Received: 27 Nov 2024 | Revised: 16 Dec 2024 | Accepted: 19 Dec 2024

Electronic Journal of Plant Breeding

Research Article

Genetic assessment in early clonal population in sugarcane (*Saccharum officinarum* L.) for productivity traits and resistance to foliar diseases

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Abstract
The study evaluated 557 progenies from commercial/near-commercial crosses, along with eight commercial checks, for productivity traits and resistance to foliar diseases in the clonal-I generation at ARS Sankeshwar during the 2022-23 season in an augmented design. The results revealed significant variability within and between families, heritability and genetic advance for all traits. Clones such as SNK 190023, SNK 191722, SNK 190362 and SNK 191801 recorded significantly higher cane yield besides showing high resistance (HR) to foliar diseases such as brown rust, red leaf spot, eye spot, brown spot and *pokkah boeng* in comparison to the checks Co 09004 (early) and Co 86032 (mid-late). Families F3 (CoVC 14062 × Co 775), F5 (CoVC 14062 × CoT 8201), F8 (Thirumadhuram × CoPant 97222), F12 (CoC 671 × 85 R 186), F14 (Co 86032 × CoSe 92423), F15 (CoVC 14062 GC), and F44 (Co 99004 GC) exhibited significant superiority over the check Co 86032 for cane yield, while CoVC 14062 × CoT 8201 and Co 99004 GC showed higher selection rates and high resistance to brown rust (100%), red leaf spot (84%), and Pokkah boeng (70%) suggesting their potential for use in future breeding programs aimed at improving sugarcane productivity and disease resistance.

Keywords: Sugarcane, Flowering behavior, Progeny evaluation, Foliar diseases

INTRODUCTION

Globally, sugarcane cultivation spans approximately 26.08 million hectares, with production of 1922.05 million tonnes and with a productivity of 73.67 tonnes per hectare (Anon. 2022). In India, it thrives in diverse agro-ecological conditions, covering an extensive area of 5.15 million hectares. The country's production amounts to 431.81 million tonnes, boasting a productivity rate of 83.89 tonnes per hectare. Uttar Pradesh, Maharashtra, Karnataka and Tamil Nādu are the leading states in sugarcane production (Anon. 2022). Addressing the challenges arising from population growth and increasing per capita consumption necessitates augmenting sugar production through enhanced productivity (Guddadamath *et al.,* 2014). Such enhancements hold the potential to significantly boost the economic well-being of farmers and stakeholders in the sugarcane sector, ensuring economic security. However, increasing productivity encounters substantial impediments including moderate yield rates, excessive flowering, vulnerability to diseases and pests, lack of consistent, high-performing sugarcane clones adaptable to diverse agro-ecological regions. Historically, developing sugarcane varieties has been crucial for boosting cane productivity. Earlier researchers have showed a negative link between

sucrose content and cane production (Khan *et al*., 2012; Kumar *et al.,* 2018; Patra *et al.,* 2022). Today, the focus is on increasing genetic variability by crossing diverse commercial/near commercial clones as parentages and identifying potential high-yielding clones. This involves crossbreeding multiple parents, evaluating diversity in these crosses, and selecting families capable of producing superior clones.

Commercially cultivated sugarcane varieties are complex polyploids, generating significant genetic variability. It is vital to separate the total variability into heritable and non-heritable components using genetic parameters like phenotypic and genotypic coefficient of variations, heritability estimates, and genetic advance under selection (Singh *et al.,* 2010). Heterosis breeding is an important genetic tool that can be capable of enhancing yields by 30 to 40 percent, while also enriching numerous other desirable qualitative and quantitative traits in crops (Duanmeesuk *et al*., 2021). The degree of standard heterosis serves as a key indicator for assessing genetic diversity and plays a pivotal role in guiding the selection of desirable lines in breeding programs (Ishaq and Olaoye, 2021; Duanmeesuk *et al*., 2021; Alarmelu *et al.,* 2021). The assessment of the nature and magnitude of heterosis for different characters serves to identify potential family combinations for exploitation as clonal varieties. This process aids in isolating transgressive segregants for developing high-yielding varieties.

Sugarcane is susceptible to various diseases caused by fungi, bacteria, viruses, nematodes, and abiotic stresses. Key foliar diseases include brown rust, smut, eye spot, red leaf spot, brown spot, and *pokkah boeng* (Ranjan *et al.,* 2018; Shan *et al.,* 2021). Emerging minor diseases such as *Pokkah boeng*, red leaf spot and brown stripe are becoming significant threat to sugarcane globally, due to expanded cultivation and continuous crop propagation, leading to both qualitative and quantitative losses (Viswanathan and Singh, 2023). Therefore, identifying disease-resistant clones are of paramount important in sugarcane research/ breeding. This study aimed to select genotypes from proven families with superior cane and sugar productivity traits, focusing on assessing standard heterosis and identifying families and progenies with high productivity and resistance to foliar diseases.

