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

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), 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.

Key words: 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. MATERIAL 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℃ 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 × 0.60 m and a row length of 6.00 m distributed across three blocks. Each block included seven commercial clonal checks (plants grown from vegetative setts) 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 (2021) [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

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 vegetative setts)				
	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)

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:

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

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

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 ≥ 100), ten progenies were randomly sampled, while in smaller families (n = 30-99 with FGP ≥ 1.0%), five progenies were randomly sampled. This approach follows the method outlined by Leite et al. (2009) and Silveira et al. (2016) [19, 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 hygrometer 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 (1977) [21]. Meanwhile, for the commercial clonal checks, three random millable canes from each commercial check in each block were assessed in for comparison.

2.3 Statistical analysis

Analyses 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

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*

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 (2019) [5], Somu and Nagaraja (2020) [22] and Khokhar *et al.* (2022) [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 (2012) [24] and Sanghera and Jamwal (2019) [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%).

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 (2021) [25] and Sreenivasa et al. (2024) [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.

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
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

Cont…

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.
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 clonal checks (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, Min.: Minimum, Max.: Maximum*

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).

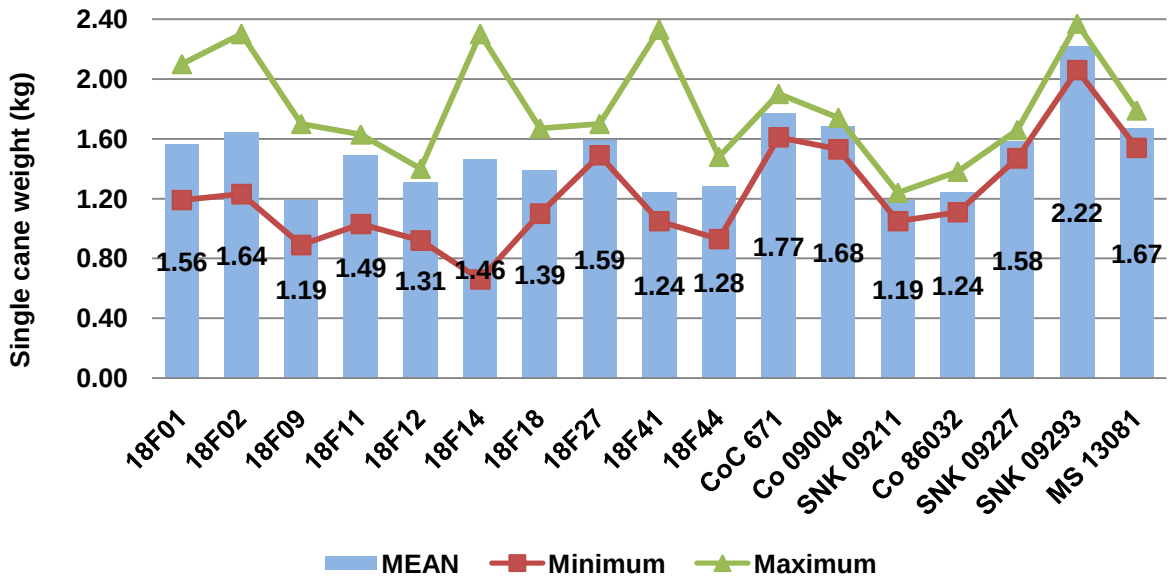

Fig 1. Mean and range of single cane weight for promising sugarcane families

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 (2021) [18].

