

Research Article**Variability for cane yield and quality characters among full-sib progenies of sugarcane (*Saccharum spp*) on family basis**Abdelmohmoud, O, Ahmed^{1*}, G. Vijayakumar², U.S. Natrajan³, and C. Babu⁴**Abstract**

Forty-six sugar cane families were studied for ratooning ability based on family mean, in a completely randomized block design with two replications at the Sugarcane Breeding Institute (ICAR), Coimbatore. Out of the 46 families, 30 biparental families were further studied for intra-family variation for population characters, cane characters, quality characters and clump yield. The family 87A298 x Co 1148 produced better variance for tillers counts where as two families CoH 110 x 984843 and 984843 x Co 1148 had shown maximum variances for number of millable cane. CoJ 72 x Co 62198 produced wider variances for stalk height and internode length where as for clump yield and internode number the variance was found to be maximum in the family 9869110 x Co 1148. The family 985931 x Co 779 showed maximum variance for stalk diameter. Two families viz., CoJ 72 x Co 62198 and Co 85002 x 971862 recorded the highest variances for hand refractometer brix at 300 days and 330 days respectively. The family 87A298 x Co 1148 showed high level of variances for clump yield and juice quality indicating the scope for simultaneous selection of clones for both the traits within this family.

Key words: Sugarcane, variability, full-sib progenies, cane yield and quality

Introduction

Cultivated sugarcane is a polyploid of interspecific origin in which *Saccharum officinarum* constitute the basic genome with parts of its genome derived from *S. spontaneum*, *S. barberi* and *S. sinense*. Thus, the present cultivated sugarcane varieties are of interspecific origin that sustains the genetic variability. Genetic improvement in sugarcane usually depends on the early identification of promising crosses which can produce commercially acceptable genotypes. The success of selection of such genotypes from these crosses is based not only on desirable agronomic characters, but also on the available genetic variations present in the population. Hence, it is of great interest, to determine the variability within different families in order to recover segregants with high agronomic merits. According to Skinner (1972), prediction of cross performance would also help to concentrate efforts on the most profitable crosses that substantially

increase the chances for selecting elite clones with good cane and sugar yield. Collins *et al*, (2003) reported that although sugarcane is grown commercially as clones, the breeding program typically commences by evaluating large number of seedlings derived from true seeds. Therefore the process of selection of promising genotypes within sugarcane crosses is one of the most critical decisions that sugarcane breeder has to make. Thus, the present study had placed an emphasis on selection of genotypes within families for cane yield characters namely tillers count, internode numbers, internode length, number of millable cane and clump yield and juice quality traits like juice brix based on the magnitude of variation available in each cross for the trait under study.

Materials and methods

The experimental material consisted of 46 sugarcane families and their parents. The parents were derived from intervarietal and interspecific crossing program thus ensuring wider genetic variability in the study material. Plant crop of the families was harvested and ratoon crop was established during June, 2004 at Sugarcane Breeding Institute Coimbatore, India in a

¹ Sugarcane Research Center, Guniad, Sudan

^{2, 4} Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

³ Sugarcane Breeding Institute (ICAR), Coimbatore, Tamil Nadu, India

* E mail: abdelmohmoud91@yahoo.co.in

completely randomized block design with two replications. The plot size was three rows each of 6m length spaced at 0.9m, each row containing 12 genotypes spaced at 50 cm apart. The standard recommended agronomic practices were adopted during the cropping season. Thirty selected biparental families each with forty genotypes each were studied for analyzing the intrafamily variance for cane yield and quality characters. Twenty genotypes per family in each replication were considered for recording observations on different characters such as population characters *viz.*, tiller counts at 120 days (TLC) and number of millable cane at harvest (NMC); cane characters at harvest such as stalk height (STH), stalk diameter (STD), single stalk weight (SSW) internode number (INN) internode length (INL); clump yield (CLY) at harvest and quality character namely hand refractometer brix (HRB) at 300 and 330 days. The main stalk in all clumps was considered while recording observations of population, cane and quality characters whereas the total stool weight after harvest was used to calculate clump yield (kg). Population characters were recorded in both the replications. Hand refractometer was used to record can juice brix. The method for recording observation for different characters per replication in each family was followed as reported by Babu (2004).