MATERIALS AND METHODS

Experimental materials and design: The experimental material comprised 557 pre-selected hybrid sugarcane progenies (First clonal generation) obtained from 48 crosses, comprising 14 biparental crosses (BPs) and 34 general crosses (GCs) along with eight commercial checks *viz*., CoC 671, Co 09004, CoSnk 09211, Co 86032, CoSnk 09227, CoSnk 09293, CoSnk 13374 and CoSnk 13436. The list of crosses with number of pre-selected progenies is presented in **Table 1**. The 48 crosses were effected during the flowering season (Nov-Dec) of 2020-21. Among them, a total of 21 crosses, including 14 bi-parental crosses (BP) and seven general crosses (GC) were effected at the National Hybridization Garden (NHG), ICAR-SBI, Coimbatore, India. In parallel, a total of 27 GC's were collected at ARS, Sankeshwar during the post-flowering period (Dec-Jan) 2020-21. During the month of May, 2021, the collected fluff was sown in a shaded nursery under controlled environmental conditions. The ground nursery experiment was conducted at ARS, Sankeshwar in an augmented design during 2021-22 cropping season and selection of progenies were done on the basis of cane and juice quality-related traits as well as on overall appearance of the cane type, including features such as colour, de-trashability and clump stand, in comparison to popular commercial checks in ground nursery.

The experiment was set up using an Augmented Randomized Block Design (Federer and Searle 1976) with a row spacing of 1.20 m. Pre-selected progenies including checks were planted with a seed rate of ten buds per meter in one row of 3.00 m length. The progenies were distributed across three blocks, wherein, each block included one row each of eight commercial checks in a consistent order. The trial was conducted during 2022-23 cropping season at ARS, Sankeshwar, India following all recommended package of practices.

Data on the agro-morphological and biochemical traits of sugarcane progenies and checks were collected. The agro-morphological traits were counted; including number of millable canes (NMC), stalk diameter (CG) (cm), stalk length (CH) (m) and single cane weight (SCW) (kg) were recorded from all individual genotypes at harvest. For biochemical traits, the composite juice extracted from three millable canes per progeny was analyzed for brix% and sucrose% using a Brix hygrometer and a Polarimeter, respectively. Additionally, CCS% was estimated following the protocol outlined by Meade and Chen (1977). Cane yield (CY) (t/ha) of was estimated by multiplying NMC and SCW. Commercial cane sugar yield (CCSY) (t/ha) was calculated as CCSY = CCS% × CY (t/ha).

Flowering Behaviour Studies: Genotypes were evaluated for flowering intensity and timing by recording the total number of flowering stalks per plot at three stages: early, mid, and late. Based on these observations, the genotypes were classified as follows.

Classification for flowering intensity is as follows

Grade	Flowering intensity %	Classification as per SBI Coimbatore (Patil *et al*., 2015)
4	0	Non Flowering
3	0-30	Shy/ Sparse Flowering
2	30-60	Moderate flowering
1	>60	Profuse flowering

Table 1. List of crosses with number of preselected progenies studied in the present investigation along with commercial checks

Family code	Parentage	NPS*	Family code	Parentage	NPS*
F1	Co 7201 × ISH 307	10	F25	Co 87015 (GC)	4
F2	MS 68/47 × Co 11015	15	F26	Co 06036 (GC)	1
F3	CoVC 14062 × Co 775	20	F27	Co 8213 (GC)	9
F4	Co 86032 × CoVC 14061	6	F28	ISH 512 (GC)	6
F5	CoVC 14062 × CoT 8201	89	F29	ISH 536 (GC)	4
F6	CoC 671 × CoVC 14061	3	F30	ISH 545 (GC)	1
F7	Co 7201 × Co 94008	8	F31	IGH 816 (GC)	3
F8	Thirumadhuram × CoPant 97222	55	F32	CoVSI 15122 (GC)	6
F9	NB 94-545 × CoH 70	10	F33	Co 11015 (GC)	2
F10	Co 2000-10 × Co 89003	2	F34	CoVC 14062 (GC)	1
F11	Co 86032 × CoH 70	2	F35	Co 13018 (GC)	6
F12	CoC 671 × 85 R 186	12	F36	MS 13081 (GC)	3
F13	Co 86032 × Co 86249	2	F37	Co 13014 (GC)	6
F14	Co 86032 × CoSe 92423	14	F38	Co 86011 (GC)	12
F15	CoVC 14062 (GC)	30	F39	CoM 88121 (GC)	3
F16	ISH 69(GC)	19	F40	ISH 69 (GC)	4
F17	CoSnk 03707 (GC)	9	F41	85 R 186 (GC)	1
F18	CoSnk 03754(GC)	1	F42	Co 85002 (GC)	5
F19	CoSnk 03044 (GC)	8	F43	Co 87015 (GC)	2
F20	ISH 69 (GC)	6	F44	Co 99004 (GC)	13
F21	ISH 157 (GC)	22	F45	ISH 545 (GC)	2
F22	MS 68/47 (GC)	36	F46	CoT 10367 (GC)	7
F23	Co 8371 (GC)	8	F47	PI 15131 (GC)	4
F24	Co 85002 (GC)	45	F48	PI 15132 (GC)	20
Commercial standards					
C1	CoC 671	C5	SNK 09227		
C2	Co 09004	C6	SNK 09293		
C3	SNK 09211	C7	SNK 13374		
C4	Co 86032	C8	SNK 13436		

