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Research Article

Pre-breeding in sugarcane (*Saccharum* sp. hybrids) for red rot resistance and economic traits

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Abstract

The present investigation is concerned with the development of genetic stocks for resistance to red rot disease caused by *Colletotrichum falcatum* Went and other important economic traits. This was studied with progenies obtained from 39 crosses involving 45 parental clones of interspecific and intervarietal origin. The progenies were subjected for screening against red rot under controlled condition testing (CCT) method. The pattern of inheritance of red rot resistance showed in general that, crosses involving resistant parents tend to have more number of resistant progenies than from crosses involving susceptible parents. Out of 39 crosses investigated for race specific resistance as a qualitative trait, 18 crosses showed a simple Mendelian segregation of monogenic nature. Parent progeny regression analysis suggested that about 50% of the variation in the population could be attributed to additive genetic variance (horizontal resistance). Two crosses involving susceptible parents *viz*., 971235 (S) x Co 1148 (S) and Co 88028 (S) x Co 775 (S) contributed 28-30% resistant progenies. These transgressive segregants are likely to be stable in their resistance due to additive genetic action and could be used as donor parents in red rot resistance breeding programmes for imparting race non-specific resistance. The present investigation has also identified some specific cross combinations for yield, quality and red rot resistance for further exploitation in breeding programme.

Key words: Pre-breeding, *Saccharum* sp. hybrids, red rot resistance

Introduction

The present day cultivars of sugarcane are the descendants of trispecific hybrids involving *Saccharum officinarum, Saccharum barberi / sinense* and *Saccharum spontaneum* and derive their ability to produce cane and sugar from the first, disease resistance, hardiness and ability to withstand adverse conditions from the third species. *S. barberi / sinense*, being considered to be derivatives of natural hybridization between *S. officinarum* and *S. spontaneum* (Parthasarathy, 1946) might have contributed gene complexes for adaptiveness and sucrose. The genetic variability created through interspecific hybridization and back crossing involving these major species has sustained the sugarcane improvement activities for more than half-a-century. Further improvement within this population essentially depends on the release and the utilization of variability available for stalk yield and quality traits. Proper exploitation of this variability in a crop like sugarcane with a complex ploidy nature and high level of heterozygosity is a complicated process. Breeding for higher yield and quality requires basic information on the extent of genetic variation in a population and its response to selection.The first Indian commercial hybrid cane Co 205 was an interspecific hybrid between *S. officinarum* Vellai and *S. spontaneum* Coimbatore (Barber, 1920). Subsequently *S. barberi*, *S. sinense* and the wild species *S. spontaneum* were utilized, along with *S. officinarum* for evolving commercial hybrids in India (Venkatraman, 1938). After the initial interspecific crosses, sugarcane breeders concentrated their attention on *inter se* crossing of their derivatives. This has resulted in further improvement in yield and

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quality of commercial hybrid cane varieties. The present day varieties have a narrow genetic base with only 11 *S. officinarum* and 2 *S. spontaneum* clones (Natarajan, 1984). Characterization of the parents allows the calculation of genetic distances, which may have predictive value for the offsprings, insofar as dominant gene action plays a major role in controlling the agronomically important traits for exploiting heterosis. Since most of the present day varieties are the product of a few selected original germplasm and further improvement through selection for *per se* performance of a few meiotic recombinant progenies, total genetic recombination present in the modern varieties is limited. Because of the small number of clones / species used in primary crosses, genetic base of modern sugarcane varieties has been reported to be narrow and is thought to be the reason for the present slow progress in sugarcane breeding (Arceneaux 1965 and D'Hont *et al.* 1995). Concern has also been expressed in this regard to the overall reduction of the gene pool available for sugarcane improvement. This necessitates the sugarcane breeders to explore new possibilities to increase genetic variability by identifying and effecting crosses between the diverse parents.

