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RESEARCH ARTICLE

Assessment of promising sugarcane (*Saccharum officinarum* L.) families for enhancement of cane and sugar productivity

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Abstract

Sugarcane is a major source of sugar, facing constant pressure to enhance productivity due to the increased cost of cultivation and fluctuating global market prices. Assessing crosses for clonal development with enhanced productivity is hitherto a proven approach. Selecting the right parent combinations is essential for creating high-yielding progenies. In this context, 33 families (crosses) were evaluated for fluff germination, seedling survival, and productivity traits in the segregating seedling generation. Overall, across diverse crosses, out of 3,020 seedlings, 2,284 survived, with certain crosses showing better performance. A total of 482 clones were selected based on productivity and visual traits of commercial importance compared to the popular check, Co 86032 and were further assessed for cane and sugar productivity traits in the first clonal generation. High heritability was observed for most traits, indicating the effectiveness of selection. Among the clones studied, SNK 191675, SNK 190690 and SNK 191748 showed significantly higher productivity than the popular check, Co 86032. Furthermore, the present study identified promising families, namely, CoVC 14062 × CoT 8201, Thirumadhuram × CoPant 97222, Co 86032 × CoSe 92423, CoVC 14062 × Co 775, MS 68/47 (GC), Co 86011 (GC) and Co 99004 (GC), which showed superior performance in both the seedling and first clonal generations in terms of germination, seedling establishment and the percentage of selectable segregants along with productivity traits. Among these, a few crosses such as CoVC 14062 × CoT 8201, Thirumadhuram × CoPant 97222, ISH 69 (GC), CoVC 14062 (GC) and Co 85002 (GC) also exhibited an acceptable narrow range of variability with significantly superior mean productivity features over commercial popular clonal check, Co 86032. Hence, such crosses are promising not only for clonal varietal development but also for the exploitation of seedlings for direct commercial cultivation.

Keywords: Family selection, fluff germination, acceptable range, CCS yield, selectable segregants

Introduction

Sugarcane (*Saccharum* spp.) is a major commercial crop in the agricultural map of India, providing food, energy and economic security. Globally, sugarcane cultivation and processing sustain nearly 100 million livelihoods, with Brazil and India collectively accounting for 56% of the world's sugarcane production (Chauhan et al. 2022). Sugarcane serves as a raw material for the sugar industry and is used for the production of various co-products such as jaggery, molasses, press mud and wax. The sugarcane crop ranks as the second largest economically viable agro-industry crop, providing approximately 75% of the world's sugar demand, with a significant contribution to the income, employment and foreign revenue for a substantial portion of the population (Priya et al. 2023). Sugarcane is cultivated in most Indian states, primarily in tropical regions like Maharashtra, Karnataka, Gujarat, Madhya Pradesh, Tamil Nadu, Andhra Pradesh, and sub-tropical regions such as Uttar Pradesh, Bihar, Uttarakhand, Haryana, Punjab, covering an area of about 5.15 million hectares, which accounts

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for approximately 2.50% of the gross cropped area. The production capacity exceeds 468.79 million tonnes with a productivity of 83.89 tonnes per hectare (Anonymous 2023).

Crop improvement in sugarcane mainly focuses on enhancing sugar content and biomass yield. Current sugarcane varieties are inter-specific hybrids of *Saccharum officinarum* L. (2n = 80) and *S. 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 (Govindraj and Amalraj 2022). However, challenges such as climatic variability, high cultivation costs and limited genetic diversity hinder sustainable productivity. Developing high sucrose and cane-yielding cultivars is a crucial goal in the sugarcane breeding program (Sanghera and Jamwal 2019a; Perera et al. 2022). However, breeders face numerous challenges, including photo and thermo-sensitivity, high polyploidy, aneuploids, poor fertility, lengthy breeding selection cycles and limited genetic diversity in germplasm (Patil et al. 2015; Dinesh Babu et al. 2022; Hemaprabha et al. 2022). 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, contributing to better recombinant progenies as productive clones after the selection cycle. On the other hand, on account of the recurrent use of commercial clones/popular varieties, some cross combinations among ancestrally related parents exhibit a commercially acceptable range of variability with superior mean values for important productivity features, making them suitable for direct commercial cultivation.

Every year, multiple crosses are produced in sugarcane breeding programs, and a few proven crosses are selected for commercial varietal development based on the performance of the progeny (Ram et al. 2022 and Sreenivasa et al. 2024). In India, the ICAR-Sugarcane Breeding Institute (SBI), Coimbatore, operates a centralized facility for the fluff supply program with the mandate to develop superior sugarcane varieties for cane yield and sucrose content combined with tolerance to biotic and abiotic stresses, suitable for cultivation in tropical, subtropical and coastal India, wherein, bi-parental crosses (BP), selfs, polycrosses (PC) and general collections (GC) are effected using novel and diverse parental clones. To augment the centralized sugarcane breeding activities, the Agricultural Research Stations (ARS), Sankeshwar (Peninsular Zone, lat 16°14′N, long 74°30′E) and Mugad (latitude 15° 26′ 39″ N, longitude 74° 54′ 46″ E) are also effecting PC and GC (open pollinated crosses), These stations have been recording fairly good seed setting, especially from the flowering season of 2010-11 (Patil et al. 2012), particularly when there is rainfall or cloudy weather in the flowering period (Nov-Dec).

After hybridization with parents to obtain high sucrose and cane yield, families must be evaluated to then select individual plants within the best families because selection in families with high genotypic values increases the probability of finding superior clones among the progenies (Kimbeng and Cox 2003; Barbosa et al. 2005; Stringer et al. 2011). Based on this hypothesis, family selection, a proven, short-term, efficient and cost-effective approach, has been routinely applied for isolating superior clones (individual clone selection) derived from well-established commercial parents for varietal development programs (Hogarth 1987; Skinner et al. 1987; Zhou et al. 2013; Patil et al. 2015; Mbuma et al. 2017; El-Taib and Ebid 2022). The identification of promising crosses and the selection of productive segregants from them is a cost-effective and efficient approach. Therefore, the present study was carried out to identify promising families to isolate elite sugarcane clones for various productivity traits in both seedling and first clonal generations, with the goal of accelerating the varietal development programme. Concurrently, with this main objective, the mean performance of families was also compared with popular commercial clones for the possibility of exploiting true seed-based seedlings for direct commercial cultivation.

Materials and methods

Experiment material

A total of 33 crosses (families) were studied, out of which 17crosses were affected at the National Hybridization Garden (NHG), ICAR-SBI, Coimbatore, India, which included 10 BP'sand sevenGC's (open pollinated crosses)during the flowering period (Nov-Dec) in 2019-20. In parallel, the remaining nine GCs were collected at ARS, Sankeshwar, Karnataka, and seven GCs at ARS, Mugad (latitude 15° 26′ 39″ N, longitude 74° 54′ 46″ E), Karnataka during the post-flowering period (Dec-Jan) in 2019-20 cropping season.

