



Evaluation of Sugarcane Families and Identification of Promising Families for Cane Yield and Juice Quality Traits in Early Selection Stages

**Mallikarjun P. K.^{a*}, Sanjay B. Patil^a, Hanamaratti N. G.^a,
C. R. Patil^b and P. V. Patil^c**

^a *Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, 580 005, Karnataka, India.*

^b *Department of Agricultural Microbiology, University of Agricultural Sciences, Dharwad, 580 005, Karnataka, India.*

^c *Department of Plant Pathology, University of Agricultural Sciences, Dharwad, 580 005, Karnataka, India.*

Authors' contributions

This work was carried out in collaboration among all authors. Conceptualization of research authors SBP, MPK. Designing of the experiments authors SBP, MPK, HNG. Contribution of experimental materials author SBP. Execution of field/lab experiments and data collection authors MPK, SBP. Analysis of data and interpretation authors MPK, SBP, HNG. Preparation of the manuscript authors MPK, SBP. All authors read and approved the final manuscript.

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ABSTRACT

The utilization of superior parental lines and identification of promising families enhance the genetic gain in sugarcane. To identify the promising families, 1620 progenies derived from twenty two crosses involving genetically diverse historical parents were evaluated for cane yield and juice quality attributing traits. The mean number of millable canes per clump (9.00), cane girth (2.32 cm),

*Corresponding author: Email: mallihonna@gmail.com;

millable cane height (217.00 cm) and Brix% in juice (20.79%) were recorded. The significant variance, high broad-sense heritability and genetic advance over mean suggested that number of millable canes per clump, single cane weight, millable cane height, Pol% in juice and Brix% in juice are suitable for family evaluation. Based on progeny performance, families of Co 86032 × CoVC 14061 and Co 0312 GC, were found significantly superior compared to most popular clonal check, Co 86032 for number of millable canes per clump, similarly, CoVC 14062 × Co 89003 and Co 86002 × ISH 69 for cane girth, and CoVC 14062 × Co 89003, Co 11015 and Co 87015 for CCS% in juice content at early selection stages. Among 22 families studied, the four families viz., Co 86032 × CoVC 14061, CoVC 14062 × Co 89003, CoVC 14062 GC, Co 87015 GC and Co 11015 GC, produced higher percentage of population selection with acceptable range for commercially important traits (Brix% in juice, cane yield components). These identified promising families can be further exploited in sugarcane varietal improvement.

Keywords: Sugarcane; family selection; heritability; brix%; germination; seedling generation.

1. INTRODUCTION

Sugarcane (*Saccharum* spp. complex) stands as one of the major cash and industrial crops in the world, serving as a fundamental raw material for the sugar industry and various agro-based sectors. Sugarcane is cultivated widely across various Indian states, especially in tropical regions like Karnataka, Tamil Nadu, Maharashtra, Andhra Pradesh, Gujarat, Madhya Pradesh and sub-tropical regions such as Uttar Pradesh, Uttarakhand, Haryana, Punjab, Bihar, covering an area of about 5.15 million hectares [1]. This cultivation constitutes around 2.50% of the gross cropped area. The production capacity of sugarcane surpasses 468.79 million tonnes, achieving a productivity of 83.89 tonnes per hectare.

Crop improvement in sugarcane is primarily focuses on enhancing sugar content and biomass yield. The current sugarcane varieties are inter-specific hybrids of *Saccharum officinarum* L. ($2n = 80$) and *Saccharum spontaneum* L. ($2n = 40-128$), resulting in significant variations in commercially important traits such as commercial cane sugar percentage (CCS%), cane yield and CCS yield among cultivated varieties and species clones [2,3]. Several factors, including cane maturity, soil conditions, climate, agricultural practices and sugarcane variety, influence cane yield and sucrose content in juice. Sustainable sugar productivity is a major concern due to adverse climatic conditions, the increasing cost of sugarcane cultivation, and the high level of sugar consumption in many developing countries in Asia, Africa and Latin America [4]. Developing high sucrose and cane-yielding cultivars is a crucial goal in the sugarcane breeding program [5,6]. However, breeders face numerous challenges, including high polyploidy, aneuploids,

poor fertility, lengthy breeding selection cycles and limited genetic diversity in germplasm [7,8]. Broadening the genetic base of sugarcane involves selecting suitable parental combinations during hybridization based on their phenotypic traits, pedigree history and genetic distance between parents. This process contributes to better recombinants and promising clones after the selection cycle.