Red rot caused by *Colletotrichum falcatum* went, is the most serious disease of sugar cane in India. It is also the oldest mentioned disease of sugarcane dating back to the times of Buddha. Barber in 1901 made the first recorded report of red rot occurrence in India. Since then a number of red rot epidemics have been reported, especially in eastern Uttar Pradesh, northern Bihar and pockets of Punjab. These epidemics have resulted in the devastation of local varieties and elimination of many early Coimbatore bred varieties including Co 312 and Co 453. In recent times, CoJ 64, which had been the most popular variety because of its highest recovery, was one among the several varieties that succumbed to red rot. The disease essentially confined to northern India and parts of north-western India and Andhra Pradesh for several decades has started spreading to other parts of southern India as well, especially in the east coast zone, taking a heavy toll of many improved varieties, the most notable one being CoC 671. As a consequence breeding for red rot resistance has emerged as an important facet of varietal evolution.

In the present study, crosses have been made using parents from interspecific origin involving diverse forms of *S. officinarum* and *S. spontaneum* that are hitherto unutilized in the sugarcane breeding programme.

Materials and Methods

Experimental materials

The experimental materials consisted of 1950 progenies obtained from 39 biparental crosses involving 11 pollen parents and 34 pistil parents of sugarcane. This present study was conducted at Sugarcane Breeding Institute (ICAR), Coimbatore, India (latitude; 11^{o} North; longitude; 78^{o}.8' East; altitude; 426.72 m MSL) during 2002-2003.

The parental materials include clones released from Sugarcane Breeding Institute, Coimbatore, varieties evolved by state Sugarcane Research Stations and promising clones selected from various research projects of Sugarcane Breeding Institute, Coimbatore. A majority of these clones are derived from interspecific hybridization between S. *officinarum* and *S. spontaneum*. These diverse *S. officinarum* and *S. spontaneum* clones (6 each) are so far unused in sugarcane breeding programmes and thus provide the much needed genetic diversity in the parent materials for sucrose content and red rot resistance. The list of such interspecific parents and the *S. officinarum* and *S. spontaneum* clones involved in their constitution is given in Table 1.

Out of these 39 biparental crosses, 23 crosses involved interspecific derivatives as parents as against 16 crosses which involved only intervarietal derivatives as parents. Thirty six seedlings per replication per cross were planted in a randomized block design @ 12 seedlings per row of 6m length along with the parents. Normal package of practices were adopted with respect to manuring, irrigation, earthing up *etc*.

Biometrical observations

All the progenies along with their corresponding parents were subjected to screening against red rot disease under controlled condition testing (CCT) method as suggested by Mohanraj *et al*. (1994 and 1997) and Viswanathan *et al*. (1998). At the age of tenth month single healthy stalk from each selected progeny was cut at the bottom and brought to the testing chamber. Then the top portion of the cane with 5-6 internodes retaining the 3-4 last emerged leaves was cut and the leaf sheaths were removed using a fine knife without injuring the nodal tissues. The top two nodes were then covered with cotton. Two canes were used for testing in the case of parents. Inoculum from the *Colletotrichum falcatum*

pathotypes isolated from the infected canes of CoC 671 was used for disease evaluation and the spore suspension was poured over the nodes wrapped with cotton. The inoculated canes were then placed vertically in a sand medium and allowed to root and remain metabolically active in the chamber. They were incubated in moist chamber under 90% relative humidity and the temperature was maintained at 32°C for 7-10 days.

Disease Rating

A week to 10 days after inoculation disease reaction was scored as levels of resistance on a scale of 1 to 5 based on the criteria reported earlier as 1 – highly susceptible, 2 – susceptible, 3 – moderately susceptible, 4 – moderately resistant and 5 – resistant (Mohanraj *et al*. 1997). The average of two readings was taken for analysis in parents.

Data Analyses

The disease scorings obtained from the different progenies were statistically analysed to estimate the vertical (race specific) and horizontal (race non-specific) resistant components present in the population. The progenies of different crosses were grouped into two categories, resistant (R and MR) and susceptible (MS, S and HS) for investigating race specific resistance (Mendelian). χ^2 test for goodness of fit was worked out for monogenic inheritance. From the disease scorings (1, 2, 3, 4 and 5) of the progenies and parents, family mean and mid parental values were calculated, and parent progeny regression was arrived to find out the proportion of horizontal resistant component present in the population.

The biometrical observations on economic traits such as sucrose per cent (SUC) and stalk yield per clump (YLD) at 360 days after planting were also recorded in the parents and their progenies at 360 days in addition to the red rot resistance score.

