	7.49	105.16	270	2.08	0.65	68.35
PIO 88-1819 x PIS44	15.15	12.21	8.05	133.28	220	2.00	0.69	91.96
PIO 88-104 x IND 82319	15.45	11.04	6.77	115.26	260	1.90	0.64	73.77
PIO 88-1715 x PIS 93-24	14.60	13.38	9.41	120.53	215	2.21	0.60	72.32
Co 86010 x PIS 38	16.95	11.65	6.96	110.19	220	2.13	0.61	67.22
CoC 671 x PIS 38	14.70	13.83	9.84	98.68	209	2.09	0.65	64.14
SE	0.26	0.29	0.26	09.06	3.39	0.05	0.02	3.43
SD	1.90	2.15	1.83	17.92	24.7	0.37	0.21	25.03
BC₁ families								
Co 8371 x 97-526	22.82	19.87	13.64	81.50	165	2.65	1.03	83.95
Co 86002 x 97-345	24.32	21.40	14.77	78.15	205	2.50	0.92	71.90
Co 86002 x 97-77	21.42	18.21	12.36	85.26	185	2.57	0.92	78.44
Co 86002 x 96-38	20.75	18.42	12.77	88.36	199	2.50	0.90	79.52
Co 86002 x 96-135	21.34	19.19	13.38	74.12	185	2.51	1.02	75.60
Co 7201 x 96-104	20.58	17.67	12.05	78.56	193	2.52	0.90	70.71
Co 88032 x 95-108	20.42	18.22	12.65	71.77	195	2.50	0.93	66.84
SE	0.12	0.15	0.12	0.96	1.9	0.02	0.02	1.24
SD	1.95	2.3	1.88	15.22	310	0.35	0.34	19.56
BC₂ families								
Co 86002 x 20 -930	23.42	20.41	14.02	84.50	200	2.57	0.97	81.97
Co 86002 x 20 -930	22.87	19.72	13.48	72.30	195	2.64	0.90	65.07
Co 86002 x 20-197	20.71	18.91	13.27	82.50	201	2.65	0.91	75.06
SE	0.33	0.37	0.29	3.47	5.89	0.06	0.07	3.84
SD	1.8	2.07	1.61	19.00	32.6	0.34	0.38	21.02

Table 3. Genetic parameters in BC₁ progenies

Characters	h ²	GCV	PCV	GA
Improved <i>S. officinarum</i> x improved <i>S. spontaneum</i>				
NMC/row	0.61	20.12	25.48	32.14
Single cane weight (kg)	0.78	20.84	26.34	0.27
Cane height (cm)	0.25	5.86	12.18	14.01
Cane diameter (cm)	0.70	2.97	3.01	0.50
Brix	0.55	15.02	19.00	3.00
Sucrose (%)	0.52	22.58	30.14	3.55
Cane yield (kg/row)	0.40	19.21	35.11	12.45
Improved <i>S. officinarum</i> x improved <i>S. robustum</i>				
NMC/row	0.64	22.16	28.00	32.14
Single cane weight (kg)	0.80	25.12	26.34	0.41
Cane height (cm)	0.34	7.25	14.15	12.14
Cane diameter (cm)	0.40	8.12	16.68	0.50
Brix	0.65	14.12	15.28	3.21
Sucrose (%)	0.71	18.58	18.96	3.60
Cane yield (kg/row)	0.68	24.35	46.24	26.23

components NMC and single cane weight was observed (Table 3). High heritability coupled with moderate genetic advance was observed for single cane weight and cane diameter. Juice quality parameters particularly sucrose showed heritability upto 55 % indicating that selection will be effective for sucrose % and brix %.

F₁ hybrids showed improved hybrid vigour for cane yield traits viz. stalk number, stalk length and cane thickness. There was a good increase in cane population and cane length and cane diameter showed heterosis over midparent in all the crosses studied. Single cane weight was, in general low, although individual clones exhibited cane weight

around 1.0 kg and did not exceed both the parents. The families exhibited higher cane yield than the better parent indicating their recombination potential and the role of non-additive gene action for the traits.