*NPS: Number of progenies studied, GC: General collections (open pollinated crosses)

Classification for time of flowering is as follows

Period of flowering	Classification
November 1st – 4th week	Early
December 1st – 4th week	Mid
January 1st – 4th week	Late

Screening of sugarcane clones for disease reaction: Three plants were randomly selected from each genotype for observations on type of symptoms and disease scoring is done for top, middle and lower leaves and based on mean of these three plants observations, host reaction was estimated. Screening against *Puccinia melanocephala* Syd & P Syd. [brown rust (BR)], *Dimeriella sacchari* Hansford. [red leaf spot (RLS)], *Bipolaris sacchari* E J Butler [eye spot (ES)] and *Cercospora longipes* E J Butler [brown spot (BS)] diseases of sugarcane were done as per guidelines outlined by Mayee and Datar (1988).

$$Disease\ incidence\ (\%) = \frac{Number\ of\ disease\ affected\ canes}{Total\ number\ of\ canes\ assessed} \times 100$$

Disease incidence scale for *pokkah boeng* (PKB) disease was recorded based on method developed by Ranjan *et al.* (2018) as follows.

Score	Reaction category
0% - 10%	Resistant
11% - 20%	Moderately resistant
More than 21%	Susceptible

Disease severity scale of brown rust, red leaf spot, brown spot and eye spot in sugarcane

Scale	Response description	PDI range	Host reaction
0	No visible Symptoms	0	Immune (I)
1	Minute specks on lower one or two leaves covering approximately 1% leaf area	1 to 11	Highly resistant (HR)
2	Specks increase in their size with light colored centre and red to brown margin on lower one or two leaves covering around 5% leaf area	12 to 22	Resistant (R)
3	Specks enlarge into lesions, irregularly shaped may coalesce observed on lower three to four leaves covering around 6%-15% leaf area	23 to 33	Moderately resistant (MR)
4	Enlarged lesions on lower three to four leaves covering around 16%-25% leaf area with sporulation noticed	33 to 55	Moderately susceptible(MS)
5	Lesions enlarged covering large area on each leaf and observed on mid leaves covering around 26%-30% leaf area with sporulation observed		
6	Lesions enlarged covering large area on each leaf and lower one or two leaves drying covering Up to 66 around 31%-40% leaf area with high sporulation		
7	Lesions enlarged and lower three to four leaves drying covering around 41%-45% leaf area with high sporulation	56 to 88	Susceptible(S)
8	Lesions of different sizes observed on all the leaves and middle leaves drying covering around 46%-50% leaf area with high sporulation		
9	All the leaves showing enlarged lesions covering more than 50% of leaf area with heavy sporulation and all the leaves drying	89 to 99	Highly susceptible(HS)

Statistical analysis: Estimates of genetic variability parameters for cane yield and juice quality parameters were statistically analyzed using R software (version R-4.2.1) (www.r-project.org). The means were compared (p=5%) using Microsoft-Excel. The promising genotypes were identified based on their performance in terms of cane and juice quality attributing traits along with flowering and disease reaction.

Standard heterosis: The magnitude of heterosis was studied using information on various cane and juice quality attributing traits. Heterosis expressed as percentage increase or decrease in the mean values of hybrid (F_1) over standard variety (SV) was estimated using the following formula as suggested by Briggle (1963) and Fonseca and Patterson (1968), respectively.