Population characters:

Tiller Counts =

$$\frac{\text{Total number of tillers}}{\text{No. of genotypes per plot}}$$

Number of millable cane =

$$\frac{\text{Total number of millable cane}}{\text{No. of genotypes per plot}}$$

Cane characters:

Stalk Height =

$$\frac{\text{Cumulative stalks height}}{\text{Number of millable Cane}}$$

Stalk diameter =

$$\frac{\text{Total stalk diameter readings}}{\text{Respective number of millable cane}}$$

Single stalk weight =

$$\frac{\text{Total stalks weight}}{\text{Respective number of millable cane}}$$

Internode number =

$$\frac{\text{Total number of internodes}}{\text{Total height of respective millable canes}}$$

Internode length =

$$\frac{\text{Total number of internode number}}{\text{Total height of respective millable cane}}$$

Quality character (Hand refractometer brix) =

$$\frac{\text{Total hand refractometer brix readings}}{\text{No. of genotypes}}$$

The average of the two replications for each character was considered as the mean performance of the family. Both between and within family variance was calculated for all characters using forty progenies per family. Analysis of variances along with expected mean squares were carried out as per Falconer, (1989). Test of significance was carried out with F test (Snedecor and Cochran, 1967).

Results and discussion

Analysis of variance between families indicated highly significant differences among genotypes from different families for population, cane and quality characters. The intra-family variation for the above characters is presented in Table 1 and 2.

Population characters: The family 87A 298 x Co 1148 showed maximum variance for tillers count at 120 days, followed by the family 984819 x Co 1148 while the lowest variance was registered by 986140 x Co 1148. Variance for number of millable cane at harvest was found to be the highest among the progenies of 984819 x Co 1148 followed by CoJ 72 x Co 62198. The family 986140 x Co 1148 recorded the lowest variance value.

Cane characters: Among the families, CoJ 72 x Co 62198 produced the highest variance for stalk height at harvest followed by Co 98003 x 971862. The family 985931 x Co 775 had showed highest variance for single stalk weight followed by 970311 x 986179 and the family 971236 x Co 62198 showed the minimum variance among genotypes for this character among the families. The families CoH 110 x 984843 and Co 88028 x Co 775 recorded the highest variance for stalk diameter followed by the family Co 87002 x 986179 and the family 971236 x Co 62198 had showed the minimum variance among the progenies for this character. Within family variance for number of internode at harvest was found to be high in the family CoJ 72 x Co 62198 followed by 9869110 x Co 1148. The least variance among the families for this character was recorded by Co 87002 x 986179. Internode length was found to be the highest with 9869110 x Co 1148 for variance within the family followed by 984819 x Co 1148 while the family 986059 x Co 94008 showed

the least variance for internode number. Two families *viz.*, 9869110 x Co 1148 and 87A 289 x Co 1148 had exhibited maximum variance among genotypes for clump yield.

Quality characters: The maximum variance value for hand refractometer brix at 300 days was recorded by CoJ 72 x Co 62198 and CoH 110 x 984843 while at 330 days the highest variance was recorded by Co 85002 x 971862 and 87A 298 x Co 1148. The least variance was shown by the family 984819 x Co 1148 among the families studied.