Experimental design and generations

The true seeds (fluffs) obtained from crosses (irrespective of the type of cross) during the year 2019-20 were evaluated in the 2020-21 cropping season. These fluffs were sown in a shaded nursery under controlled environmental conditions, with temperatures maintained between 30 to 35°C and high humidity levels between 80 to 85% during the month of May 2020 at ARS, Sankeshwar, Karnataka. Simultaneously, settlings of commercial checks *viz.*, CoC 671, Co 09004, CoSnk 09211, Co 86032, CoSnk 09227 and CoSnk 09293 were raised in seedling trays for comparative analysis. In August 2020, the seedlings and settings (commercial checks) were transplanted into the ground nursery after 45 to 55 days of nursery growth based on seedling vigor. The experiment was set up using an augmented design-II (Federer & Searle, 1976), with a spacing of 1.20 × 0.60 m and a row length of

6.00 m. It was distributed across three blocks, each with 11 families, evaluating a total of 33 families during the 2020-21 cropping season at ARS, Sankeshwar, Karnataka, India. In the ground nursery, each family is represented by 40 random seedlings in a four-row plot, with ten seedlings per row. Additionally, each block included one row with ten seedlings, each of six commercial checks, planted in a consistent order within each block. The remnant seedlings from the 33 crosses were transplanted into the extended blocks of the ground nursery for comparative analysis of germination and seedling establishment parameters (Supplementary Fig. 1).

In a seedling generation, 482 hybrid progenies (clones) were selected based on the cane and juice quality-related traits as well as the overall appearance of the cane type, including features like color, detrashability and clump stand, etc., compared to the popular check, Co 86032. These selected progenies were evaluated for productivity traits during the 2021-22 cropping season at ARS, Sankeshwar, Karnataka, in an augmented design-II (Federer & Searle 1976) with a row spacing of 1.20 m apart. Each genotype was planted with a seed rate of ten eye buds per meter in one row of 3.00 m in length. The selected progenies were distributed across three blocks. Additionally, each block included one row each of eight commercial checks *viz.*, CoC 671, Co 09004, CoSnk 09211, Co 86032, CoSnk 09227, CoSnk 09293, CoSnk 13374 and CoSnk 13436, planted with same seed rate in a consistent order within each block (Supplementary Fig. 1). The crop was cultivated following the recommended package of practices for the region.

Observations recorded

Data was recorded for the number of seedlings germinated per cross (NSG) at 45 days after fluff sowing. The fluff germination percentage (G%) was calculated using a formula consistent with the procedure used in the All India Coordinated Research Project (AICRP) on sugarcane and, as previously reported by Singh and Singh (2021). After transplanting all the germinated seedlings into the ground nursery, each individual progeny was assigned a number and tagged for identification. The number of seedlings that survived per cross (NSE) was recorded at 360 days after transplanting (DAT) and the seedling survival percentage (S%) was calculated using the following formula:

$G\% = ((NSG)/(WFS \times 250)) \times 100$

$S\% = ((NSE)/(NSG)) \times 100$

$PSS\text{-}I = ((NSS) / (NSE)) \times 100$

$PSS\text{-}II = ((NSC) / (NCE)) \times 100$

Additionally, the percentage of selectable segregants per cross in seedling generation (PSS-I) was determined by considering the number of segregants selected per cross (NSS) for advancement at the harvest stage, based on their superiority over the popular checks for productivity traits as well as cane features. Similarly, the percentage of selectable clones per cross in the first clonal generation (PSS-II) was calculated by considering the number of selectable clones per cross (NSC) for advancement to the second clonal generation at harvest. The parentage of all crosses, along with the locations where the fluff was collected (FCL), is listed in Table 1. In the seedling generation, traits such as the number of millable canes per clump (NMC/C) and cane girth (CG) were recorded from all individually tagged progeny populations, along with commercial clonal checks at 360 DAT. For the analysis of juice quality parameters such as Brix%, Pol% and CCS%, ten random progenies (three millable canes per progeny) from each of the 33 families were sampled, following methodologies outlined by Leite et al. (2009); Bajpai et al. (2014); de Moraes et al. (2021) for the number of sampling for juice quality analysis. The average of three millable canes per progeny (clump) was used to determine single cane weight (SCW). The composite juice extracted from three millable canes per progeny was analyzed for Brix% and Pol% using a Brix hygrometer and a Polariscope, respectively. Additionally, CCS% was estimated following the protocol outlined by Meade and Chen (1977). In the settling generation, data were recorded for the number of millable canes per plot (NMC/plot) of each genotype at harvest. Three mother canes from each plot were sampled randomly and their average measurements for CG (cm) and SCW (kg) were recorded. Cane yield (CY) and CCS yield (CCSY) were calculated following the method outlined by Silveira et al. (2016). Similarly, three mother canes of all the checks were assessed from each block at harvest for comparison.

Statistical analysis

The percentage of fluff germination and seedling survivability were statistically analyzed using the formulas mentioned above. Analysis of variance (ANOVA) and estimates of genetic variability parameters for cane and sugar productivity traits were statistically analyzed using the augmentedRCBD package in 'R' software (version R-4.2.1) (https://www.r-project.org/). The data was analyzed to determine the mean performance of families (crosses) in both the seedling and first clonal (settling) generation for important productivity traits. The means of cane and sugar productivity traits of clones were further analyzed and compared with commercial clonal checks at a 5% significance level ($p = 5\%$) using Microsoft Excel.

Results and discussion

Evaluation of seedling generation for germination, survivability and productivity traits

Sugarcane improvement can be accomplished through biparental/poly crosses or by general collections involving desired parents. Identification of promising families is vital to ensure a better frequency of selectable segregants. This is crucial because the process of identifying productive desired segregants and developing a new sugarcane variety involves lengthy selection cycles. The yield potential of these selected clonal varieties mainly depends on the choice of parental combinations. Thus, hybridization among promising parents plays a critical role in creating hybrid clones that can outperform the existing commercial hybrids. In this regard, a total of 33 crosses were produced, resulting in the germination of 3,020 seedlings, out of which 2,306 seedlings survived in field conditions at 360 DAT. The overall germination and survivability of sugarcane seedlings were observed to be 2.10% and 76.36%, respectively. Notably, the Co 85002 GC family recorded the highest fluff germination of 8.1%, followed by CoVC 14062 GC (7.2%) and CoVC 14062 × CoT 8201 (6.3%). Highest seedling survival percentage was noticed in families such as Co 87015 GC (94.4%), followed by MS 68/47 GC (91.1%) and Thirumadhuram × CoPant 97222 (90.8%). Conversely, the lowest survival frequency after transplanting was recorded in ISH 502, GC (47.6%) (Table 1). Similar findings were reported by Sanghera and Jamwal (2019a) and Sudhagar et al. (2023). These true seed germination and subsequent seedling establishment parameters of crosses are of prime importance from the point of view of exploiting them for possible commercial cultivation as seedling populations instead of isolating individual progeny for clonal varietal development.