$$Standard\ heterosis\ (SH\%) = \frac{F1 - SV}{SV} \times 100$$

RESULTS AND DISCUSSION

Genetic parameters of selected clones in first clonal generation: The mean, range, genotypic coefficients of variability (GCV), phenotypic coefficients of variability (PCV), heritability (h^2_{BS}) and the genetic advance over mean (GAM) for cane yield and juice quality parameters are shown in **Table 2**. The analysis revealed that PCV values exceeded their corresponding GCV values for all traits, indicating influence of environmental or non-genetic factors in expression of these traits. The lowest values for both GCV and PCV (6.62% & 6.16%) were observed for Purity%, while the highest were recorded for flowering and CCSY (**Table 2**). These results align with the studies by Kumar *et al.* (2018) and Tolera *et al.* (2023). High heritability estimates classified as per Robinson *et al.* (1949), were observed for all traits studied, implying effective selection potential for these traits. Additionally, all traits showed high heritability and GAM, except for cane diameter and Purity% (**Table 2**), indicating preponderance of additive genetic effects in the determination of these traits. Hence, these traits can be improved through simple phenotypic selection. The maximum GAM was observed for NMC/plot, followed by CY, CCSY and SCW, indicating substantial potential for cane productivity improvement through breeding efforts. These findings align with results reported by Delvadia and Patel (2006); Patra *et al.* (2022).

Inter family variability for productivity traits: Among the top 15 families for cane yield compared to the popular check Co 86032, the family Co 86011 GC exhibited the highest variance for cane yield, ranging from 22.83 to 183.00 t/ha, followed by the family CoVSI 15122 GC, while the lowest variance were recorded by CoC 671 × 85 R 186 and Co 86032 × CoSe 92423, respectively (**Table 3**). Variance for CCS yield was highest among the progenies of Co 86011 GC ranging from 4.82 to 39.74 t/ha, followed by Thirumadhuram × CoPant 97222 (**Table 3**). The family CoC 671 × 85R186 recorded the lowest variance value for CCS yield. Similar finding was

Table 2. Estimates of genetic variability parameters along with inter family variance of 48 crosses (families) for various traits

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	h^2_{BS} (%)	GAM (%)	Inter family variance
			Min	Max					
1	Number of millable canes ('000 ha^{-1})	82.64	2.55	266.44	41.81	41.67	99.33	85.67	3.42
2	Single cane weight (kg) at harvest	1.9	1.06	3.44	20.67	20.11	94.71	40.38	4.78
3	Stalk length (m)	2.63	1.85	3.53	11.62	11.43	96.73	23.19	2.11
4	Stalk diameter (cm)	2.66	1.98	3.53	10.57	9.77	85.54	8.65	4.01
5	Harvest index %	91.19	81.63	96.46	2.72	2.57	88.88	14.99	0.91
6	Brix (%) at harvest	21.47	15.46	26.38	8.37	8.09	93.80	19.37	2.12
7	Sucrose (%) at harvest	20.15	13.70	23.97	10.01	9.69	93.85	19.37	2.48
8	Commercial cane sugar (%) @ Harvest	14.72	9.59	17.89	10.88	10.48	92.8	20.83	2.90
9	Juice Purity (%) at harvest	93.74	84.97	98.77	2.93	2.51	73.47	4.44	1.51
10	Cane yield (t/ha) at harvest	146.66	22.83	267.61	22.15	20.97	89.66	40.96	7.16
11	Commercial cane sugar yield (t/ha) at harvest	21.56	3.26	42.08	24.62	23.81	93.49	47.49	6.29

GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, h2BS: Heritability in broad sense, GAM: Genetic advance over mean

Table 3. Family wise mean, range and intra family variance of top fifteen sugarcane families for cane and sugar yielding traits at harvest in first clonal generation

F.C.	NPS	Cane yield (t/ha)				Commercial cane sugar yield (t/ha)			
		Mean	Range		Variance	MEAN	Range		Variance
			Min.	Max.			Min.	Max.	
F8	13	167.54	131.18	267.61	1811.03	34.86	23.10	57.89	110.19
F5	35	164.06	137.44	223.11	532.51	35.10	26.79	46.75	23.76
F7	5	163.72	141.78	193.11	413.18	36.53	31.40	44.67	25.97
F14	7	158.54	142.80	178.04	212.38	35.87	30.32	40.23	15.36
F22	9	157.56	136.24	204.80	671.68	29.83	24.80	39.18	23.64
F15	7	156.87	133.31	215.98	878.98	34.09	26.29	48.18	59.11
F3	4	151.33	141.28	180.53	378.94	31.53	28.22	37.84	18.48
F12	6	148.86	137.76	171.89	155.83	32.90	31.08	37.05	4.45
F27	5	146.09	100.80	171.76	768.85	30.19	21.62	36.82	41.57
F23	4	145.47	100.32	178.72	1136.76	30.93	17.09	36.72	86.92
F24	25	143.37	84.05	244.35	1290.67	31.71	19.62	55.62	71.26
F25	4	141.88	126.47	173.77	492.27	31.54	28.37	37.25	15.48
F32	4	141.85	74.39	190.63	2377.04	29.23	17.05	34.26	67.28
F17	4	141.22	131.17	154.70	131.23	30.49	29.48	32.12	1.34
F38	7	138.94	22.83	183.00	3059.66	30.43	4.82	39.74	143.72
				Commercial checks					
Co 09004		142.43	137.22	148.5	63.62	34.72	34.1	35.54	1.04
Co 86032		135.08	125.04	143.89	177.66	30.55	28.66	32.14	6.06
CD @ 5%		7.16				6.29			
CV		8.29				4.37			

FC: Family code, NPS: Number of progenies selected, CD: Critical difference, CV: Coefficient of variation

reported by Abdelmahmoud *et al.* (2009) for the cross 986140 × Co 1148 for NMC at harvest. Sugarcane, being a polyploidy heterozygous plant, this variability might be arisen due to genetic differences resulting from the act of crossbreeding as well as autogamy.