Clump yield: 9869110 x Co 1148 was found to generate the highest variance among genotypes followed by Co 85002 x 971862 whereas the least variance for this trait was registered by the family 986059 x Co 94008. Creation of maximum genetic variability is the basic requirement for initiating any breeding program. In this study, two families *viz.*, 986110 x Co 1148 and 87A 289 x Co 1148 had shown higher variance of 44.14 and 44.10 respectively for clump (stool) yield. This indicated that there is a wide scope for selection of clones with higher clump yield within these two families. The family 87A 289 x Co 1148 also showed high variance for H.R brix at 330 days. It indicates that the simultaneous selection for cane yield and high H.R brix is possible within this family. Ortiz (1984) found that selection of different cane and sugar characters at the low selection pressure (20 - 25%) was effective. The latter family had also shown the highest variance for tillers count at 120 days indicated that selection for clones with good number of tillers for high clump yield within this family is definitely possible. Chen *et al.* (1991) reported that genotypes with high cane yield and sugar content can be selected based on stalk diameter, stalk height and number of millable canes per clump and clump weight. Falconer (1960) generalized this and mentioned that selection for specific character results in correlated response in certain other characters. The family CoH 110 x 984843 had recorded the highest variance among genotypes for stalk diameter which indicated that selection for genotypes with good stalk diameter is effective in this family. This family also showed higher variation for hand refractometer brix value at 300 days which will favour for the selection of clones with good stalk diameter and higher juice brix.

Among the families studied, CoJ 72 x Co 62198 and CoH 110 x 984843 recorded the highest variance for H. R. brix trait at 300 days. The latter family also registered the highest variance for stalk height and internode number that indicated indirect selection for cane yield though it's yield components mainly stalk height and internode number is effective since both

these characters are positively associated. According to Quintus (1923) and Singh and Singh (1954), among the yield components affecting the cane yield of sugarcane, number of millable canes per unit area, single stalk weight, stalk diameter, stalk height and number of internodes are important. Chen *et al.* (1991) reported that genotypes with high cane yield and sugar content can be selected based on stalk height, stalk diameter, number of millable cane per clump and clump weight. Direct selection for elite clones with the high juice brix at 300 days in the family CoJ 72 x Co 62198 is also possible as it showed the highest variance for this character. The variance among the progenies of the family 985931 x Co 775 and 970311 x 986197 was found to be the highest for single stalk weight and it can be exploited for selecting clones with high single stalk weight. Also indirect selection for genotypes with higher cane yield in these families through single stalk weight can also be achieved since single stalk yield is one of the components that contribute to the cane yield. Punia *et al.* (1983) found that number of millable canes and single stalk weight among the cane characters that contributed most to cane yield. Among the characters, clump weight was found with the highest variance. The families 9869110 x Co 1148 and 87 A 298 x Co 1148 which recorded the highest variance for clump weight (Table.1) indicated that selection for clones with high cane yield from these families will be effective and when repeated these crosses may further generate more variability for clump yield. The later family was also exhibited the highest variance for number of tillers among the family studied, indicated the presence of strong association between clump yield and number of tillers. Srivastava *et al.* (1993) reported that cane yield was mainly governed by production of tillers and number of millable canes. Thus direct and indirect selection for cane yield through number of tillers might be possible within this family.

The present study had brought out some useful information on the genetic variability. Among the families, 9869110 x Co 1148 followed by 87A 298 x Co 1148 are the best combinations to generation wide variation to select elite genotypes for clump weight and these crosses should be repeated further for selection of clones with improved clump weight. Genetic improvement under selection for clones with high number of millable stalks is possible with 984843 x Co 1148 and Co J 72 x Co 62198 where as for the selection of clones with higher stalk weight, 985931 x Co 775 and 970311 x 986179 were the best. The highest variability for juice brix among the progenies of Co J 72 x Co 62198 indicated selection of clones with good juice quality is possible in this family.