Across the 33 crosses, 482 hybrid clones were selected during the seedling generation based on their overall appearance of the cane type, including features like color, detrashability, clump stand, flowering, etc., along with their performance either superior to or on par with commercial checks in terms of cane productivity and juice quality traits. In the current study, the overall percentage of selectable segregants was observed to be 20.90%. Among the families studied, MS 68/47 GC (80.49%) recorded the highest percentage of selectable segregants, followed by MS 68/47 × Co 11015 (42.86%) and CoVC 14062 × Co 775 (42.55%) (Table 1). However, out of the 33 families studied, 15 exhibited a population selection of more than 20.0%. The crosses with a higher proportion of selectable seedlings could be an important parameter for the identification of productive families (Kimbeng and Cox, 2003 and Mbuma et al. 2017). In contrast, due to reduced seedling establishment and subsequent vigor compared to clonal checks, low selection rates were observed in families such as CoSnk 03754 GC (6.67%) followed by Co 87015 GC (8.33%) and ISH 536 GC (8.51%) also recorded relatively lower mean values for productivity traits in the seedling generation. These results are consistent with previous studies (Sanghera and Jamwal 2019a; Singh and Singh 2021; Sreenivasa et al. 2024).

For better statistical analysis, only 14 crosses (each with over 40 seedlings) were assessed for tonnage and juice quality parameters, compared to commercial checks. The families need to exhibit mean performance equal to or better than the popular clonal commercial check, Co 86032, to be considered for their possibility of utilizing for direct commercial cultivation. In the context of commercial acceptability attributes, certain families *viz*., NB 94-545 GC, ISH 157 GC, MS 68/47 GC, CoVSI 15122 GC and Co 99004 GC, exhibited high progeny mean performance, with significantly superior over the popularly grown check, Co 86032 in terms of SCW. The crosses *viz*., Co 7201 × ISH 307, Thirumadhuram × CoPant 97222, Co 86032 × Co 86249, ISH 69 (GC) and CoSnk 03707 (GC) recorded superiority over check, Co 86032 for NMC/C (Table 1), another important contributing parameter for cane yield. For juice quality, families *viz.,* CoVC 14062 × Co 775, Co 86032 × CoSe 92423, CoVC 14062 × CoT 8201 and CoC 671 × 85 R 186 exhibited significantly high progeny mean for CCS% of up to 15.0% over the mid-late popular check, Co 86032 (14.32%) (Table 1). These juice quality traits are of prime importance for the sugar industry's acceptance. The Brix value (%) in the juice was highest in the Co 86032 × CoSe 92423 family, where the maternal parent, Co 86032, a proven high-quality mid-late variety, contributed significantly to its progenies. These crosses not only recorded superior mean juice quality parameters but also exhibited highly acceptable cane productivity traits such as NMC/clump, cane girth and single cane weight.

Overall considering the cane and sugar productivity traits, the crosses *viz*., CoVC 14062 × CoT 8201, Thirumadhuram × CoPant 97222, Co 86032 × CoSe 92423, CoVC 14062 × Co 775, MS 68/47 (GC), Co 86011 (GC) and Co 99004 (GC) were shown promise compared to popular check, Co 86032. Though these identified crosses meet the requirements of both seedling nursery production and subsequent commercial cultivation, there is a need for enhancing germination and subsequent seedling establishment parameters for viable economic seedling nursery production of identified crosses, along with confirming their cane and sugar productivity traits performance across seasons and agro-ecologies to realize the benefit of seedling (true seeds) instead of setts/settling cultivation. However, none of the families were superior over the early checks CoC 671 and Co 09004, indicating the need to incorporate more early high-sugar clones as parents to obtain transgressive segregants for early high sugar. The performance of the crosses in this study suggests an increased potential and scope for enhancing cane and sugar productivity in mid-late maturity compared to early maturity with the present deployment of parental clones under study.

Evaluation of first clonal generation for cane and sugar productivity traits

The analysis of the variance of 482 clones derived from 33 crosses, along with eight commercial checks, revealed a

Table 1. Seedling establishment characteristics, mean productivity traits and selection rates of sugarcane families in seedling generation

FC	Crosses (families)	Ground nursery (Seedling generation) harvest @ 360 DAT											
		NSG	NSE	G%	S%	NMC/ clump	CG	SCW	Brix%	Pol%	CCS%	NSS	PSS-I
FCL: NHG, SBI, Coimbatore, 2019-20													
1	Co 7201 × ISH 307	41	32	1.40	78.00	12.0* (3–28)	2.20	0.85	21.97	19.67	13.69	10	31.25
2	MS 68/47 × Co 11015	42	35	1.40	83.30	7.0 (3–13)	2.52	1.46	20.18	18.00	12.50	15	42.86
3	CoVC 14062 × Co 775	66	47	1.60	71.20	9.0 (1–18)	2.40	1.46	23.67*	22.20*	15.78*	20	42.55
4	Co 86032 × CoVC 14061	41	34	1.50	82.90	9.0 (1–22)	2.20	1.09	22.08	20.48	14.48	6	17.65
5	CoVC 14062 × CoT 8201	440	356	6.30	80.90	6.0 (1–21)	2.60*	1.47	23.59*	21.42*	15.01*	90	25.28
6	Thirumadhuram × CoPant 97222	303	275	3.40	84.16	11.0* (1–35)	2.20	1.41	21.88	19.04	13.07	55	20.00
7	NB-94-545 × CoH 70	40	31	1.30	77.50	9.0 (1–18)	2.70*	1.60	16.63	13.36	8.80	9	29.03
8	CoC 671 × 85 R 186	45	31	1.50	68.90	8.0 (2–18)	2.60*	1.84	23.12	21.02*	14.93*	12	38.71
9	Co 86032 × CoSe 92423	82	58	1.30	70.70	10.0 (1–18)	2.40	1.59	24.02*	21.78	15.25*	15	25.86
10	Co 86032 × Co 86249	40	31	1.10	77.50	11.0* (1–27)	2.30	1.56	22.71	20.64	14.46	3	9.68
11	CoVC 14062 (GC)	179	141	7.20	78.80	10.0 (1–31)	2.40	1.74	21.76	19.27	13.34	18	12.77
12	NB 94-545 (GC)	44	35	1.40	79.50	7.0 (1–18)	2.60*	1.94*	19.01	16.68	11.50	6	17.14
13	ISH 69 (GC)	304	199	4.10	65.50	11.0* (1–38)	2.20	1.54	20.54	17.48	11.87	18	9.05
14	CoSnk 03707 (GC)	39	30	0.80	76.90	11.0* (1–25)	2.20	1.40	21.71	18.38	12.45	9	30.00
15	CoSnk 03754 (GC)	91	45	1.30	49.50	10.0 (1–28)	2.10	1.21	21.21	18.33	12.54	3	6.67
16	ISH 157 (GC)	138	107	2.00	77.50	10.0 (1–27)	2.40	1.99*	21.02	18.19	12.45	20	18.70
17	CoN 07072 (GC)	80	43	2.70	53.80	10.0 (1–26)	2.30	1.49	21.92	19.39	13.42	8	18.60
FCL: ARS Sankeshwar, 2019-20													
18	MS 68/47 (GC)	45	41	1.50	86.70	7.0 (1–18)	3.10*	2.08*	18.52	15.77	10.71	33	80.49
19	Co 8371 (GC)	45	32	3.00	71.11	10.0 (2–26)	2.50	1.29	19.92	17.12	11.68	8	25.00
20	Co 85002 (GC)	302	219	8.10	72.50	9.0 (1–25)	2.40	1.77	21.97	19.70	13.72	45	18.72
21	Co 87015 (GC)	36	34	0.60	94.40	6.0 (1–11)	2.50	1.85	21.81	19.50	13.56	4	11.76
22	Co 8213 (GC)	55	37	1.40	67.30	8.0 (3–15)	2.60*	1.83	21.28	18.88	13.08	9	24.32