Results and Discussion

The data collected on the disease scorings of individual progenies and parents was statistically analysed and the results on the mode of inheritance of red rot resistance were reported in terms of race specific (vertical resistance) and race non-specific (horizontal resistance) resistance. Out of the seven crosses tested under R x R category two crosses showed goodness of fit for 3:1 segregation while there were significant deviations in the other five crosses (Table 2). However, in R x S category out of the 19 crosses, the expected ratio of 1:1 was observed in 16 crosses, the other three showing significant deviation. In the S x S category 13 crosses were studied. Although all progenies were expected to be susceptible according to Mendelian segregation, frequent occurrence of resistant progenies was also observed.

The family wise mean values on mid parent and families are given in Table 3. Using the mean values on mid parent and family, linear regression was worked out. The results of the analysis of variance for regression showed that the linear regression was found to be significant. From the graphical representation (Fig. 1), it is clear that, nearly 50 per cent of the variation could be attributed to linearity.

Progenies combining yield and sucrose, yield and red rot resistance and all the three characters are also presented in the Table 4. It shows the percentage of progenies superior in performance over the general mean by one critical difference for clump yield, sucrose per cent and resistance to red rot disease.

Inheritance of resistance

Information on inheritance of red rot resistance in the present day varieties as well as in the advanced interspecific genetic stocks is essential to formulate appropriate breeding strategies The mode of inheritance was investigated both for race-specific and race non-specific components. It was found that out of seven crosses under R x R category, two crosses showed goodness of fit for 3:1 segregation while there were significant deviations in the other five crosses. Out of 19 crosses under R x S category, 1:1 segregation was observed in 16 crosses, the other three showing significant deviations. Natarajan *et al*. (2001a) studied inheritance of red rot in terms of vertical and horizontal resistance and reported that, 10 out of 20 crosses showed goodness of fit for simple Mendelian ratios and the rest displayed significant deviations.In the S x S category, 13 crosses were studied. Although all progenies are expected to be susceptible according to Mendelian segregation, frequent occurrence of resistant progenies was observed**.** This gave a clear indication that race specific resistance alone could not wholly explain the pattern of inheritance. Hence parent-progeny regression was worked out to find out the level of additive gene action (race non-specific) that

confers red rot resistance. It was found that nearly 50% of the variation could be attributed to this component of resistance (Fig 1). Natarajan *et al.* (2001a) reported that, around 47 per cent of the variation observed was due to horizontal resistance.

The presence of substantial levels of additive genetic variance (horizontal resistance) in the population signifies the fact that resistance break down, a consequence of vertical resistance, could be avoided and stable resistance achieved. This may be due to the involvement of *S. spontaneum* in the parental clones which impart horizontal resistance to their progenies. Natarajan *et al.* (2001b) reported that, an increase in *S. spontaneum* chromosome in the progenies increases horizontal resistance component of resistance.

A natural phytosystem builds up horizontal resistance and the scope for evolution of vertical resistance is very much limited since it leads to the death of both the host and pathogen. *S. spontaneum* being a natural phytosystem with a contiguous distribution in the red rot endemic areas together with its ability to propagate naturally by both seed and vegetative means, forms an ideal candidate for evolution and maintenance of horizontal resistance. However, during the course of breeding sugarcane varieties for red rot resistance employing specific isolates of the pathogen, there is the possibility of the breeder and pathologist unwittingly shifting the host-pathogen system from one of HR-friendly to VR-friendly. This has been very well established in other crops and there are enough indications in sugarcane as well against red rot.

Natarajan *et al.* (2001b) also reported that, crosses involving susceptible parents may tend to produce resistant progenies with stable resistance due to additive genetic action. In the present study also, two crosses involving susceptible parents *viz.,* 971235 [S] x Co 1148 [S] and Co 88028 [S] x Co775 [S] produced resistant progenies to the tune of 30 per cent and 28 per cent respectively (Table 3). These transgressive segregants are the products of additive genetic action and are bound to show stable resistance (horizontal resistance). Such transgressive segregants that have arisen from the susceptible parents on both sides can also be used as potential genetic stocks in resistance breeding programmes for imparting race non-specific resistance. In fact there are a number of such varieties that are already available, some of which are listed below.