The selected hybrids, viz. 95-77, 96-77, 97-12, 97-256, 97-130, 97-196, 97-66, 97-170, 97-34, 97-526, 97-72, 97-77, 97-145 and 97-157 showed a significant advantage over the parents for sucrose% and were used extensively and backcrossed with improved *S. officinarum* and commercial clones. Coefficient of variation ranged from 19.06 % (cane height) to 65.17 % (NMC). The hybrids showed a wide range for fibre (12.3 – 20.0%), brix % (12.70 - 21.45%) and sucrose% (10.29 -19.07). The hybrids were tall

and vigorous with remarkable thickness and good ratooning ability. Sucrose % was low as expected and these observations agree with Roach (1969) and Walker (1972) who reported reduced sucrose content in interspecific hybrids of *S. spontaneum*.

Selection in first generation and back-crossing appeared to retain the advantage of the F₁ upto two back crosses. Selection intensities at various clonal evaluations for yield potential and other important agronomic traits in the back cross population have reached the level in competition with commercial clones. Through three generations of nobilization of improved *S. spontaneum* with improved *S. officinarum*, BC₁ and BC₂ hybrids were eligible for breeding purpose. Heritability among the back cross families was from low to high and ranged from 0.25 (cane height) to 0.78 (cane weight) in

BC₁ involving *S. spontaneum*. The back cross population showed substantial improvement for single cane weight and cane diameter with no significant improvement for cane height. In the second back cross population created, coefficient of variation for number of millable canes (11.01%) and cane height (9.84%) was comparatively less than that for quality parameters (Brix %: 21.23% and sucrose % : 18.14%). The study suggested that further backcrossing of BC₂ hybrids with commercial and improved clones will be able to produce more transgressive recombinants with improved quality. Sucrose % showed an overall improvement of 34.39 % and 36.89 % at 300 days and 28.21% and 33.90% at 360 days in BC₁ and BC₂ populations respectively over the improved *S. spontaneum* parents and comparable with *S. officinarum* parents (Table 4).

Table 4. Genetic improvement (%) for yield and quality traits in F₁ and backcross generation (improved *S. officinarum* x improved *S. spontaneum*)

Generation	NMC	SCW (kg)	Cane dia (cm)	Cane ht (cm)	Sucrose (%) 300d	Sucrose (%) 360d
BC ₂	45.30	1.00	2.70	208.00	16.40	18.80
BC ₁	47.10	1.10	2.80	210.10	16.10	18.00
F ₁	88.46	0.98	1.93	227.83	14.88	16.80
% improvement in F ₁ over improved <i>S. spontaneum</i>	13.41	75.00	211.29	42.97	24.21	19.66
% improvement in BC ₁	98.12	-7.30	-2.46	24.07	34.39	28.21
% improvement in BC ₂	90.44	-12.34	-3.86	22.84	36.89	33.90
Improved <i>spontaneum</i> parents	78.00	0.56	0.62	159.35	11.98	14.04
improved <i>officinarum</i> parents	23.77	1.19	2.85	169.33	15.67	17.74

Proportion of red rot and smut resistant types was high in this group and 710 genetic stocks combining red rot resistance, ratooning ability and drought tolerance were identified. Twenty nine clones with 100 t/ha of yield and 20% fibre content of cane were identified as promising selections for further improvement and 34 clones with high fibre and biomass were identified which offer scope for identification of energy canes from this group.