		NSG	*NSE*	*G%*	*S%*	*NMC/ clump*	*CG*	*SCW*	*Brix%*	*Pol%*	*CCS%*	*NSS*	*PSS-I*
23	ISH 512 (GC)	35	30	1.30	85.70	8.0 (2–14)	2.40	1.47	21.08	18.39	12.64	5	16.67
24	ISH 536 (GC)	55	47	1.20	85.50	9.0 (1–21)	2.20	1.59	21.08	18.81	13.07	4	8.51
25	CoVSI 15122 (GC)	40	36	1.10	90.00	8.0 (1–21)	2.40	1.96*	21.98	19.99	14.01	6	16.67
26	Co 13018 (GC)	40	30	1.10	75.00	7.0 (1–16)	2.40	1.50	22.38	20.77	14.69	6	20.00
FCL: ARS Mugad, 2019-20													
27	Co 86011 (GC)	52	44	3.50	84.60	9.0 (3–18)	2.50	1.43	20.68	18.54	12.91	12	27.27
28	Co 85002 (GC)	59	51	1.50	86.40	8.0 (1–27)	2.50	1.80	22.24	20.06	14.01	5	9.80
29	Co 87015 (GC)	50	36	1.30	72.00	9.0 (3–15)	2.30	1.27	22.47	20.55	14.44	3	8.33
30	Co 99004 (GC)	43	37	2.50	86.00	9.0 (2–28)	2.30	1.99*	22.45	20.45	14.34	13	35.14
31	ISH 502 (GC)	63	30	0.50	47.60	10.0 (3–18)	2.50	1.55	20.09	17.51	12.03	4	13.33
32	CoT 10367 (GC)	42	34	0.50	81.00	7.0 (1–26)	2.10	1.14	22.60	20.44	14.29	4	11.76
33	PI 15131 (GC)	43	38	1.10	88.40	9.0 (2–22)	2.30	1.54	22.64	20.98*	14.73	4	10.53
Total/ Mean		3020	2306	2.10	76.36	9.00	2.39	1.55	21.52	19.17	13.31	482	20.90
SE ±						0.30	0.03	0.05	0.25	0.30	0.51		
Commercial checks (Plants grown withsettlings) harvest @ 360 DAT													
C1	CoC 671					4.0 (3–7)	2.60	1.71	24.85	23.97	17.24		
C2	Co 09004					8.0 (4–17)	2.80	2.14	24.35	23.26	16.66		
C3	CoSnk 09211					5.0 (3–12)	2.40	2.01	21.34	18.22	12.39		
C4	Co 86032					9.0 (5–16)	2.40	1.80	22.85	20.54	14.32		
C5	CoSnk 09227					10.0 (3–15)	2.60	1.69	22.34	20.34	14.26		
C6	CoSnk 09293					7.0 (3–12)	3.10	1.75	22.85	20.78	14.56		
CD @ 5%						2.27	0.19	0.14	0.74	0.44	0.54		

* Significantly superior over popular grown check Co 86032, FCL= Fluff collected locations, NSG = Number of seedlings germinated per cross, NSE = Number of seedlings survived per cross, G% = Fluff germination percentage per cross, S% = Seedling survival percentage per cross, NMC/ clump = number of millable canes per clump, CG = Cane girth (cm), SCW = Single cane weight (kg), Brix% = Brix per cent in juice, Pol% = Sucrose content in juice, CCS% = Commercial cane sugar per cent, NSS = number of selected segregants per cross advancement at the harvest stage, PSS-I = percentage of selected segregants advanced to first clonal generation from ground nursery and GC = General collections

significant mean sum of squares for all traits, considering different sources of variation, including treatment effects (ignoring blocks), genotypes and checks (Table 2). Similarly, the mean square due to checks *v/s* genotypes (varieties) was significant for all the traits except NMC/plot, which indicated that the test entries were Significantly different from the checks. The low standard errors for all traits, except cane yield, suggest that the experimental work was highly precise (Skinner et al. 1987; Kimbeng and Cox 2003). In the case of commercial checks, no adjustments were needed as they were present in all blocks. However, adjustments were required for the test entries because they appeared only once in the experiment. To estimate the error mean square and block effects, repeated checks were used, following the approach outlined by Federer and Searle (1976). However, the adjusted block effects were non-significant for all traits except for cane girth, indicating the homogeneity of the evaluation blocks. Previous studies by Sanghera and Jamwal (2019b); and Somu and Nagaraja (2020) also analyzed using an augmented design, which is proved to be an efficient approach for conducting large-scale sugarcane breeding experiments.

Estimates of genetic variability for the first clonal generation of sugarcane

Various statistical parameters such as mean, standard deviation, coefficient of variation (CV) and genetic variability parameters were calculated to assess the extent of variability within the population of 482 clones selected across 33 families (Table 3). Among the traits studied, the highest CV was observed for cane yield (27.67%). While moderate level of variation was observed for all the traits except for Brix% (8.40%), indicating significant variability in these studied traits. These findings align with results reported by Anna Durai et al. (2015); and Sanghera and Jamwal (2019b). The mean values across families for the number of millable cane per plot, cane girth (cm), single cane weight (kg), Brix%, Pol%, CCS%, cane yield (t/ha) and CCS yield (t/ha) were 29.0, 2.64 cm, 1.85 kg, 21.43, 19.09, and 14.73%; 142.50 and 21.89 t/ha, respectively, were comparable to the popular check Co 86032 (Table 4), indicating enough scope for the selection and advancement of productive clones, leading to the development of varieties with enhanced productivity. The observed ranges for these traits were as follows: 15 to 52 for NMC/ plot, 1.95 to 3.38 cm for cane girth, 1.16 to 2.80 kg for single cane weight, 17.44 to 26.56% for Brix%, 14.53 to 22.63% for Pol%, 10.97 to 17.94% for CCS%, 66.50 to 224.00 t/ha for cane yield and 8.72 to 33.72 t/ha for CCS yield. These results are consistent with those reported by Sudhagar et al. (2023); and Tolera et al. (2023).