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References

- Babu, C. 2004. Family performance of sugarcane (*Saccharum* spp. hybrids) for yield, quality and red rot (*Colletotrichum falcatum* Went) resistance and its relationship with genetic diversity based on STMS markers and coancestry of crosses, Ph.D. Thesis, Tamil Nadu Agricultural University, Coimbatore, India.
- Collins, A. Kemberge. and Micke C. Cox. 2003. Early generation selection of sugarcane families and clones in Australia: A Review. *Journal Society of Sugar Cane Technol.*, **23**: 216 – 227.
- Chen, Z.J. Lin, Y.Q. Chen, R.K. and Zhange, X.L. 1991. Selection for brix in sugarcane hybrid progenies. *Journal of Fijian Agricultural College*. **20**: 123 – 129.
- Falconer, D.S. 1989. *Introduction to Quantitative Genetics*. 3rd Edn. Longman Burnt Mill.
- Falconer, D.S. 1960. *Introduction to Quantitative Genetics*. Oliver and Boyd Edinburgh.
- Ortiz, R. 1984. Efficiency of various selection methods in the early stages of selection in sugarcane breeding. *Cultivos Tropicales*.
- Punia, M.S. Chandhary, B.S. and Hooda, R.S. 1983. *Genetic divergence in sugarcane*. *Indian Journal of Agric. Sci.*, **53**: 434 – 436.
- Singh, M. and Singh, H. 1954. Certain Correlation studies in sugarcane. *Proceeding Bienn. Conference sugarcane Research Development Workers*, **2**:70 – 78.
- Skinner, J. C. 1972. Selection in sugarcane: A review. *Proceeding International. Society of Sugar Cane Technol.*, **14**:149 –162.
- Snedecor, G. W. and Cochran. 1967. *Statistical methods*. Oxford and IBH Pub Co. Ltd. New Delhi.
- Srivastava, A.K. Gosh, A. K. and Agnithorti, V. P. 1993. *Sugarcane ratoon*, Oxford & IBH Publishing Co. Pvt. Ltd., India.
- Quintus, R.A. 1923. *Cultivation of sugarcane in Java*. Norman Roger. London.

Table 1. Intra-family variance for population and quality characters

	Source of variation	Mean square			
		TLC120	NMC	HBR300	HRB330
a.	Inter- families	101.12**	89.35**	50.55**	43.83**
b.	Intra- families	28.15	30.35	05.90	11.97
1.	87A 298 x Co 1148	51.01	50.62	04.79	30.08
2.	970311 x 986179	28.97	25.73	07.60	21.08
3.	971235 x Co 1148	36.41	28.57	08.62	11.94
4.	971235 x Co 62198	24.18	32.28	05.52	03.85
5.	971236 x Co 62198	22.13	25.70	02.94	11.57
6.	9844195 x CoA 7602	13.38	11.05	05.52	05.39
7.	984819 x Co 1148	49.15	68.33	06.44	02.77
8.	985040 x Co 1148	16.98	12.63	03.71	12.82
9.	985931 x Co 775	19.02	16.72	5.00	7.08
10.	986095 x Co 94008	13.69	11.57	04.03	04.98
11.	986095 x Co 62198	25.66	25.45	04.40	11.14
12.	986140 x Co 1148	11.69	10.97	2.33	11.89
13.	9869110 x Co 1148	44.51	43.04	02.38	11.94
14.	9871144 x Co 775	28.85	28.40	02.72	5.63
15.	987124 x Co 775	21.94	17.08	03.99	03.39
16.	Co 85002 x 971862	20.42	28.84	04.13	33.73
17.	Co 86010 x Co 775	16.65	12.21	6.04	18.68
18.	Co 8371 x 971862	16.79	14.66	07.78	17.90
19.	Co 86249 x Co 775	14.45	13.73	03.37	11.68
20.	Co 87002 x 986179	22.51	15.50	04.80	04.00
21.	Co 88028 x Co 775	22.61	20.08	04.52	07.11
22.	Co 98003 x 971862	20.42	23.16	05.00	06.15
23.	CoH 110 x 984843	47.68	53.93	11.93	18.14
24.	CoH 110 x 986179	39.59	27.37	10.87	05.78
25.	CoH 76 x 985094	16.97	18.66	04.55	23.30
26.	CoJ 72 x Co 62198	36.04	55.33	20.49	25.59
27.	CoM 9220 x 987001	26.67	26.61	04.90	03.87
28.	CoM 9220 x 984843	16.44	18.93	04.20	27.12
29.	ISH 1 x Co 94008	23.26	20.38	07.23	04.06
30.	RS 93-2182 x Co 93009	30.60	43.43	09.59	11.75