Improved *S. officinarum* x improved *S. robustum*

ANOVA of F_1 and back cross families showed significant differences among the genotypes and families for yield and yield-related traits. Histograms showing frequency distribution of various agronomic traits in the F_1 and backcross families showed continuous distribution for the traits studied and skewness ranged from -0.04 to 1.18. BC_1 families demonstrated almost normal distribution (skewness: -0.48 to 0.79). The genotypic variation coefficient was higher for cane weight (46.81%), cane length (39.96%), cane diameter (40.12%) and Brix % (43.20%). The results indicate that the breeding program for these characters can be continued in this group. The hybrids had moderate cane population with thick canes (2.8 cm) and were moderately vigorous with less flowering. A high degree of variability was observed in F_1 and BC_1 for various qualitative and quantitative traits and the estimates were of high order. GCV in progenies involving improved *S. officinarum* x *S. robustum* was higher for NMC and single cane weight (Table 3) and low for cane length and cane diameter. Single cane weight was in general moderate and individual clones exhibited cane weight around 1.20 kg. The

selected hybrids, viz. 98-3, 98-13, 98-269, 98-270 and 98-77 showed significant advantage over the parents for sucrose% and cane thickness and these were used extensively and backcrossed with improved *S. officinarum* and commercial clones. The hybrids showed a wide range for Brix (14.24 - 23.30%) and sucrose (12.25 – 21.49%). Though the BC_1 families showed an increase for cane yield, the selected families, viz. PIR 89-327 x Co 86011 and PIR 88-3350 x Co 86249 had 25 % higher yield than the parents (Table 5). Most of the back cross families inherited flowering as indicated by Chi square statistics. High heritability values were observed for cane diameter (40.0 %) and HR brix (60.0%). Higher estimates of heritability coupled with higher genetic advance for NMC and moderate sucrose indicated that the heritability is due to additive effects and could be used as indicator for selection for these traits (Table 3). High heritability values were observed for cane yield traits in *S. spontaneum* crosses and moderate to high heritability for cane yield traits in *S. robustum* crosses (Bakshi Ram and Hemaprabha, 1992; Rao and Rao, 1977; Nagarajan et al. 2000). High heritability combined with low genetic advance for single cane weight indicates the non-additive effect. The characters with wider range, viz. number of millable canes, single cane weight, sucrose, brix and cane yield had higher magnitude of GCV and PCV except cane height. Single cane weight, number of millable canes and quality parameters showed high genetic advance indicating the additive gene effect for the trait.

First stage nobilized hybrids showed an improvement of 12.25 % and 8.50% for sucrose % at 300 and 360 days over the improved *S. robustum* parents and comparable with improved *S. officinarum*

Table 5. Mean values of agronomic and quality traits in selected families of improved *S. officinarum* and improved *S. robustum*

Crosses	Brix	Sucrose (%)	CCS (%)	Purity (%)	NMC row	Cane ht (cm)	Cane dia (cm)	SCW (kg)	Yield /row (kg)
F₁ families									
PIR 88-3350 x Co 86249	21.57	18.42	12.53	85.40	100.5	220	2.80	1.18	128.03
Co 7201 x PIR 88-3350	21.25	19.07	13.28	89.74	98.5	185	2.45	1.00	98.50
PIR 88-3350 x Co 89003	20.50	18.17	12.58	88.63	100.4	205	2.56	1.01	101.48
PIR 89-327 x Co 86011	23.30	21.49	14.99	91.55	89.24	207	2.68	1.00	89.24
PIR 93-319 x Co 94012	22.00	19.91	13.92	90.50	102.2	210	2.70	1.12	114.28
SE	0.26	0.29	0.26	1.42	09.06	3.39	0.05	0.02	3.43
SD	1.90	2.15	1.83	10.36	17.92	24.7	0.37	0.21	25.03
BC₁ families									
Co 86249 x 98-268	23.15	21.49	15.21	92.86	78.25	270	2.86	1.63	127.54
98-258 x Co 8353	22.75	20.83	14.64	91.56	63.48	230	2.54	1.56	98.98
98-258 x Co 92008	23.25	20.67	14.34	88.91	65.24	230	2.62	1.63	106.34
98-84 x Co 8353	22.75	20.64	14.45	90.73	68.96	210	2.58	1.01	69.65
CoC 671 x 98-77	22.45	20.45	14.34	91.10	52.93	195	2.72	1.17	61.92
SE	0.23	0.22	0.2	0.42	2.69	5.06	0.05	0.04	3.57
SD	1.44	1.38	1.26	2.63	16.82	31.6	0.32	0.26	22.31