Several research projects have demonstrated that, following hybridization with parents to obtain high sucrose and cane yield, families must undergo evaluation. Subsequently, individual plants within the best families should be selected. This is because selecting in families with high genotypic values increases the probability of finding superior clones among the progenies [9,10,11]. Based on this hypothesis, family selection, a proven, short-term, efficient and cost effective approach, has been routinely applied to assess superior clones (individual clone selection) derived from well-established commercial parents for varietal development programs [12,13,14,7,15,16]. The identification of promising crosses and the selection of productive segregants from them constitute a cost effective and efficient approach. Therefore, the present study aims to identify promising families based on cane yield and quality traits in the seedling generation, with the goal of accelerating the varietal development programmes.

2. MATERIALS AND METHODS

2.1 Plant Material and Experimental Conditions

The study was conducted at the ground nursery of the Agricultural Research Station (ARS), Sankeshwar, Karnataka, India. The experimental

material consisted of 22 crosses (crosses), including bi-parental crosses (BP's), general collections (GC's) and polycrosses (PC's). These 22 families, corresponding to the 2019 series, were effected at three crossing locations; (i) National Hybridization Garden (NHG), ICAR-Sugarcane Breeding Institute (SBI), Coimbatore, (ii) ARS, Sankeshwar and (iii) ARS, Mugad (Table 1). True seeds (fuzz) of the 22 crosses (segregating seedling populations), were germinated under controlled conditions in a shade nursery, by maintaining a temperature of 30-35°C and high humidity (80-85%) in April 2020. Later, they were transplanted into the ground nursery at 55-60 days of nursery growth.

2.2 Experimental Design and Data Collection

A total of 1620 segregating seedlings from 22 families were transplanted in the field during the first week of June, 2020. The experiment was set up using an augmented design-II [17], with a spacing of 1.20 m x 0.60 m and a row length of 6.00 m distributed across three blocks. Each block included seven commercial standards (plants grown from clones) viz., CoC 671, Co 09004, SNK 09211, Co 86032, SNK 09227, SNK 09293 and MS 13081. The crop was cultivated following the recommended package of practices for the region.

Data was recorded for the weight of fluff per cross (WFS) in grams before sowing the TSS families in the shade nursery. Subsequently, the true seeds were evenly spread in a thin layer on a finely prepared seedbed to facilitate the growth of healthy segregating seedling populations. The number of seedlings germinated per cross (NSG) was recorded at 45 days after sowing, and the fluff germination percentage (FGP) was calculated using a formula consistent with previously reported by Singh and Singh [18]. After transplanting the seedlings into the ground nursery under field conditions, each individual progeny within the TSS families was assigned a number and tagged for identification. The number of progenies survived per cross (NPS) was recorded at 60 days after transplanting, and the seedling survival percentage (SSP) was calculated using the following formula:

$$\text{Fluff germination percentage (FGP)} = \frac{\text{Number of seedlings germinated}}{\text{weight of fluff sown (g)} \times 250} \times 100$$

$$\text{Seedling survival percentage (SSP)} = \frac{\text{Number of progenies survived}}{\text{Number of seedlings germinated}} \times 100$$

Traits such as the number of millable cane per clump (NMC/ clump), cane girth (CG) (cm), cane height (CH) (cm) and the number of internodes (NI) were recorded from individually tagged progeny populations (TSS families) along with checks at harvest. For the analysis of industrially essential traits, three millable canes per progeny were collected. The number of samples varied depending on family size. In larger families ($n \geq 100$), ten progenies were randomly sampled, while in smaller families ($n = 30-99$ with FGP $\geq 1.0\%$), five progenies were randomly sampled. This approach follows the method outlined by Leite et al. [19] and Silveira et al. [20]. The collected millable canes were crushed to extract juice separately from each sample and progeny. This juice was then subjected to analysis for Brix *per cent* and sucrose *per cent* (Pol %) in the juice using a brix hydrometer and a polariscope, respectively. Additionally, the commercial cane sugar (CCS %) was worked out based on the values of Pol% and Brix%, as per Meade and Chen [21]. Meanwhile, for the commercial clonal checks, three random millable canes from each commercial check in each block were assessed for comparison.