The results of the genetic variability analysis showed that the PCV values were higher than their corresponding GCV values for all the studied traits. This suggests that environmental or non-genetic factors influence each trait. Phenotypic variability encompasses both genotypic (heritable) and environmental (non-heritable) variations (Tolera et al. 2023). The lowest values for both GCV and PCV were observed for Brix%, while the highest values were recorded for CCS yield. These findings align with the studies conducted by Kumar et al. (2018) and Somu and Nagaraj (2020). The GCV should be considered along with heritability estimations, as it provides a reliable indication of the amount of heritable variation present. In the current experiment, high heritability estimates were observed for all the traits studied, as classified by Robinson et al. (1949). This implies that simple selection for these traits would be effective. The study revealed that all traits had high heritability estimates, along with high GAM, except for Brix% and Pol%, which had moderate GAM (Table 3). Considering GAM, in addition to heritability, is more informative when selecting the best genotypes (Johnson et al. 1955). These findings are consistent with the results reported by Ahmed and Obeid (2012); and Sanghera and Jamwal (2019b). The maximum GAM was observed for cane yield (51.11%), followed by NMC/ plot (42.65%), indicating potential for substantial improvement in cane productivity through breeding.

Cane and sugar productivity traits in the first clonal generation

The pre-selected clonal population of 482 genotypes exhibited a wide range of cane and sugar productivity traits when compared to the commercial checks. Among the top 25 promising clones listed in Table 5, several were significantly superior to the popularly grown check, Co 86032, in terms of commercially important traits (CCS%, Cane yield and CCS yield). Notably, three of these clones, *viz.,* SNK 190062, SNK 190412, and SNK 192184, recorded significantly higher cane yield compared to the popularly grown check, Co 86032, as well as the best cane-yielding check, Co 09004 (Table 5). These genotypes exhibited a 35 to 40% yield advantage over the popular check, Co 86032, indicating their potential as improved commercial varieties with desirable cane features. Our results are in consensus with findings from previous studies conducted by Abo Elenen et al. (2018), Sanghera and Jamwal (2019a); Khokhar et al. (2022). A similar trend was observed for CCS yield, wherein 12 promising genotypes exhibited 16 to 36% superiority over the best CCS yielding check, Co 09004 (Table 5). Hence, these genotypes hold significant promise as commercial varieties in the region. Among the various juice quality parameters, the sucrose content in juice is a crucial and deciding trait for industrial acceptability. Out of the 25 promising clones, three clones, *viz.,* SNK 190690, SNK 190680 and SNK 190145, exhibited significantly superior sucrose content compared to the best early high sucrose check, CoC 671. However, the cane productivity traits of SNK 190680 were significantly

Table 2. Analysis of variance for cane and sugar productivity traits in first clonal generation of sugarcane

Sources of variation	d.f.	Mean sum of squares							
		NMC/ plot	Cane girth	SCW	Brix%	Pol%	CCS%	CY	CCSY
Treatment (ignoring Blocks)	489	77.49**	0.12**	0.27**	2.87**	3.76**	4.35**	1068.39**	54.25**
Treatment: Check	7	97.88**	0.33**	0.85**	4.54**	3.49**	1.98**	1529.70**	30.55**
Treatment: Genotypes	481	75.56**	0.11**	0.24**	2.60**	3.50**	4.20**	1054.99**	52.20**
Treatment: Genotypes *vs*. Check	1	0.14^{NS}	0.32**	0.05*	49.99**	60.8**	36.8**	493.26*	24.98**
Block (eliminating Treatments)	2	7.87^{NS}	0.05*	0.03^{NS}	0.01^{NS}	0.02^{NS}	0.03^{NS}	76.69^{NS}	3.00^{NS}
Residuals	14	16.26	0.01	0.04	0.2	0.3	0.35	109.08	15.80
Standard Errors (SEd)									
A test treatment and a control treatment		1.84	0.13	0.11	0.56	0.62	0.53	12.79	1.66
Control treatment means		1.23	0.09	0.07	0.37	0.41	0.35	8.53	1.11
Two test treatments (Different Blocks)		2.25	0.16	0.14	0.69	0.75	0.64	15.67	2.03
Two Test Treatments (Same Block)		2.12	0.15	0.13	0.65	0.71	0.61	14.77	1.92
CD @ 5%									
A test treatment and a control treatment		3.95	0.28	0.24	1.2	1.32	1.13	27.43	3.56
Control treatment means		2.63	0.19	0.16	0.80	0.88	0.75	18.29	2.37
Two test treatments (Different Blocks)		4.83	0.34	0.29	1.47	1.62	1.38	33.60	4.36
Two test treatments (Same Block)		4.56	0.32	0.27	1.39	1.52	1.30	31.68	4.11

$^{NS}p > 0.05$; * $p <= 0.05$; ** $p <= 0.01$, d.f.: degrees of freedom, CD: Critical difference
NMC/ plot = Number of millable canes per plot, SCW = Single cane weight (kg), Brix% = Brix *per cent* in juice, Pol% = Sucrose content in juice, CCS% = Commercial cane sugar per cent, CY = Cane yield (t/ha) and CCSY = Commercial cane sugar yield (t/ha)

Table 3. Estimates of genetic variability parameters across different cross combinations for productivity traits in first clonal generation of sugarcane

Traits	NMC/plot	Cane girth (cm)	Single cane weight (kg)	Brix %	Pol %	CCS %	Cane yield (t/ha)	CCS yield (t/ha)
Mean	29.00	2.64	1.85	21.43	19.09	14.73	142.50	21.89
σ^2_p	75.56	0.11	0.24	2.60	3.50	4.20	1054.99	55.20
σ^2_g	59.30	0.10	0.20	2.40	3.20	3.85	945.91	39.40
GCV	26.55	11.98	24.17	7.23	9.37	13.32	21.58	28.67
PCV	29.97	12.56	26.48	7.52	9.80	13.91	22.79	33.94
ECV	13.90	3.79	10.81	2.09	2.87	4.02	7.33	18.16
σ	7.65	0.29	0.40	1.80	2.01	1.60	39.43	5.22
h^2_{BS}	78.48	90.91	83.33	92.31	91.43	91.67	89.66	71.38
GAM	42.65	20.57	37.12	15.97	19.83	20.51	51.11	35.06
CV %	26.38	10.98	21.62	8.40	10.53	10.86	27.67	23.85

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, ECV = Environmental coefficient of variation, σ: Standard deviation, h^2_{BS} = Broad sense heritability (%): GAM = Genetic advance over mean (%), CV = Coefficient of variation, NMC/plo =: Number of millable canes per plot, Brix% = Brix per cent in juice, Pol%: Sucrose content in juice, and CCS% = Commercial cane sugar per cent