Among the traits, SCW exhibited the highest inter-family variance. The families Co 86032 × CoH 70 and ISH 157 GC, which recorded the highest variance for SCW, indicated that selection for clones with high single cane weight and cane yield from these families will be effective, and repeating these crosses with higher number of segregating progenies would further enhances variability for cane yield. This variability is an important consideration in sugarcane breeding programs aimed at isolating productive progenies as high-yielding varieties. The highest variance components for sucrose was exhibited by Co 7201 × ISH 307, followed by MS 13081 GC and NB 94-545 × CoH 70, and the lowest variance was recorded by Co 86032 × CoH 70. Results clearly indicated that variations were observed for both quality and yield traits among the families. The families with the highest variance resulted in the progenies with maximum *per se* values for CCS % and single cane weight, the important quality and yield-contributing traits, respectively. Among the heterotic productive clones, namely SNK 191703, SNK 190342, SNK 190356, SNK 192088, SNK 190711, and SNK 192145, were also advanced to the second clonal generation for evaluation. Based on both visual selection and the superior data recorded for cane and sugar productivity parameters, most of the clones that were advanced also exhibited acceptable flowering and other desirable features, including resistance (HR) to foliar diseases (**Table 4**).

Disease Reaction: Out of 557 progenies evaluated, 310 progenies found highly resistant (HR) against multiple foliar diseases such as Brown spot (BS), Red leaf spot (RLS), Brown rust (BR), and Eye spot (ES), as well as *Pokkah boeng* (PKB). The data on disease reactions among the top ten genotypes were observed and presented in **Table 4**. The data on the incidence of Pokkah boeng revealed that among top ten genotypes for cane yield and CCS yield, SNK 191703, SNK 190342, SNK 190356, SNK 192088, SNK 190711, SNK 192145 and SNK 190145 showed resistant reaction (Table 4) while, the genotype SNK 191722 was graded as moderately resistant and genotypes *viz*., SNK 193062 and SNK 191801 were graded as susceptible to PKB disease. The most economic and effective control measure against PKB disease is to select and plant resistance varieties (Huang *et al.,* 2018; Shan *et al.,* 2018).

All the top ten genotypes showed immune reaction for brown spot and brown rust diseases (**Table 4**). The progeny screening was conducted under natural incidence conditions where foliar diseases incidence is regular and not been artificially challenged against the pathogens causing foliar diseases. Under these conditions, the inoculum load for the foliar diseases was sufficient, 44.34% progenies recorded susceptible to highly susceptible reactions. Despite this, some progenies recorded least disease ratings (highly resistant reaction). However, these progenies need to be screened further under artificial high disease pressure conditions in the advanced stages of selection. The study identifies the family CoVC 14062 × CoT 8201, which had more number of progenies showing resistance (HR) to multiple foliar diseases hence; it can be considered as the most promising combination for breeding resistance to multiple foliar diseases in sugarcane.

Identification of proven families and heterotic progenies: Among the 557 genotypes studied, the most promising non-flowering genotypes *viz*., SNK 190023, SNK 191722, SNK 190362, and SNK 191801, showed significantly higher heterotic performances compared to popular checks Co 86032 and Co 09004 for cane and CCS yield, respectively (**Table 5**). Additionally, these genotypes exhibited resistance to foliar diseases (**Table 4**). Overall, these clones emerge as promising genotypes and were advanced for further clonal generation assessments to confirm both tonnage and juice quality features. These findings are consistent with Patil *et al.* (2015) in early clonal generations. Furthermore, the genotypes *viz*., SNK 192088, SNK 190023, SNK 191722, SNK 190362, and SNK 191801 showed higher tonnage and delayed flowering. Among them, SNK 192088 showed moderate flowering, while SNK 191722, SNK 190362, and SNK 191801 exhibited non-flowering characteristics and displayed immunity or resistance against foliar diseases, while, SNK 190362, and SNK 191801 scored susceptibility to *pokkah boeng* disease (**Table 4**). Despite susceptibility to PKB disease, these genotypes performed well in terms of productivity traits. Therefore, these highly productive non-flowering clones should be extensively evaluated before their commercial cultivation in a protective/PKB-free environment. Furthermore, flowering clones could be suitably exploited as parents to combine productivity with PKB resistance, while the genotype, SNK 191722 exhibit potential for productivity traits with disease resistance and non/shy flowering.