2.3 Statistical Analysis

Analysis of variance (ANOVA) for cane yield and juice quality traits were statistically analyzed using the data collected in augmentedRCBD package in 'R' software (version R-4.2.1). Estimates of genetic variability parameters for cane yield and juice quality traits were calculated. The mean and range of cane yield and juice quality traits of clones were further analyzed and compared with commercial clonal checks at a 5% level of significance, using a Microsoft excel.

3. RESULTS AND DISCUSSION

The data presented in Table 2 revealed that the analysis of variance (ANOVA) based on one-way (single factor analysis) showed highly significant differences ($p < 0.01$) among the evaluated families (crosses) for all traits. The variation within seedlings is largely due to differences between TSS families; therefore, these seedlings are expected to yield high cane and juice quality traits in the next stage of selection. The ANOVA based on augmented block design for all the

studied traits revealed highly significant differences ($p < 0.01$) among all evaluated treatments. This indicates the presence of sizable variability and the potential for significant improvement in these traits through selection. However, there was no significance for block effects (eliminating treatments), indicating homogeneity of evaluation blocks. The mean squares due to families differed significantly for all studied characters, indicating sufficient genetic variation in genotypes for all the studied traits. Similar results were reported by Sanghera and Jamwal [5], Somu and Nagaraja [22] and Khokhar *et al.* [23]. Highly significant ($p < 0.01$) variance estimates of families versus checks were observed for all the studied traits, indicating that the test entries (seedlings) were significantly different from the check variety. Similar results were reported by Ahmed and Obeid [24] and Sanghera and Jamwal [5], who observed significant differences for the contrast of the

checks versus new genotypes for the parameters.

3.1 Performance of Families for Cane Yield Related Traits

A total of 22 families (crosses) were evaluated, resulting in the germination of 1620 seedlings. The overall germination and survival frequency of sugarcane seedlings were observed to be 2.9% and 82.6%, respectively (Table 3). Notably, the CoM 6806 GC family recorded the highest fluff germination *per cent* of 9.4%, followed by CoVC 14062 GC (7.9%) and Co 86032 × CoVC 14061 (6.3%). The highest seedling survival percentage was noticed in families such as Co 11015 GC (96.7%), followed by CoVC 14062 × Co 89003 (95.0%) and Co 86032 × CoVC 14061 (93.6%). Conversely, the lowest survival frequency after transplanting was recorded in Co 06036, GC (70.0%) and ISH 100 GC (70.0%).

Table 1. Details about the true sugarcane seed families (BiP's, GC's and PC's) effected across locations for obtaining progeny populations

Sl. No.	FC	Crosses (Parentage)	FCL	WFS (g)
1	18F01	CoVC 14062 × Co 89003	CO	14.00
2	18F02	Co 86032 × CoVC 14061	CO	8.00
3	18F33	CoH 119 × CoC 8001	CO	39.00
4	18F34	Co 2000-10 × CoVC 14061	CO	31.00
5	18F40	Co 86002 × ISH 69	CO	22.00
6	18F09	CoM 6806 (GC)	CO	17.00
7	18F10	Co 98006 (GC)	CO	7.00
8	18F11	Co 99004 (GC)	CO	19.00
9	18F12	CoJn 862072 (GC)	CO	35.00
10	18F14	CoVC 14062 (GC)	CO	14.00
11	18F16	CoA 7602 (PC)	CO	5.00
12	18F18	Co 8371 (PC)	CO	14.00
13	18F19	ISH 20 (GC)	SNK	24.00
14	18F20	Co 06036 (GC)	SNK	42.00
15	18F21	Co 312 (GC)	SNK	71.00
16	18F22	ISH 307 (GC)	SNK	32.00
17	18F26	CoSnk 03632 (GC)	SNK	23.00
18	18F27	Co 11015 (GC)	SNK	8.00
19	18F41	Co 87015 (GC)	SNK	17.00
20	18F42	Co 95021 (GC)	M	10.00
21	18F43	Co 8213 (GC)	M	15.00
22	18F44	SNK 049 (GC)	M	5.00
Commercial standards (plants grown from clones)				
	C1	CoC 671		
	C2	Co 09004		
	C3	SNK 09211		
	C4	Co 86032		
	C5	SNK 09277		
	C6	SNK 09293		
	C7	MS 13081		