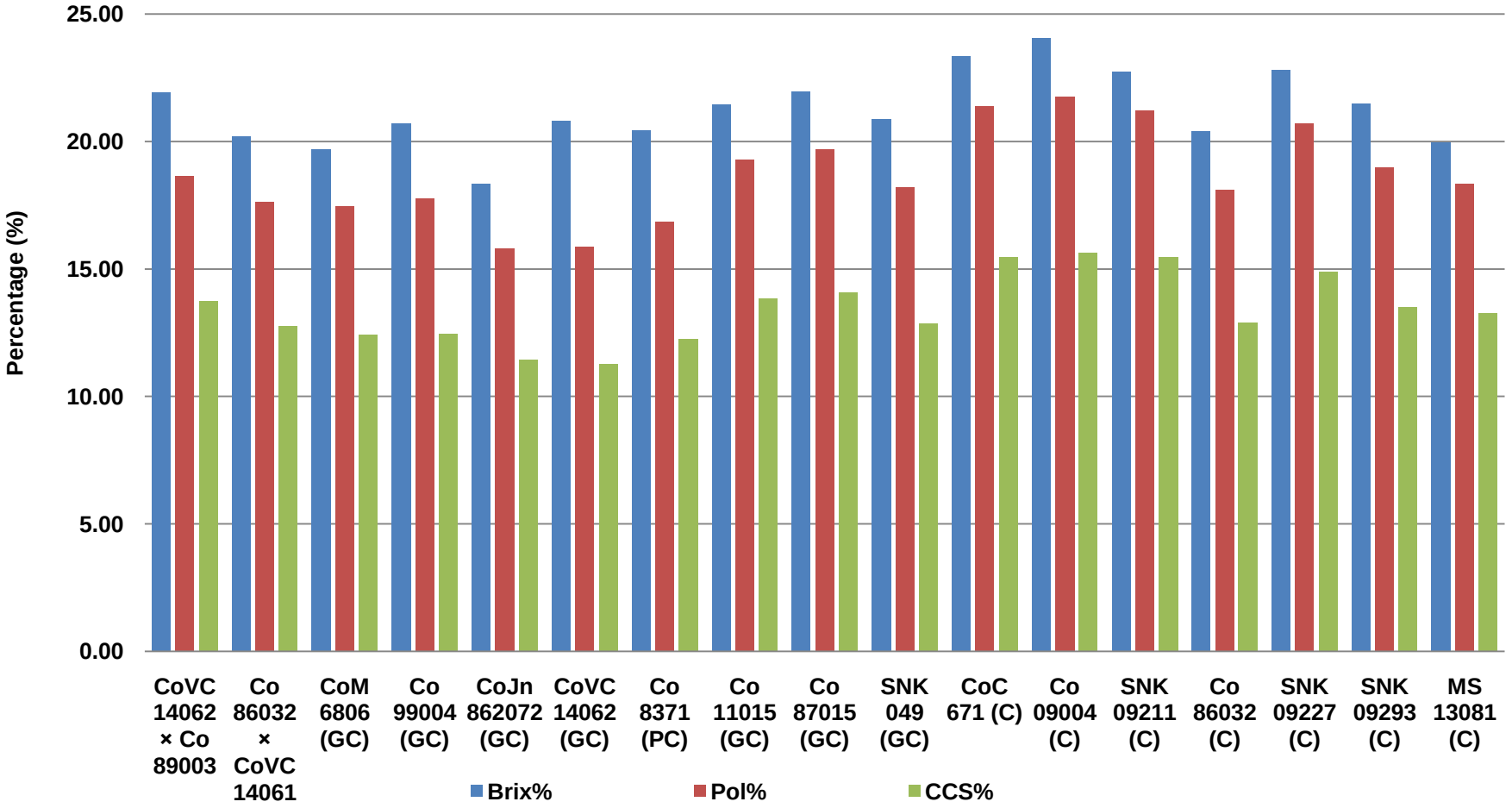

Fig. 2. Comparative performance of promising crosses based on sugar yield related traits in seedling generation of sugarcane

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.

REFERENCES

1. Mallikarjun PK,Sanjay B Patil. Study of genetic variability in productivity and juice quality traits among first clonal generation sugarcane clones (*Saccharum* spp.). The Pharma Innovation Journal. 2023;12(9):1806-1811.
2. Govindaraj P, Amalraj VA. Expedition collection, characterization and diversity analysis of the new wild sugarcane germplasm from Manipur. Indian Journal of Plant GeneticResources.2022;35(2):199-208.
3. Anna Durai A,Karuppaiyan R. Potential parents for developing climate-resilient sugarcane varieties in India: A Breeding Perspective. In: Verma KK, Song XP, Rajput VD, Solomon S, Li YR, Rao GP, editors. Agro-industrial perspectives on sugarcane production under environmental stress. Springer Nature, Singapore; 2023.
4. Pal R, Singh K, Singh O, Singh V, Jain R,Solomon S. Effect of plant growth regulators (PGRS) on germination, yield and quality of sugarcane in sub-tropical Indian Agricultural Research Journal.2021;58:657-661.
5. Sanghera GS, Jamwal NS. Identification of potential crosses based on vigour, cane characteristics and HR Brix for first clonal selection in sugarcane. Indian Journal of Sugarcane Technology.2019;34(1):12-16.
6. Perera MF, Budeguer F, Enrique R, Ostengo S, Noguera AS,Racedo J. Potential and Advanced Strategies for Sugarcane improvement. In: Gaur RK, editor. Omics Approaches for Sugarcane Crop Improvement. CRC Press, Boca Raton, Florida, United States; 2022.
7. Patil SB, Guddadamath SG,Khadi BM. Genetic enhancement of sugarcane productivity combining non flowering feature. Sugar technology.2015;17:386-394.
8. Hemaprabha G, Mohanraj K, Jackson PA, Lakshmanan P, Ali GS, Li AM et al. Sugarcane genetic diversity and major germplasm collections. Sugar Technology, 2022;24:279-297.
9. Kimbeng CA, Cox MC. Early generation selection of sugarcane families and clones in Australia: a review. J. Am. Soc. Sugar Cane Tech.2003;23:20-39.
10. Barbosa MHP, de Resende MDV, Bressiani JA, da Silveira LCI,Peternelli LA. Selection of sugarcane families and parents by Reml/Blup. Crop Breeding and Applied Biotechnology.2005;5:443-450.