Resistant variety	**Susceptible parents**
Co 7704	
Co 740 x Co 6806	
Co 8021	
Co 740 x Co 6806	
Co 86010	
Co 740 x Co 7409	
Co 93009	
Co 678 x Co 775	
CoSi 95071	
CoC 671 x MS 68/47	
CoC 90063	
Co 6304 x CoC 671	

Economic types

A breeding programme would have served its purpose well if it brings forth economically superior types apart from generating useful information. Since sugarcane is exploited commercially as a clone, the rationale for family selection is not to produce superior families with commercial value, but rather to identify families with a higher frequency of superior clones (Kimbeng and Cox, 2003). The top scoring families for yield, sucrose per cent, red rot resistance, combination of yield with sucrose, yield with red rot resistance and families combining all the three characters are presented in the Table 5.

Conclusion

The present investigation has identified a large number of promising selections for yield, quality and red rot resistance for further testing and release for commercial cultivation and some specific cross combinations for yield, quality and red rot resistance for further exploitation in breeding programme. The specific crosses *viz*., 987032 x Co 93009 and Co 85002 x 971862 identified for the combination of all the three characters could be utilized to identify outstanding progenies combining yield, quality and resistance to red rot disease in future breeding programmes.

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Table 1. Interspecific origin of the parents used in the study

S.No.	Parents	Species involved	
		Saccharum officinarum	*Saccharum spontaneum*
1	970311	28 NG 210, NG 77-99	SES 87A
2	971235	-	SES 275
3	971236	-	SES 275
4	973402	NG 77-99, 28 NG 51, NG 77-63, NG 77-137	SES 44A, SES 538
5	9844195	28 NG 221, NG 77-99, 28 NG 51,28 NG 210, NG 77-137	SES 515-7, SES 44A, SES 538
6	984727	28 NG 221	SES 91, SES 515-7
7	984819	28 NG 221	SES 515-7
8	984843	28 NG 221	SES 515-7
9	985040	28 NG 221	SES 515-7
10	985094	28 NG 221	SES 515-7
11	985735	28 NG 221	SES 44 A
12	985931	-	SES 91
13	986046	-	SES 91
14	986095	-	SES 91
15	986140	-	SES 91
16	986179	-	SES 91
17	9869110	NG 77-99, 28 NG 51, 28 NG 210, NG 77-137	SES 44A, SES 538

NG – New Guinea
SES – *Saccharum spontaneum* Expedition Scheme

Table 2. Mendelian segregation for red rot resistance

S.No.	Cross	'R' progenies	'S' progenies	χ^2
	R x R (3:1)			
1	Co 87002 [R] x 986179 [R]	13	21	13.57**
2	CoM 9220 [R] x 984843 [R]	21	15	5.33*
3	CoM 9220 [R] x 987001 [R]	21	15	5.33*
4	ISH 1 [R] x Co 94008 [R]	14	17	14.72**
5	RS 93-2182 [R] x Co 93009 [R]	26	6	0.67
6	9844195 [R] x Co A7602 [R]	19	17	9.48**
7	987032 [R] x Co 93009 [R]	28	4	2.67
	R x S (1:1)			
8	Co 8371 [S] x 971862 [R]	7	29	13.44**
9	Co 85002 [S] x 971862 [R]	18	18	0
10	Co 86010 [R] x Co 775 [S]	13	23	2.78
11	Co 86249 [R] x Co 775 [S]	12	23	3.46
12	Co 98003 [S] x 971862 [R]	19	17	0.10
13	Co 98006 [S] x 987001 [R]	21	15	1.00
14	CoC 671 [S] x Co 94008 [R]	11	23	4.24*
15	CoH 110 [S] x 984843 [R]	22	14	1.78
16	CoH 110 [S] x 986179 [R]	19	17	0.10
17	87A298 [R] x Co 1148 [S]	14	22	1.78
18	970311 [S] x 986179 [R]	17	19	0.10
19	973402 [R] x Co 775 [S]	11	22	3.66
20	984727 [S] x 984843 [R]	6	30	16.00**
21	984819 [R] x Co 1148 [S]	21	14	1.40
22	985931 [R] x Co 775 [S]	21	15	1.00
23	986095 [S] x Co 94008 [R]	16	19	0.26
24	9869110 [R] x Co 1148 [S]	20	16	0.44
25	9869110 [R] x Co 62198 [S]	11	22	3.66
26	987080 [R] x Co 1148 [S]	19	15	0.48
	S x S			
27	971235 [S] x Co 1148 [S]	11	25	
28	971235 [S] x Co 62198 [S]	4	32	
29	971236 [S] x Co 62198 [S]	5	31	
30	Co 88028 [S] x Co 775 [S]	10	26	
31	CoH 76 [S] x 985094 [S]	3	32	
32	CoJ 72 [S] x Co 62198 [S]	1	35	
33	985040 [S] x Co 1148 [S]	2	34	
34	985735 [S] x Co 62198 [S]	2	20	
35	986046 [S] x Co 775 [S]	6	29	
36	986095 [S] x Co 62198 [S]	1	34	
37	986140 [S] x Co 1148 [S]	-	34	
38	987124 [S] x Co 775 [S]	3	33	
39	9871144 [S] x Co 775 [S]	4	31	