FC: Family code, FCL – Fluff collected locations, CO: NHG, SBI, Coimbatore, SNK: ARS, Sankeshwar, M: ARS, Mugad, GC – General collections, PC – Poly crosses, WFS – Weight of fluff sown per cross (g)

Table 2. Analysis of variance of block adjusted for cane yield and juice quality related traits of 22 TSS families in seedling generation of sugarcane

Source of Variation	d.f.	NMC/ Clump	Cane girth	Cane height	Single cane weight	Brix %	Pol %	CCS %
Between TSS families	21	162.54**	5.22**	20636.14**	0.33**	7.12*	13.73**	9.94**
Within TSS families	1598	22.80	0.13	2445.78	0.11	3.31	4.82	2.41
Treatment (ignoring Blocks)	1626	24.58**	0.20**	2696.49**	0.16**	4.39**	4.88**	3.76**
Treatment: Check	6	10.58**	0.14**	5179.92**	0.33**	5.76**	5.74**	3.36**
Treatment: Seedlings	1619	24.61**	0.19**	2681.72**	0.14**	3.77**	4.06**	3.33**
Treatment: Seedlings vs. Check	1	66.84**	3.98**	11702.24**	0.82**	42.01**	59.77**	38.11**
Block (eliminating Treatments)	2	0.11 ^{NS}	0.01 ^{NS}	29.12 ^{NS}	0.01 ^{NS}	0.01 ^{NS}	0.05 ^{NS}	0.06 ^{NS}
Residuals	12	0.63	0.01	252.80	0.01	0.11	0.13	0.09

NS $P > 0.05$; * $P < 0.05$; ** $P < 0.01$

NMC: Number of millable canes

Table 3. Mean values and range of important cane yield related traits of the 22 TSS families in seedling generation at harvest

Sl. No.	Family code	NP	FGP	SSP	NMC/ clump			Cane girth (cm)			Cane height (cm)			Number of internodes		
					Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.
1	18F01	38	1.14	95.0	7.00	2	14	2.59*	1.86	3.23	216	95	268	22.00*	12.00	29.00
2	18F02	117	6.25	93.6	12.00*	2	28	2.31	1.52	3.09	244.	110	320	21.00*	14.00	26.00
3	18F09	389	9.41	77.2	9.00	1	29	2.43	1.70	3.53	235	68	374	18.00	8.00	26.00
4	18F10	29	2.00	82.9	6.00	4	16	2.35	1.61	3.48	237	122	325	18.00	12.00	26.00
5	18F11	63	1.47	90.0	8.00	2	17	2.34	1.68	3.21	257*	159	351	19.00	14.00	25.00
6	18F12	70	2.86	78.0	7.00	1	26	2.29	1.05	3.29	206	65	356	20.00*	10.00	27.00
7	18F14	257	7.86	93.4	10.00*	3	32	2.48	1.60	3.77	253*	83	367	20.00*	9.00	29.00
8	18F16	14	1.60	70.0	9.00	2	16	2.48	2.06	2.90	259*	138	289	21.00*	16.00	26.00
9	18F18	64	2.00	91.4	10.00*	1	23	2.45	1.42	3.52	203	74	279	19.00	12.00	25.00
10	18F19	25	1.67	72.5	10.00*	1	25	2.47	1.61	2.98	251*	143	303	18.00	13.00	20.00
11	18F20	25	1.09	83.3	10.00*	3	23	2.24	1.25	2.92	195	110	264	22.00*	17.00	25.00
12	18F21	10	1.08	76.6	13.00*	2	23	2.05	1.67	2.87	232	138	304	18.00	12.00	22.00
13	18F22	24	1.01	86.0	7.00	2	14	2.48	1.74	3.50	236	95	354	21.00*	11.00	26.00
14	18F26	29	1.7	72.5	9.00	1	30	2.26	1.68	3.35	264*	136	373	18.00	14.00	25.00
15	18F27	118	6.10	96.7	8.00	3	20	2.39	1.59	3.12	242	111	354	22.00*	13.00	30.00
16	18F33	11	1.04	90.0	11.00*	5	21	2.61*	2.14	3.01	211	84	251	19.00	11.00	25.00