In present study, although many genotypes showed positive heterosis for cane and sugar yield over the commercial checks, Co 86032 and Co 09004, but the number of genotypes showing the significant superiority over checks is relatively less especially for commercial cane sugar percentage. This indicates the need for the inclusion of more number of high juice quality parents in the hybridization program (**Table 5**). The clones which were significantly superior over checks for cane yield and sugar yield were identified and compared. The families F8 (Thirumadhuram × CoPant 97222), F12 (CoC 671 × 85R186), and F15 (CoVC 14062 GC) were found to be the most promising, as they recorded higher frequencies of heterotic progenies over the commercial check Co 86032, both for CCS% and cane/sugar yield. Meanwhile,

Table 4. Performance of top ten progenies of first clonal generation for cane and sugar yield traits along with flowering and disease reactions

S. No.	F.C.	Genotypes	CY	CCSY	CCS%	Brix%	Pol%	CG	SCW	F. I.	Disease reaction				
											BS	RLS	BR	ES	PKB
1	F8	SNK 191703	160.23*	27.6*	17.24*	24.77*	23.50*	2.71*	1.98*	1	I	I	I	I	R
2	F8	SNK 191722	170.47*	28.28*	16.60*	23.77*	22.60*	2.60	1.85*	**4**	I	I	I	I	MR
3	F12	SNK 190342	188.44*	30.09*	15.95*	23.58*	21.93	2.83*	2.18*	1	I	HR	I	I	R
4	F15	SNK 190356	153.86*	24.97*	16.20*	23.58*	22.17*	2.25	1.29	1	I	R	I	I	R
5	F56	SNK 192088	217.84*	35.91*	16.49*	23.42	22.40*	2.80*	2.06*	2	I	HR	I	I	R
6	F25	SNK 190711	172.42*	28.81*	16.71*	23.38	22.59*	2.14	1.84*	1	I	I	I	I	R
7	F15	SNK 190362	193.11*	30.73*	15.90*	23.08	21.74	2.78*	1.76*	**4**	I	HR	I	I	S
8	F2	SNK 192145	173.35*	27.63*	15.94*	22.92	21.73	2.56	2.58*	2	I	I	I	I	R
9	F8	SNK 191801	162.80*	27.16*	16.70*	22.92	22.45*	2.96*	2.53*	**4**	I	R	I	HR	S
10	F12	SNK 190145	170.29*	27.28*	16.00*	22.89	21.78	2.84*	2.24*	1	I	HR	I	I	R
Commercial checks															
C1		CoC671	100.72	17.17	17.06	24.64	23.29	2.67	1.56	1	I	R	I	I	R
C2		Co 09004	142.43	24.41	17.13	24.39	23.28	2.86	1.82	3	I	HR	I	I	R
C3		SNK09211	139.43	22.87	16.41	23.64	22.38	2.33	1.37	4	I	R	I	I	R
C4		Co 86032	135.08	20.08	14.90	22.63	20.66	2.48	1.44	4	I	I	I	I	R
C5		SNK 09227	141.11	22.22	15.78	22.38	21.42	2.6	1.44	4	I	MS	I	I	R
C6		SNK09293	131.25	20.63	15.72	21.88	21.22	2.79	1.80	2	I	HR	I	I	R
C7		SNK 13374	169.30	26.15	15.45	22.92	21.26	3.19	2.57	4	I	I	I	I	R
C8		SNK 13436	172.84	26.54	15.37	21.05	20.65	3.30	2.75	4	I	I	I	I	R
		CD @ 5%	18.29	2.37	0.75	0.80	0.88	0.19	0.16						
		CV	6.82	6.79	3.12	1.19	2.38	4.23	4.03						

*Significantly superior over popular check Co 86032, CY- cane yield, CCSY- commercial cane sugar yield, CCS- commercial cane sugar, CG – cane diameter, SCW- Single cane weight, FI – flowering intensity, BS- Brown spot, RLS- Red leaf spot, BR – Brown rust, ES- Eye spot, PKB- *pokkah boeng*, I – Immune, HR – Highly resistant, MR – Mild resistant, R – Resistant, S – Susceptible, CD: Critical difference, CV: Coefficient of variation

the families F2 (MS 68/47 × Co 11015) and F25 (Co 87015 GC) exhibited superiority in cane/sugar yield and also showed promise for improving juice quality parameters. High and low positive heterosis observed was mainly due to varying genetic composition between parents of different crosses for the component traits (Rajesh and Gulsan, 2001).