/ Significant deviations from Mendelian segregation*

R – Resistance

S – Susceptible

Table 3. Red rot resistance scores of families

S.No	Family	No. of progenies tested	Percentage of 'R' progenies	Mean values	
				Family	MP
1	Co 87002 [R] x 986179 [R]	34	38.2	2.94	4.00
2	CoM 9220 [R] x 984843 [R]	36	58.3	3.64	4.00
3	CoM 9220 [R] x 987001 [R]	36	58.3	3.39	4.00
4	ISH 1 [R] x Co 94008 [R]	31	45.2	3.13	4.00
5	RS 93-2182 [R] x Co93009 [R]	32	81.3	4.38	4.00
6	9844195 [R] x Co A7602 [R]	36	52.8	3.19	4.25
7	987032 [R] x Co 93009 [R]	32	87.5	3.88	4.25
8	Co 8371 [S] x 971862 [R]	36	19.4	2.56	3.00
9	Co 85002 [S] x 971862 [R]	36	50.0	3.22	3.00
10	Co 86010 [R] x Co 775 [S]	36	36.1	2.86	3.00
11	Co 86249 [R] x Co 775 [S]	35	34.3	3.01	3.00
12	Co 98003 [S] x 971862 [R]	36	52.8	3.36	3.25
13	Co 98006 [S] x 987001 [R]	36	58.3	3.19	3.25
14	CoC 671 [S] x Co 94008 [R]	34	32.4	2.85	2.50
15	CoH 110 [S] x 984843 [R]	36	61.1	3.44	3.25
16	CoH 110 [S] x 986179 [R]	36	52.8	3.33	3.25
17	87A298 [R] x Co 1148 [S]	36	38.9	2.64	3.50
18	970311 [S] x 986179 [R]	36	47.2	3.17	3.50
19	973402 [R] x Co 775 [S]	33	33.3	2.70	3.00
20	984727 [S] x 984843 [R]	36	16.7	2.42	3.25
21	984819 [R] x Co 1148 [S]	35	60.0	3.40	3.50
22	985931 [R] x Co 775 [S]	36	58.3	3.17	3.00
23	986095 [S] x Co 94008 [R]	35	45.7	3.17	3.50
24	9869110 [R] x Co 1148 [S]	36	55.6	3.25	3.50
25	9869110 [R] x Co 62198 [S]	33	33.3	2.82	3.00
26	987080 [R] x Co 1148 [S]	34	55.9	3.26	3.50
27	971235 [S] x Co 1148 [S]	36	30.6	2.72	2.50
28	971235 [S] x Co 62198 [S]	36	11.1	2.42	2.00
29	971236 [S] x Co 62198 [S]	36	13.9	2.25	2.00
30	Co 88028 [S] x Co 775 [S]	36	27.8	2.58	2.50
31	CoH 76 [S] x 985094 [S]	35	8.6	2.37	2.75
32	CoJ 72 [S] x Co 62198 [S]	36	2.8	1.80	2.50
33	985040 [S] x Co 1148 [S]	36	5.6	1.89	3.00
34	985735 [S] x Co 62198 [S]	22	9.1	2.50	2.75
35	986046 [S] x Co 775 [S]	35	17.1	2.63	2.25
36	986095 [S] x Co 62198 [S]	35	2.9	1.86	2.50
37	986140 [S] x Co 1148 [S]	34	0.0	1.71	3.00
38	987124 [S] x Co 775 [S]	36	8.3	2.31	2.00
39	9871144 [S] x Co 775 [S]	35	11.4	2.20	2.25