Sl. No.	Family code	NP	FGP	SSP	NMC/ clump			Cane girth (cm)			Cane height (cm)			Number of internodes		
					Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.
17	18F34	20	1.95	77.4	9.00	3	29	2.59*	1.57	3.31	212	100	279	19.00	13.00	26.00
18	18F40	24	1.60	92.3	10.00*	3	19	2.64*	1.79	3.64	201	97	255	18.00	13.00	25.00
19	18F41	198	5.47	80.5	7.00	1	27	1.66	0.46	2.59	242	77	354	22.00*	12.00	29.00
20	18F42	28	1.60	70.0	11.00*	2	32	2.32	1.73	3.40	208	120	276	15.00	10.00	21.00
21	18F43	12	1.02	70.1	14.00*	4	31	2.12	1.50	2.46	271*	135	324	17.00	13.00	21.00
22	18F44	55	4.67	78.6	7.00	1	16	2.22	1.36	3.02	226	128	320	19.00	14.00	25.00
Adjusted mean		1620	2.9	82.6	9.00			2.32			217			20.00		
Commercial standards (Plants grown from clones)																
C1	CoC 671				5.00	5	6	2.55	2.50	2.60	209	200	216	17.00	16.00	18.00
C2	Co 09004				7.00	6	8	2.70	2.70	2.70	209	205	218	22.00	21.00	22.00
C3	SNK 09211				10.00	9	10	2.57	2.53	2.60	211	201	221	20.00	19.00	20.00
C4	Co 86032				7.00	5	9	2.44	2.30	2.73	207	193	232	18.00	18.00	19.00
C5	SNK 09227				10.00	9	11	2.92	2.87	2.97	255	234	279	22.00	21.00	23.00
C6	SNK 09293				7.00	6	7	3.02	2.83	3.15	288	276	300	20.00	19.00	21.00
C7	MS 13081				6.00	5	7	2.98	2.93	3.03	304	289	317	22.00	21.00	23.00
Critical difference (5%)																
A Test Treatment and a Check					2.14			0.15			42.76			1.79		
Control Treatment Means					1.42			0.07			28.29			1.19		
Coefficient of Variance					8.87			4.08			7.31			3.38		

* Significantly superior over popularly grown check Co 86032, NP: Number of progenies studied per cross, FGP: Fluff germination percentage, SSP: Seedling survival percentage, NMC: Number of millable canes
Min.: Minimum, Max.: Maximum

From, Table 3 reveals that NMC/ clump, cane girth, cane height and the number of internodes varied significantly among evaluated families. NMC/ clump varied from 6.00 for the cross 18F11 (Co 99004 GC) to 13.00 of 18F21 (Co 312 GC) and NMC/ clump for the popular check variety, Co 86032 was 7.00. Similar results were reported by Pathy and Mohanraj [25] and Sreenivasa et al. [26]. Cane girth differed significantly among the evaluated families, cane girth varied from 0.46 cm for the family 18F41 (Co 87015 GC) to 3.77 cm for cross 18F14 (CoVC 14062 GC). Four families; 18F01 (CoVC 14062 × Co 89003), 18F33 (ISH 502 GC), 18F34 (ISH 554 GC) and 18F40 (ISH 307 GC), recorded significantly greater cane girth values than the check variety Co 86032 (2.44 cm). The number of internodes varied from 8.00 for the cross 18F09 (CoM 6806 GC) to 30.00 of 18F21 (Co 11015 GC) and the number of internodes for the popular check variety, Co 86032 was 18.00.

Single cane weight differed among the evaluated families, with single cane weight varying from 0.66 kg for the cross 18F14 (CoVC 14062 GC) to 2.33 kg for cross 18F41 (Co 87015 GC). The family 18F01 (CoVC 14062 × Co 89003), 18F02 (Co 86032 × CoVC 14061) and 18F27 (Co 11015 GC) showed significant superiority over the popularly grown check, Co 86032 for the single cane weight (Fig. 1).