Table 4. Cane characteristics and selection rates recorded for sugarcane families in the first clonal generation

FC	Crosses (families)	First clonal trial (Settling generation)										
		NCE	NMC/ plot	CG	SCW	Brix%	Pol%	CCS%	CY	CCSY	NSC	PSS-II
1	Co 7201 × ISH 307	10	36.0*	2.6	1.9	20.1	18.6	13.1	190.0*	24.9*	2	20.0
2	MS 68/47 × Co 11015	15	34.0*	2.7	1.5	21.1	19.9	14.2	141.7	20.1	2	13.3
3	CoVC 14062 × Co 775	20	37.0*	2.5	1.8	20.7	19.2	13.6	185.0*	25.1*	5	25.0
4	Co 86032 × CoVC 14061	6	31.0	2.7	1.7	19.9	18.4	13.0	146.4	19.0	1	16.7
5	CoVC 14062 × CoT 8201	90	32.0	2.8*	2.1*	21.4	20.2	14.4	186.7*	26.8*	35	38.9
6	Thirumadhuram × CoPant 97222	55	32.0	2.8*	2.1*	20.7	19.6	14.0	185.6*	26.1*	15	27.3
7	NB-94-545 × CoH 70	9	21.0	2.8*	2.7*	19.1	17.3	12.1	157.5	19.1	1	11.1
8	CoC 671 × 85 R 186	12	27.0	2.5	2.0*	22.2	20.8	14.8	150.0	22.2	6	50.0
9	Co 86032 × CoSe 92423	15	36.0*	2.3	1.6	23.8*	21.6*	15.1*	160.0	24.2*	7	46.7
10	Co 86032 × Co 86249	3	30.0	2.5	1.4	21.9	20.1	14.1	116.7	16.5	2	66.7
11	CoVC 14062 (GC)	18	28.0	2.6	2.0*	21.7	20.0	14.1	155.6	21.9	7	24.1
12	NB 94-545 (GC)	6	29.0	3.3*	2.0*	19.5	17.3	12.0	161.1	19.3	1	16.7
13	ISH 69 (GC)	18	33.0	2.8*	1.9	20.4	19.9	14.4	174.2*	25.0*	1	5.6
14	CoSnk 03707 (GC)	9	36.0*	2.7	1.4	21.7	20.4	14.5	140.0	20.3	4	44.4
15	CoSnk 03754 (GC)	3	29.0	2.5	1.9	20.9	18.9	13.2	153.1	20.2	1	33.3
16	ISH 157 (GC)	20	29.0	2.7	1.9	21.1	19.4	13.7	153.1	20.9	2	10.0
17	CoN 07072 (GC)	8	36.0*	2.5	1.6	20.9	19.2	13.5	160.0	21.6	1	12.5
18	MS 68/47 (GC)	33	27.0	3.2*	2.3*	19.0	17.6	12.4	172.5*	21.5	9	27.3
19	Co 8371 (GC)	8	27.0	2.7	1.9	20.9	20.1	14.4	142.5	20.6	4	50.0
20	Co 85002 (GC)	45	27.0	2.6	1.9	22.1	21.1	15.1*	142.5	21.5	25	55.6
21	Co 87015 (GC)	4	35.0*	2.5	1.5	22.3	21.5*	15.5*	145.8	22.5	3	75.0

22	Co 8213 (GC)	9	28.0	2.7	2.0*	20.6	18.9	13.3	155.6	20.7	5	55.6
23	ISH 512 (GC)	5	29.0	2.3	1.7	21.9	18.5	12.5	136.9	17.1	1	20.0
24	ISH 536 (GC)	4	28.0	2.6	1.9	20.9	19.3	13.6	147.8	20.1	2	50.0
25	CoVSI 15122 (GC)	6	22.0	2.8*	2.3*	21.0	19.5	13.8	140.6	19.4	4	66.7
26	Co 13018 (GC)	6	22.0	2.7	1.7	24.1*	22.2*	15.7*	103.9	16.3	5	83.3
27	Co 86011 (GC)	12	35.0*	2.7	1.9	21.9	20.4	14.5	184.7*	26.7*	7	58.3
28	Co 85002 (GC)	5	30.0	2.7	1.7	22.3	21.1	15.1*	141.7	21.3	3	60.0
29	Co 87015 (GC)	3	34.0*	2.6	1.6	21.7	20.3	14.4	151.1	21.8	2	66.7
30	Co 99004 (GC)	13	33.0	2.3	1.9	23.6*	20.4	14.0	165.0	23.3*	6	46.2
31	ISH 502 (GC)	4	18.0	2.7	2.3*	21.4	20.1	14.3	115.0	16.4	1	25.0
32	CoT 10367 (GC)	4	21.0	2.7	1.4	18.9	17.3	12.2	81.7	9.9	2	50.0
33	PI 15131 (GC)	4	24.0	2.7	2.1*	20.2	18.2	12.7	140.0	17.8	2	50.0
Total/ Mean		482	29.0	2.6	1.8	21.4	19.1	14.7	142.5	21.9	174	
SE ±			0.5	0.0	0.0	0.1	0.1	0.1	2.2	2.4		
Commercial checks used in the study												
C1	CoC 671		33.0	2.7	1.6	24.6	22.0	15.3	146.7	22.4		
C2	Co 09004		32.0	2.9	1.8	23.4	21.2	14.8	160.0	23.7		
C3	CoSnk 09211		36.0	2.3	1.4	23.6	21.2	14.8	140.0	20.7		
C4	Co 86032		30.0	2.5	1.7	22.6	20.0	13.8	141.7	19.6		
C5	CoSnk 09227		35.0	2.6	1.5	22.4	20.3	14.2	145.8	20.7		
C6	CoSnk 09293		26.0	2.8	1.8	21.9	20.1	14.1	130.0	18.4		
C7	CoSnk 13374		23.0	3.1	2.5	22.9	20.0	13.7	159.7	21.9		
C8	CoSnk 13436		22.0	3.3	2.7	21.1	19.6	13.9	165.0	22.9		
	CD @ 5%		3.9	0.3	0.3	1.2	1.3	1.1	27.4	3.6		

* Significantly superior over popular grown check Co 86032, SE = Standard Error, CD = Critical difference, NCE = number of clones evaluated per cross, NMC/ plot = number of millable canes per plot, CG = Cane girth (cm), SCW = Single cane weight (kg), Brix% = Brix per cent in juice, Pol%: Sucrose content in juice, CCS%: Commercial cane sugar *per cent*, CY: Cane yield (t/ha), CCSY: Commercial cane sugar yield (t/ha), NSC = Number of selectable clones per cross in first clonal trial, PSS-II = percentage of selectable clones advanced to second clonal trial from first clonal trial, and GC= General collections

inferior and the other two clones were significantly superior over Co 86032 in tonnage features.