MP – Mid parent

Table 4. Percentage of progenies in individual families superior to grand mean by at least one CD

S. No.	Families	YLD	SUC	RRS	YLD+SUC	YLD+RRS	YLD+SUC + RRS
1	Co 8371 x 971862	25	52	19	13	3	0
2	Co 85002 x 971862	27	**75**	50	**16**	14	**11**
3	Co 86010 x Co 775	16	**58**	36	3	8	3
4	Co 86249 x Co 775	11	5	33	0	8	0
5	Co 87002 x 986179	17	26	38	0	9	0
6	Co 88028 x Co 775	16	41	27	8	11	5
7	Co 98003 x 971862	**44**	25	52	11	**25**	8
8	Co 98006 x 987001	27	22	58	5	22	8
9	CoC 671 x Co 94008	11	38	32	0	9	0
10	CoH 76 x 985094	13	**58**	8	8	0	0
11	CoH 110 x 984843	25	27	**61**	8	22	5
12	CoH 110 x 986179	**47**	16	50	5	**25**	5
13	CoJ 72 x Co 62198	38	36	2	14	3	0
14	CoM 9220 x 984843	22	47	52	8	17	8
15	CoM 9220 x 987001	19	44	58	14	11	5
16	ISH 1 x Co 94008	29	9	41	0	5	0
17	RS 93-2182 x Co 93009	18	25	**81**	3	19	3
18	87A298 x Co 1148	36	30	38	14	11	5
19	970311 x 986179	16	13	47	0	8	0
20	971235 x Co 1148	27	27	30	8	8	5
21	971235 x Co 62198	22	**80**	11	14	3	2
22	971236 x Co 62198	19	**83**	11	**16**	0	0
23	973402 x Co 775	18	30	33	6	6	0
24	9844195 x CoA 7602	27	16	52	5	14	3
25	984727 x 984843	16	13	16	0	0	0
26	984819 x Co 1148	31	11	**60**	2	16	3
27	985040 x Co 1148	**44**	11	5	3	3	3
28	985735 x Co 62198	9	13	9	0	0	0
29	985931 x Co 775	36	30	**58**	5	16	5
30	986046 x Co 775	28	31	17	11	8	5
31	986095 x Co 62198	37	57	2	**28**	0	0
32	986095 x Co 94008	17	31	45	5	5	3
33	986140 x Co 1148	17	17	0	0	0	0
34	9869110 x Co 1148	25	27	55	11	11	3
35	9869110 x Co 62198	15	39	33	6	9	0
36	987032 x Co 93009	37	25	**87**	12	**28**	**13**
37	987080 x Co 1148	**41**	8	55	5	23	6
38	987124 x Co 775	19	55	8	9	3	0
39	9871144 x Co 775	**40**	22	11	8	5	3
	Mean	**25**	**32**	**35**	**7**	**10**	**3**

YLD - Clump yield (kg) SUC - Sucrose (%) RRS - Red rot resistance

Table 5. Best families identified for important traits

S. No.	Families					
	YLD	**SUC**	**RRS**	**YLD + SUC**	**YLD + RRS**	**YLD + SUC + RRS**
1	CoH 110 x 986179	971236 x Co 62198	987032 x Co 93009	986095 x Co 62198	987032 x Co 93009	987032 x Co 93009
2	Co 98003 x 971862	971235 x Co 62198	RS 93-2182 x Co 93009	Co 85002 x 971862	CoH 110 x 986179	Co 85002 x 971862
3	985040 x Co 1148	Co 85002 x 971862	CoH 110 x 984843	971236 x Co 62198	Co 98003 x 971862	
4	987080 x Co 1148	Co 86010 x Co 775	984819 x Co 1148			
5	971144 x Co 775	CoH 76 x 985094	CoM 9220 x 987001			

YLD - Clump yield (kg) SUC - Sucrose (%) RRS - Red rot resistance

Fig. 1. Parent-progeny regression for red rot resistance