Most of the crosses exhibited higher cane height than Co 86032, but five families viz., 18F11 (Co 99004 GC), 18F14 (CoVC 14062 GC), 18F16 (CoA 7602 PC), 18F19 (ISH 20 GC), 18F26 (CoSnk 03632 GC) and 18F43 (Co 8213 GC), recorded significantly greater cane height (257, 253, 259, 251, 264 and 271 cm), respectively. Data in Fig. 2 revealed that commercially important traits such as, Brix%, Pol% and CCS% varied significantly among evaluated crosses. Three families viz., CoVC 14062 × Co 89003, Co 11015 GC and Co 87015 GC, had the highest means over the popular check variety, Co 86032 (20.4%, 18.1% and 12.9%) for Brix%, Pol% and CCS%, respectively (Fig. 2). These were the best crosses across all other crosses for most studied traits in the seedling generation, suggesting the possibility of evaluating a large number of clones of these crosses, followed by the selection of superior clones within these crosses during the next selection stages [27,28,7,16]. Based on the parameter of percentage population selected with specific crosses, Co 86032 × CoVC 14061 (18F02) was observed superior having 49.57% selection rate i.e. 21.74% of total population among the different crosses followed by CoVC 14062 GC (36.00%) and Co 87015 GC (31.82%) (Table 2). Similar results were observed by Singh and Singh [18,29,30,31].