Among the 482 clones evaluated, four specific clones *viz.,* SNK 191675, SNK 190690, SNK 190145 and SNK 191748, derived from families MS 68/47 × Co 11015, Co 86032 × CoSe 92423, CoVC 14062 × CoT 8201 and MS 68/47 GC, respectively, exhibited significant superiority over the popular check, Co 86032 in terms of cane and sugar productivity traits (Table 5). The mean performance of these families in the seedling and first clonal generation also exhibited promise for commercially important traits, such as cane yield, CCS% and CCS yield. A total of 175 genotypes were selected for advancement to the second clonal generation, exhibiting significant potential for commercial exploitation. However, it is essential to assess their tolerance to major pests and diseases, their ratooning ability in subsequent selection stages and their performance in multi-location trials to ensure their suitability for commercial cultivation. These results clearly depict the importance of family selection in a seedling generation, followed by individual selection in the first clonal generation within the promising sugarcane families.

Comparative analysis of productivity traits in both seedling and first clonal generation of sugarcane

The comparative analysis showed significant variability in productivity traits between the seedling and first clonal generations. While the seedling generation focused on early growth parameters like fluff germination, seedling establishment, and morphological traits, the first clonal generation emphasized traits directly related to cane yield and juice quality. Single cane weight directly influences cane yield. In a comparative analysis of selection strategies in sugarcane, Brasileiro et al. (2016) found that mass selection

Table 5. Mean performances of 25 promising genotypes and their family code for commercially important traits in the first clonal generation of sugarcane

Genotype	FC	NMC/plot	CG (cm)	SCW (kg)	Brix%	Pol%	CCS%	CY (t/ha)	CCSY (t/ha)
SNK 190015	1	27.00	2.95*	2.16*	22.60	20.06	15.53*	162.00	25.16
SNK 191675	2	30.00	2.73	2.22*	24.50*	21.14	16.21*	185.00*	29.99*
SNK 192595	2	35.00*	2.83	1.84	21.04	19.16	14.95	178.89	26.74*
SNK 191273	3	26.00	2.85	2.34*	24.06*	21.36*	16.54*	169.00	27.95*
SNK 190145	5	30.00	2.78	2.10*	23.10	21.44*	16.83*	175.00*	29.45*
SNK 190161	5	34.00*	2.79	1.88	22.60	20.06	15.53*	177.56*	27.57*
SNK 190288	5	34.00*	2.86	1.96	22.60	18.59	14.03	185.11*	25.97
SNK 190548	6	37.00*	2.74	1.85	21.94	17.31	12.86	190.14*	24.45
SNK 190392	6	32.00	2.89	2.15*	21.44	16.89	12.54	191.11*	23.97
SNK 190412	6	33.00	3.03*	2.13*	21.44	16.64	12.29	195.25*	24.00
SNK 190631	7	22.00	3.38*	2.80*	18.94	16.21	12.40	171.11	21.22
SNK 192087	8	28.00	2.85	2.19*	22.94	20.75	16.16*	170.33	27.53*
SNK 190690	9	32.00	2.51	2.02	23.56*	22.62*	17.94*	179.56	32.21*
SNK 190062	9	45.00*	2.66	1.58	21.10	18.04	13.79	197.50*	27.24*
SNK 190680	9	33.00	2.78	1.69	24.56*	22.49*	17.14*	154.92	26.55*
SNK 191748	18	28.00	2.98*	2.31*	22.65	20.20	15.66*	179.67*	28.14*
SNK 191688	18	25.00	2.80	2.67*	24.00*	19.70	14.85	185.42	27.53*
SNK 191829	18	32.00	2.94*	2.05	21.65	18.15	13.79	182.22	25.13
SNK 191724	18	29.00	2.88	2.04	21.49	19.25	14.95	164.33	24.57
SNK 192184	19	30.00	3.18*	2.32*	21.94	19.20	14.80	193.33*	28.61*
SNK 192067	27	30.00	2.77	2.07	23.44*	19.19	14.46	172.50	24.94
SNK 192075	27	30.00	2.93*	1.99	22.44	19.85	15.35*	165.83	25.46
SNK 192054	30	25.00	2.72	2.54*	22.94	20.99	16.41*	176.39	28.95*
SNK 190541	30	32.00	2.51	2.02	23.56*	20.81	16.22*	175.00	28.39*
SNK 192038	30	31.00	2.93*	2.17*	21.94	19.16	14.75	186.86*	27.56*
Mean		29.00	2.64	1.85	21.43	19.09	14.73	142.50	21.89
S.D.		7.65	0.29	0.40	1.80	2.01	1.60	36.43	5.22
Minimum		15.00	1.95	1.16	17.44	14.53	10.97	66.50	8.72
Maximum		52.00	3.38	2.80	24.56	22.63	17.94	224.00	33.72
Commercial checks used in the study									
Co 09004		32.00	2.90	1.80	23.40	21.18	14.81	160.00	23.70
Co 86032		30.00	2.65	1.70	22.20	20.00	13.84	141.67	19.61
CD @ 5%		3.95	0.28	0.34	1.20	1.32	1.13	27.43	3.56
CV		26.38	10.98	21.62	8.40	10.53	10.86	27.67	23.85

*Significantly superior over popular grown check Co 86032 for commercially important traits (CCS%, CY and CCSY), SD: Standard Deviation, CD: Critical difference, CV: Coefficient of variation, FC: Family code, NMC/ plot: Number of millable canes per plot, CG: Cane girth (cm), SCW: Single cane weight (kg), Brix%: Brix *percent* in juice, Pol%: Sucrose content in juice, CCS%: Commercial cane sugar *percent*, CY: Cane yield (t/ha) and CCSY: Commercial cane sugar yield (t/ha) accounted for 38% of individuals within families with averages below the overall mean of the tested population. In contrast, in the present study, this figure was approximately 20%. Conversely, methods focused on selecting families with higher genotypic values are investigated through individual selection (Oliveira et al. 2013). This allows breeders to explore more criteria for the most promising families, enabling the better calculation of selection intensity based on the potential of each family. Therefore, the probability of identifying clones with high genotypic value for a given trait, which is then fixed through vegetative propagation, is high (Barbosa et al. 2004).