11. Stringer JK, Cox MC, Atkin FC, Wei X, Hogarth DM. Family selection improves the efficiency and effectiveness of selecting original seedlings and parents. Sugar Technology.2011;13(1):36-41.
12. Hogarth DM. Genetics of sugarcane. In: Heinz DJ, editor. Sugarcane Improvement through Breeding. Elsevier, Amsterdam; 1987.
13. Skinner JC, Hogarth DM, Wu KK. Selection methods, criteria, and indices. In: Heinz DJ, editor. Sugarcane Improvement through breeding. Elsevier, Amsterdam; 1987.
14. Zhou MM, Kimbeng CA, Andru S, Tew TL, Pontif MJ, Gravois KA. Evaluating sugarcane families for yield potential and repeatability using random coefficient models. Crop Science. 2013;53(6):2352-2362.
15. Mbuma NW, Zhou MM, van der Merwe R. Identifying elite families and determining optimum family selection rates in sugarcane breeding. Crop Science.2017;57(5):2525-2537.
16. El-Taib AB,Ebid M. Development and evaluation of the performance of some sugarcane hybrids to detect the elite ones. Assiut J. Agri. Sci.2022;53(1):1-11.
17. Federer WT, Searle SR. Model considerations and variance component estimation in augmented completely randomized and randomized complete blocks designs. Cornell University, Ithaca, New York; 1976.
18. Singh V, Singh K. Identifying potential sugarcane families for cane yield and juice quality traits in early selection stages. Agricultural Research Journal.2021;58(3):390-398.
19. Leite MSDO, Peternelli LA, Barbosa MHP, Cecon PR, Cruz CD. Sample size for full-sib family evaluation in sugarcane. Pesquisa Agropecuária Brasileira.2009;44:1562-1574.
20. Silveir LCID, Brasileiro BP, Kist V, Weber H, Daros E, Peternelli LAet al. Selection in energy cane families. Crop Breeding and Applied Biotechnology.2016;16(4):298-306.
21. Meade CP, Chen JCP. Cane sugar hand book, John Wiley and Sons, Inc. New York; 1977.
22. Somu G, Nagaraja TE. Genetic variability, heritability and genetic advance in first clonal stage of sugarcane. International Journal of Chemical Studies. 2020;8(2):959-963.
23. Khokhar JS, Jamwal NS, Sanghera GS, Singh P. Evaluation of sugarcane (*Saccharum officinarum*) germplasm for quality, yield traits and effects of flowering on cane traits. Indian Journal of Agricultural Sciences.2022;92(7):842-846.
24. Ahmed AO, Obeid A. Investigation on variability, broad sense heritability and genetic advance in sugarcane (*Saccharum* spp). International Journal of Agricultural Sciences.2012;2(9):839-844.
25. Pathy TL,Mohanraj K. Estimating best linear unbiased predictions (BLUP) for yield and quality traits in sugarcane. Sugar Technology.2021;23(6):1295-1305.
26. Sreenivasa V, Amaresh, Aswini Nunavath, Dhanya VG, Abhishek GJ, Mahadevaiah C et al. Evaluation of superior cross combinations and identification of better parental stocks from early clonal trials in sugarcane. Archieves of Current Research International. 2024;24(2):32-38.
27. Simmonds NW. Family selection in plant breeding. Euphytica, 1996;90(2):201-208.

28. Shanthi RM, Bhagyalakshmi KV, Hemaprabha G, Alarmelu S,Nagarajan R. Relative performance of the sugarcane families in early selection stages. Sugar Technology.2008;10(2):114-118.