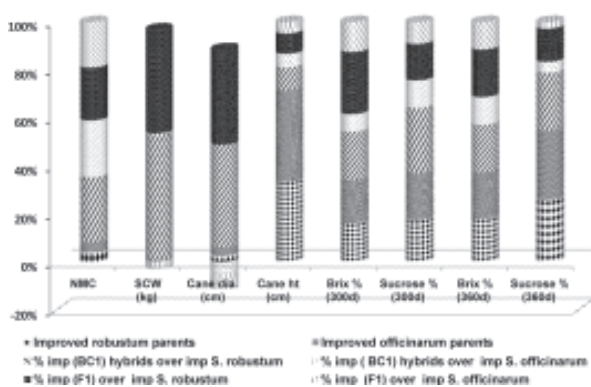


Fig 1. Genetic improvement (%) for yield and quality traits in F₁ and back cross generation (improved *S. officinarum* x improved *S. robustum*)

parents with an improvement of 7.34 % and 1.69% for sucrose % at 300 and 360 days (Fig. 1). Three hybrids, viz. Co 07010, Co 07011 and Co 07017 were identified as commercial types for testing and one clone Co 07032 was identified as biomass type. When these clones were introgressed further with improved parents and commercials, the improvement for quality and yield traits was appreciable.

BC₁ hybrids showed an improvement of 21.91% and 14.79 % for sucrose % at 300 and 360 days respectively. Among the yield related traits, number of millable canes and single cane weight exhibited a

Table 6. Correlation coefficients among various traits in backcross population

Yield	Yield	NMC	SCW	Cane dia
BC₁ (improved <i>S. officinarum</i> x improved <i>S. spontaneum</i> group)				
NMC	0.613			
SCW	0.636	-0.181		
Cane diameter	0.293	-0.263	0.616	
Cane length	0.557	0.111	0.616	0.099
BC₂ (improved <i>S. officinarum</i> x improved <i>S. spontaneum</i> group)				
NMC	0.671			
SCW	0.421	-0.340		
Cane diameter	0.300	-0.257	0.773	
Cane length	0.234	-0.357	0.818	0.502
BC₁ (improved <i>S. officinarum</i> x improved <i>S. robustum</i> group)				
NMC	0.517			
SCW	0.673	-0.254		
Cane diameter	0.223	-0.457	0.651	
Cane length	0.506	0.064	0.529	-0.019

substantial improvement compared to their *S. robustum* parents and showed an improvement of 9.23 % and 2.82% over improved *S. officinarum* parents. BC₁ showed improvement for both yield and quality parameters suggesting further back crossing in this group to impart resistance and drought tolerance. Eight clones, namely 98-3, 98-13, 98-176, 98-200, 98-221, 98-269, 98-270 and 98-272 surpassed the standards for yield and quality and were identified as high quality types.

Correlation between various yield and yield related traits

The correlation between cane yield and the yield component characters was positive and highly

significant. This suggests that selection for these components would be effective in yield improvement. The correlation coefficient results (Table 6) indicated that the cane yield was positively and significantly correlated with cane girth ($r=0.293^*$), cane weight ($r = 0.636^*$), cane length ($r = 0.557^{**}$) and number of millable canes ($r=0.613$). Stalk diameter had the lowest correlation with cane yield than any other attribute in both the populations. Correlation between stalk number and stalk diameter were reported to be negative in the studies of Smith and James (1969) and Kang et al. (1983). Positive correlation among the yield traits, viz. cane weight and number of millable canes not only indicates that increase in yield is attributed to

these component traits to a large extent but also makes selection easier for yield. Similar pattern of correlation of yield and its related traits have been reported by earlier workers (Yahaya et al. 2009). The pol % and CCS % were negatively correlated with cane yield in first back cross population with improved *S. spontaneum* background.