Hence, in the case of single cane weight, it directly contributes to cane yield. The present study revealed varying average single cane weights among different crosses and clones in both seedling and first clonal generations. In the seedling generation, single cane weight ranged from 0.85 to 2.08 kg across 33 crosses, with a mean of 1.55 kg. In the first clonal generation, among 482 clones, average single cane weight varied from 1.16 to 2.80 kg, with a mean of 1.85 kg. MS 68/47 (GC), NB 94-545 (GC), and CoVSI 15122 (GC) were significantly superior to the popularly grown check, Co 86032 in both generations for single cane weight. Conversely, the lowest single cane weight was observed in Co 7201 × ISH 307 and CoT 10367 (GC) (Tables 1 and 4). Similarly, cane girth, another important trait linked directly to cane yield, showed variations among different crosses in both generations. In the seedling generation, the average cane girth for the 33 crosses ranged from 1.30 to 4.10 cm, with a mean of 2.39 cm (Table 1 and Fig. 1). In the first clonal generation, cane girth ranged from 1.9 to 3.4 cm, averaging 2.64 cm. Crosses *viz.*, CoVC 14062 × CoT 8201, NB-94-545 × CoH 70, NB 94-545 (GC), and MS 68/47 (GC) significantly outperformed the popularly grown check, Co 86032 in both the generations for cane girth. Conversely, lower cane girth was recorded in CoT 10367 (GC) and ISH 512 (GC) (Tables 1 and 4). Similar trends in results were reported by Abo Elenen et al. (2018); Sanghera and Jamwal (2019a).

In the seedling generation, the average number of millable canes per clump (NMC/C) of 33 crosses ranged from 1.00 to 38.00, with a mean of 9.00. Meanwhile, among the 482 clones in the first clonal generation, the range of the average NMC/ plot varied from 2.00 to 37.00, with a mean of 29.00. The mean performance of NB 94-545 (GC), MS 68/47 (GC), and CoVSI 15122 (GC) was significantly superior to the popularly grown check, Co 86032, in both the seedling and first clonal generation for NMC. Conversely, the lowest millable canes were observed in CoT 10367 (GC), Co 87015 (GC), and Co 86032 × Co 86249 in both generations (Table 1 and Table 4). In terms of sugar productivity traits, the Brix% in the seedling generation ranged from 16.6 to 24.0%, with an average of 21.5%, while in the first clonal generation, it varied from 17.4 to 26.6%, with an average of 21.4% at harvest. The mean performance of the cross, Co 86032 × CoSe 92423, was significantly superior to the popularly grown check, Co 86032, in both the generations for Brix% in juice, while the lower Brix% was observed in crosses *viz.*, NB-94-545 × CoH 70, MS 68/47 (GC) and NB 94-545 (GC) (Tables 1 and 4). The wide range, combined with significantly superior means compared to Co 86032, indicates the presence of a higher frequency of progenies with high Brix values. This enhances the scope for isolating progenies with high juice quality for further advancement. These results are consistent with the findings of Abo Elenen et al. (2018), who reported a Brix% range of 13 to 24% in different cross combinations. Overall, crosses with high mean with a wide range of variability for cane and sugar productivity traits are more promising for the isolation of transgressive segregants for clonal varietal development, while narrower ranges are desired for direct commercial cultivation of seedlings. The probability of identifying such crosses in poly aneuploidy crops such as

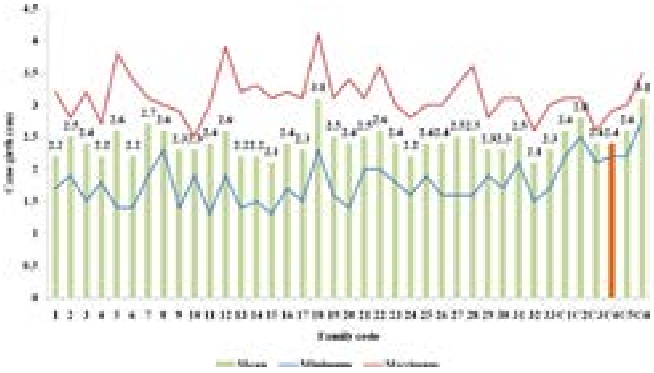

Fig. 1. Mean and range of cane girth for 33 sugarcane crosses in seedling generation

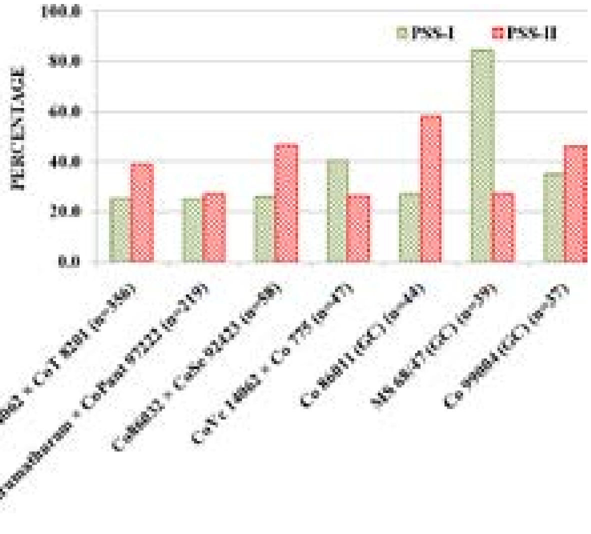

Fig. 2. Selection rates of promising sugarcane families in both seedling and first clonal generation. N = number of seedlings evaluated per cross in seedling generation, GC = General collections (open pollinated crosses), PSS-I = percentage of selected segregants advanced to first clonal generation from seedling generation, PSS-II = percentage of selectable clones advanced to second clonal generation from first clonal generation

sugarcane is rare but can be expected, as most of the proven parental combinations share a common ancestry.

In the current investigation, among the bi-parental crosses, CoVC 14062 × CoT 8201, Co 86032 × CoSe 92423, Thirumadhuram × CoPant 97222 and among the general collections, MS 68/47, Co 86011 and Co 99004 were found to be promising families in terms of fluff germination, survival ability and the percentage of selectable segregants in both seedling and first clonal generation (Tables 1, 2 and Fig. 2). Furthermore, the progenies from these combinations exhibited high mean values and showed a significant yield advantage over the current commercial cultivars. They also showed a good range of variations in yield attributing traits *viz.,* NMC, cane girth, single cane weight, Brix%, Pol% and CCS%. This suggests that these promising parents can be relied upon for the development of economically valuable segregants that combine both cane (tonnage) and sugar productivity (juice quality) traits. Additionally, the general collections of Co 87015 and Co 13018 exhibited significantly superior juice quality parameters over the popular check, Co 86032, with highly acceptable tonnage features (NMC and SCW), leading to high PSS-II, enhancing the scope for isolating high sucrose segregants combining better tonnage much preferred by industry. Overall, these promising parents have the potential to contribute to the creation of new genetic materials for commercial sugarcane cultivation and also for the development of trait-specific improved clones for future improvement programs. Among these families *viz*., CoVC 14062 × CoT 8201, Thirumadhuram × CoPant 97222, ISH 69 (GC), CoVC 14062 (GC) and Co 85002 (GC) could be promising for direct commercial exploitation, as they exhibited a relatively narrower and exploitable range of variability for productivity traits.

Authors' contributions

Designing of the experiments (SBP, MPK); Contribution of experimental materials (SBP); Execution of field/lab experiments and data collection (MPK, SBP); Analysis of data and interpretation (MPK, SBP, NGH, CRP and PVP); Preparation of the manuscript (MPK, SBP, CRP and PVP). All authors made contributions and approved final manuscript.

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