Among the families studied, F44 (Co 99004 GC) showed the highest percentage (38%) of progeny advancement rate followed by F31 (IGH 816 GC) and F36 (MS 13081 GC) in first clonal generation (**Fig. 1**), indicating their potential for isolating productive progenies for clonal generations. The families *viz*., Co 85002 GC, Co 99004 GC, and MS 68/47 GC emerged as the promising families for generating variation, particularly for selecting elite genotypes with improved single cane weight. Furthermore, genetic improvement for selecting clones with a high number of millable canes can be achieved with families PI 15132 GC, Co 7201 × ISH 307, Co 86032 × CoSe 92423, and Thirumadhuram × CoPant 97222, while families Co 86032 × CoSe 92423, Thirumadhuram × CoPant 97222, and MS 68/47 × Co 11015 are optimal combinations for higher percentages of clones exhibiting high cane yield.

For juice quality traits, families such as CoC 671 × 85 R 186, Co 86011 GC, and Co 86032 × CoSe 92423, CoVC 14062 × CoT 8201, MS 68/47 GC, Co 99004 GC, and Co 85002 GC were adjudged as the best families compared to other families where as family F8 (Thirumadhuram × CoPant 97222) showed higher variance indicating presence of higher amount of variability for juice quality traits. Nonetheless, in comparison to the popular high quality early checks CoC 671 (23.29%) and Co 09004 (23.28%), the mean sucrose % recorded in these families are 13.44% lower and these results indicate less scope for improving sucrose content over best checks with these parental combinations and need for inclusion of high sucrose clones of diverse sources for hybridization. However, there is good scope for identifying progenies over Co 86032 in terms of both cane yield and juice quality

Table 5. Heterotic performance of selected progenies over standard checks for cane and CCS yields

S. No.	F.C.	Genotypes	Cane yield (t/ha)			CCS yield (t/ha)		
			Mean value	SH % over Co 86032	SH% over Co 09004	Mean value	SH % over Co 86032	SH% over Co 09004
1	F12	SNK 190145	170.29**	25.74	19.56	27.28**	35.86	11.76
2	F12	SNK 190201	218.92**	61.65	53.704	29.94**	49.1	22.65
3	F12	SNK 190288	193.18**	42.64	35.632	31.32**	55.98	28.31
4	F12	SNK 190327	138.66	2.38	-2.647	22.52	12.15	-7.74
5	F15	SNK 190356	153.86	13.61	8.025	24.97	24.35	2.29
6	F17	SNK 190541	131.18	-3.14	-7.899	21.32	6.18	-12.66
7	F17	SNK 190549	139.81	3.23	-1.84	21.86	8.86	-10.45
8	F17	SNK 190620	232.73**	71.85	63.4	37.66**	87.55	54.28
9	F23	SNK 190667	146.65	8.28	2.963	21.54	7.27	-11.76
10	F25	SNK 190690	142.8	5.44	0.26	23.84	18.73	-2.34
11	F25	SNK 190691	178.04**	31.46	25.002	25.62	27.59	4.96
12	F31	SNK 190913	215.98**	59.48	51.639	33.69**	67.78	38.02
13	F31	SNK 190914	173.76	28.3	21.997	27.61**	37.5	13.11
14	F36	SNK 191273	157.49	16.29	10.574	21.73	8.22	-10.98
15	F8	SNK 191703	160.23**	18.31	12.497	27.6**	37.45	13.07
16	F8	SNK 191722	170.47**	25.87	19.687	28.28**	40.84	15.85
17	F8	SNK 191723	146.47	8.15	2.836	26.16	30.28	7.17
18	F8	SNK 191762	113.63	-16.1	-20.22	18.16	-9.56	-25.6
19	F8	SNK 191768	244.35**	80.43	71.558	39.06**	94.52	60.02
20	F8	SNK 191810	174.58**	28.91	22.572	21.73	8.22	-10.98
21	F8	SNK 191829	119.58	-11.7	-16.043	19.29	-3.93	-20.98
22	F10	SNK 191869	127.06	-6.18	-10.791	20.94	4.28	-14.22
23	F56	SNK 192088	217.84**	60.85	52.945	35.91**	78.83	47.11
24	F2	SNK 192152	175.8**	29.81	23.429	23.41	16.58	-4.1
25	F2	SNK 192153	183**	35.13	28.484	26.02	29.58	6.6
26	F17	SNK 192319	122.8	-9.33	-13.782	18.8	-6.37	-22.98
Overall mean			**146.66**			**21.56**		
Range			22.83-267.61			3.26-42.08		
Commercial checks								
Co 86032			135.08			20.08		
Co 09004			142.43			24.41		
CD @ 5%			8.29			4.37		
CV			7.16			6.29		

FC: Family code, CCS: Commercial cane sugar, CD: Critical difference, CV: Coefficient of variation, SH: Standard heterosis

traits. Regarding CCS yield, families like Co 85002 GC, Co 86011 GC, CoC 671 × 85 R 186, Co 86032 × CoSe 92423, Thirumadhuram × CoPant 97222, and CoVC 14062 × CoT 8201 are ideal for generating variation to select elite genotypes for enhanced CCS yield.