**Significant at 1% level of significance

Inter-family df=32; Intra-family df=1287; Family df = 39

TLC120: Tillers count at 120 days; NMC: Number of millable cane; HRB 300 and 330: Hand refractometer brix at 300 330 days respectively

**Table 2. Intra-family variance for cane characters and clump yield**

Source of variation	Mean square					
	STH	SSW	INN	STD	INL	CYD
a. Inter- families	7752.49**	0.78**	243.58**	1.61**	0.78**	42.19**
b. Intra- families	1111.62	0.11	31.48	0.21	0.11	25.19
1. 87A 298 x Co 1148	123.62	0.06	43.58	0.15	0.06	44.10
2. 970311 x 986179	89.29	0.24	16.21	0.2	0.24	26.65
3. 971235 x Co 1148	1637.22	0.06	29.05	0.19	0.06	16.67
4. 971235 x Co 62198	848.57	848.57	0.33	0.06	848.57	20.13
5. 971236 x Co 62198	853.85	0.03	40.28	0.16	0.03	25.24
6. 9844195 x CoA 7602	824.62	0.09	43.28	0.14	0.09	26.06
7. 984819 x Co 1148	896.09	0.06	29.45	0.1	0.06	29.61
8. 985040 x Co 1148	831.79	0.09	22.26	0.27	0.09	20.03
9. 985931 x Co 775	1331.99	0.25	17.96	0.29	0.25	25.36
10. 986095 x Co 94008	620.45	0.07	26.81	0.19	0.07	08.81
11. 986095 x Co 62198	1064.04	0.11	38.87	0.32	0.11	26.10
12. 986140 x Co 1148	55.191	0.15	16.01	0.16	0.15	08.91
13. 9869110 x Co 1148	974.12	0.07	46.41	0.23	0.07	44.14
14. 9871144 x Co 775	1206.65	0.09	43.92	0.28	0.09	29.88
15. 987124 x Co 775	653.59	0.06	20.46	0.08	0.06	24.12
16. Co 85002 x 971862	1633.34	0.07	3631	0.15	0.07	17.01
17. Co 86010 x Co 775	980.48	0.14	18.45	0.32	0.14	13.95
18. Co 8371 x 971862	1705.81	0.11	30.76	0.19	0.11	13.01
19. Co 86249 x Co 775	1088.32	0.08	40.74	0.18	0.08	08.97
20. Co 87002 x 986179	708.32	0.13	14.72	0.35	0.13	16.39
21. Co 88028 x Co 775	506.15	0.11	18.4	0.39	0.11	21.87
22. Co 98003 x 971862	1842.55	0.11	30.2	0.19	0.11	32.85
23. CoH 110 x 984843	1268.11	0.09	33.64	0.39	0.09	38.33
24. CoH 110 x 986179	1253.39	0.09	27.62	0.14	0.09	24.35
25. CoH 76 x 985094	1059.1	0.18	28.25	0.13	0.18	24.66
26. CoJ 72 x Co 62198	1980.45	0.15	53.4	0.18	0.15	26.93
27. CoM 9220 x 987001	760	0.21	17.76	0.15	0.21	21.27
28. CoM 9220 x 984843	1311.82	0.08	29.69	0.08	0.08	31.37
29. ISH 1 x Co 94008	1365.38	0.12	27.72	0.21	0.12	16.36
30. RS 93-2182 x Co 93009	1313.85	0.13	33.39	0.23	0.13	28.78

**Significant at 1% level of significance

Inter-family df=32; Intra-family df=1287; Cross df= 39

STH: Stalk height; STD: Stalk diameter; SSW: Single stalk weight; INN: Internode number; INL: Internode length; CYD: Cane yield