Single cane weight had the highest positive coefficient followed by number of millable canes and cane length. This may imply that these two characters were important in determining cane yield in the back cross populations. In general, the order of importance for components of cane yield was single cane weight, number of millable canes, cane length and stalk diameter. Miller and James (1974) in their studies also indicated that stalk number, stalk diameter and stalk length were important for determining cane yield. In BC₂ population, yield was positively correlated with NMC (0.671**) followed by cane weight and cane diameter. In the hybrid derivatives of improved *S. robustum*, single cane

weight showed positive correlation with yield followed by other traits. This shows that selection in BC₁ for single cane weight provides scope for yield improvement in this group in further backcrossing. The traits that showed high heritability showed statistically significant and strong correlation for yield. Earlier studies by Badaloo and Ramdoyal (2003) indicated that positive correlations among the yield traits in *S. spontaneum* crosses implied the scope to widen the genetic base and that improvement in cane yield can be achieved by indirect selection of number of millable canes, cane weight and cane length.

Selection of promising clones from base broadening programme

The products of base broadening programme have reached several stages of selection in many countries and varieties of commercial use from *S. spontaneum* have been released for cultivation in Barbados (Kennedy 2001). In our broadened genetic

Table 7. Promising families for various traits

S. No.	Trait	Families
1	Brix and sucrose %	PIO 90-202 x PIR 96-404, PIR96-285 x Co 98010 , PIO 00845 x CoA 7602, PIR 96-475 x CoA 7602, PIR 96-285 x CoT 8201, PIR 001002 x Co 94008, PIR 001002 x Co 775, Co 88025 x 97-130, Co 8371 x 97-256, Co 98003 x 96-259, PIO 88-100 x 97-196, Co 86249 x 98-268, 98-221 x 97-34, Co 8371 x 97-526, Co 86002 x 97-72, Co 86002 x 97-77, 98-272 x 97-157 98-176 x 97-157, CoC 671 x 98-77
2	Cane yield and its traits	Co 86002 x 96-38, Co 86002 x 96-195, Co 7201 x 96-104, Co 7201 x 96-195, Co 88028 x 95-104, Co 88032 x 95-108 , Co 86249 x PIR 88-3350
3	Red rot	Co 86002 x 96-38, Co 86002 x 96-195 , Co 7201 x 96-104, Co 7201 x 96-195, Co 88032 x 95-108, ISH 100 x 96 -234, CoC 671 x 97-472

base (BGB) pool, promising clones were selected on the basis of higher mean values for yield and related traits in comparison with the standard Co 86032. One hundred fifty nine clones were superior for cane yield, 101 for quality, 33 for high fibre % and 34 for high biomass. A large number of promising selections for yield, quality and red rot resistance and some specific cross combinations (Table 7) for yield, quality and red rot resistance were identified for further exploitation in breeding programme.

A large number of clones from this programme have been selected for high sucrose, cane yield and resistance to red rot. These clones with diverse genetic background maintain considerable variability for cane yield and other agronomic characters.

In these BGB clones, fibre % upto 27 % was observed and there is potential for utilization of these clones for alternate purpose. At present, 1029 clonal selections with multipurpose utility representing various levels of introgressions of improved *S. officinarum*, improved *S. spontaneum* and improved *S. robustum* are being used in many combinations with commercial parents. The range of variability for quality and fibre characters was high in F_1 of *S. spontaneum* and the potential for high fibre and high biomass production makes these clones useful to produce cane for other than commercial sugar production. BC_1 clones in both the groups outperformed with respect to cane yield, cane thickness and sucrose % in comparison with F_1 .

The study also suggested possibility of further back crossing with commercial hybrids in improved *S. robustum* group (upto BC_4) to identify clones of

commercial importance. Introgression of genes through backcross-breeding enriches the breeding pool with genes for desirable economic characters and resistance to diseases as evidenced from our study and elsewhere in the world and offer an efficient source of genetic diversity. Improved selection methodology assisted by molecular markers will make it more efficient to realize the greater reshuffling of genes created in this new gene base and allows utilization of the developed pre-breeding material by breeders.

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