The study evaluated pre-selected first clonal generation progenies for their flowering behavior, cane and sugar yield along with disease reaction. Several crosses, such as CoVC 14062 × CoT 8201 and Co 99004 GC showed promising results, producing transgressive segregants with desirable traits like non-flowering behavior, resistant to foliar diseases coupled with high cane and sugar yields. Out of 557 genotypes studied, 58 were found significantly productive over the check Co 86032 in terms of cane and sugar yield. Notably, SNK 190023, SNK 191722, SNK 190362 and SNK 191801 exhibited non-flowering with highly resistance (HR) to diseases scored. Among the top productive progenies, SNK 192088, SNK 191639 and SNK 190620 showed significantly higher heterotic

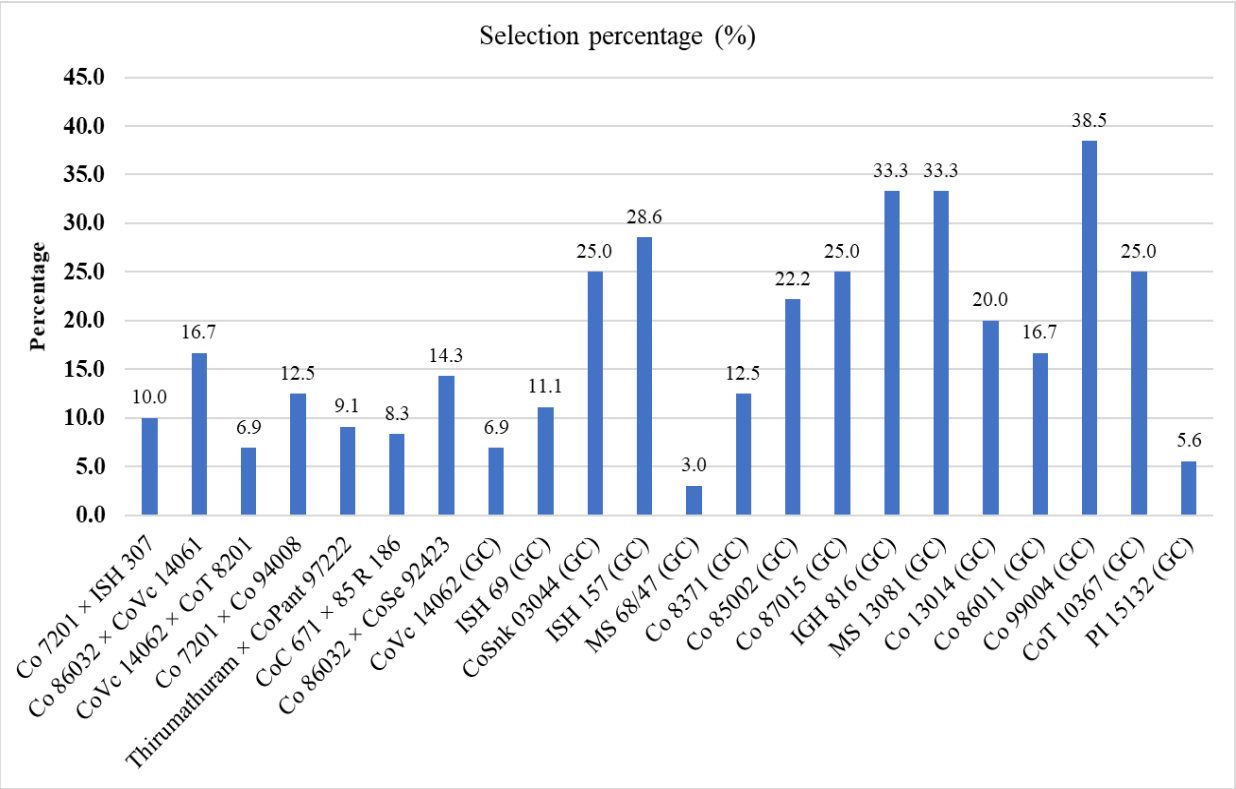

Fig. 1. Family-wise (BP, PC & GC) number of clones advanced to clonal II from clonal I generation of sugarcane

performances over checks Co 09004 and Co 86032 for cane and sugar yield, along with their shy/non-flowering features.

ACKNOWLEDGMENT

The authors extend sincere thanks to the University of Agricultural Sciences, Dharwad and ARS, Sankeshwar, for their unwavering support and encouragement in facilitating this research work.

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