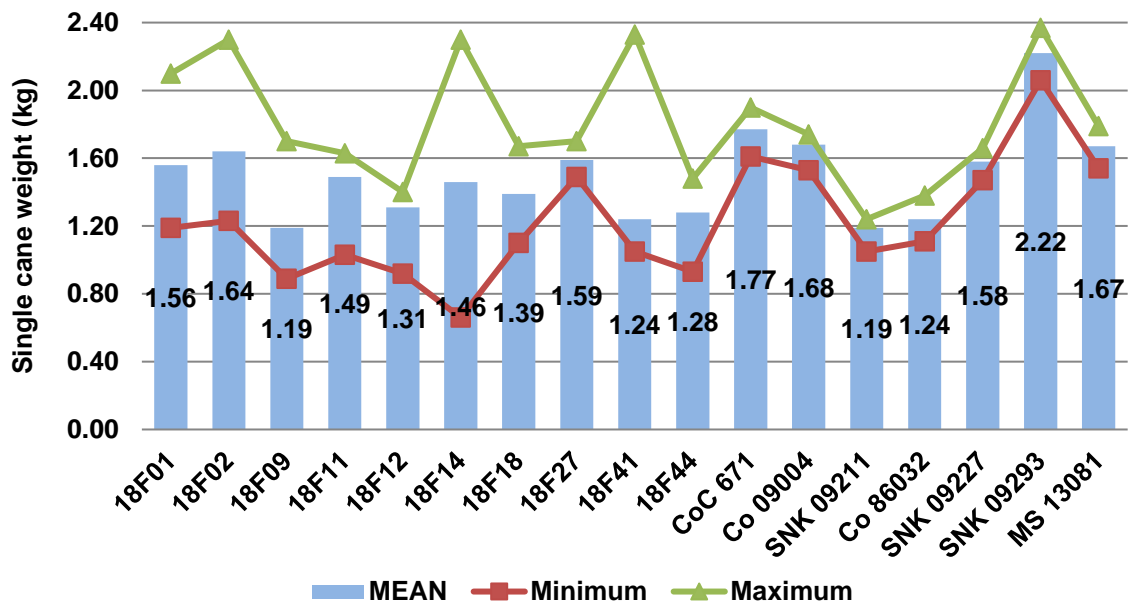


Fig. 1. Mean and range of single cane weight for promising sugarcane families

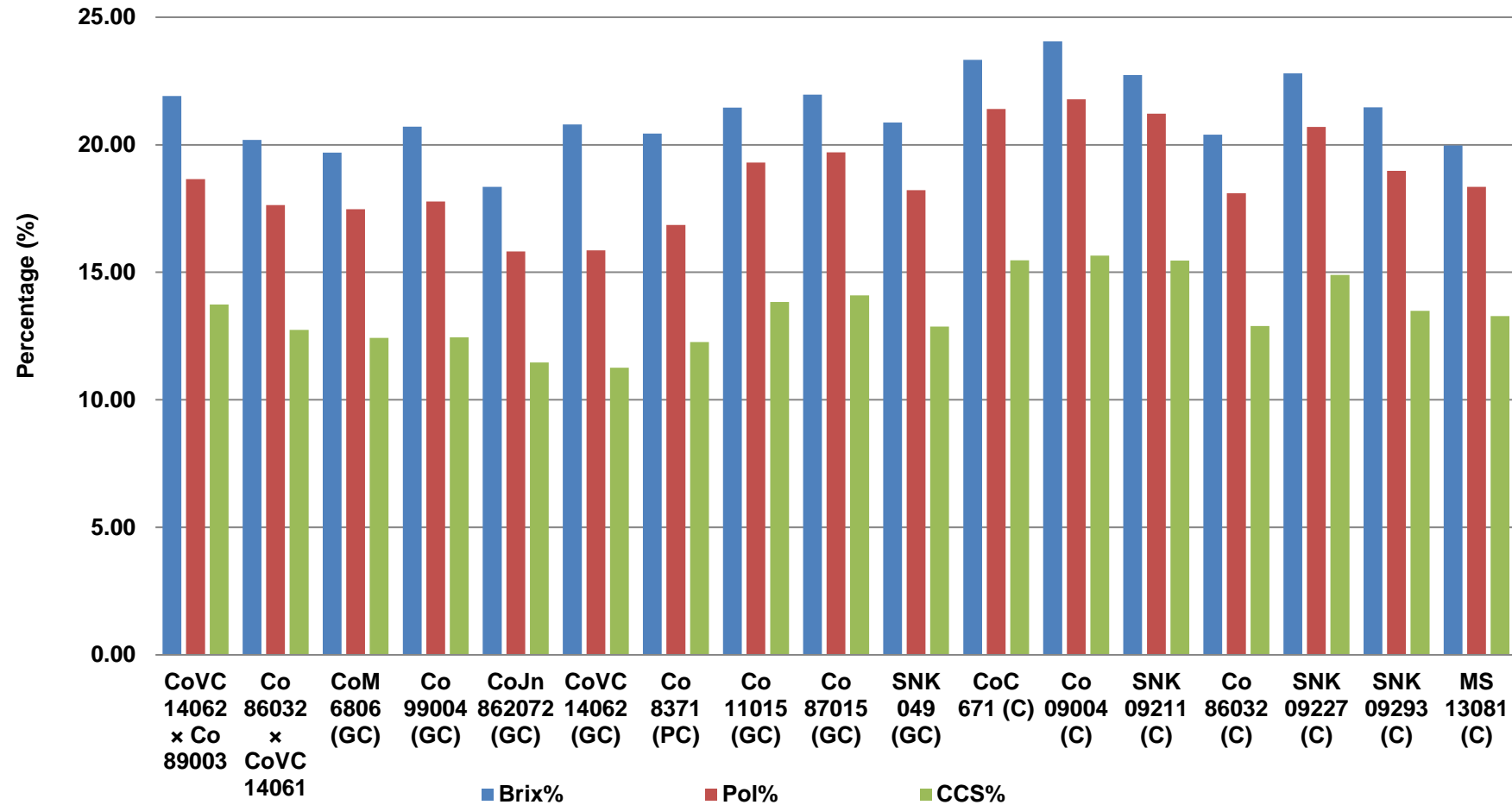


Fig. 2. Comparative performance of promising crosses based on sugar yield related traits in seedling generation of sugarcane
GC: General collections, PC: Poly crosses, C: Commercial standard varieties

4. CONCLUSION

In sugarcane varietal development, there is a continuous need for high yielding as well as high sugared clones. If potential parental combinations can be identified, it can save labour and monetary resources during subsequent clonal selections. In current study, families like Co 86032 × CoVC 14061, Co 11015 GC, Co 87015 GC and CoVC 14062 GC, have been identified for different traits viz., Brix%, Pol%, CCS%, NMC per clump, cane girth (cm) and cane height (cm) that can be used as potential parents for the improvement of each trait in future sugarcane breeding programmes.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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