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Identification of Promising Sugarcane Clones Based on Cane Yield and Quality Traits in First Clonal Selection Stage

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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. Identification of productive hybrid progenies for varietal development plays a crucial role in enhancing productivity, which is a cost-effective approach. In this context, an investigation was conducted to identify promising clones for cane yield and quality traits. Significantly higher estimates of genetic variability, heritability and genetic advance were evident for all the traits except cane girth, Brix per cent in juice and sucrose content in juice. Correlation and path analysis revealed that the traits such as the number of millable canes per plot, single cane weight, sucrose content in juice and commercial cane sugar yield showed a significant positive association with cane yield. Among the 150 hybrid progenies studied, the clones SNK 180011, SNK 180028, SNK 180070, SNK 180662 and SNK 181126 are the most promising clones with high cane yield and sugar productivity features. These results hold significant importance for identifying promising clones to enhance cane and sugar productivity.

Keywords: Augmented design, Cane yield, Promising clones, Sugarcane

1. INTRODUCTION

Sugarcane is a perennial, multipurpose crop that provides food, energy and economic security to the farmers. One of its distinctive and valuable characteristics is the high concentration of sugar accumulation in the internodes, making it a key crop for sugar production. Globally, sugarcane is responsible for nearly 75% raw table sugar production. India occupies the second position with sugarcane production of 431.81 million tonnes after Brazil with a productivity of 83.89 tonnes per hectare. Sugarcane cultivation is widespread across most Indian states, primarily in tropical regions like Karnataka, Tamil Nadu, Maharashtra, Andhra Pradesh, Gujarat, Madhya Pradesh and sub-tropical regions such as Uttar Pradesh, Uttarakhand, Haryana, Punjab and Bihar. Among these states, Uttar Pradesh leads with an area of 2.18 million hectares and a production of 177.43 million tonnes, followed by Maharashtra and Karnataka during the 2021-22 (Mallikarjun and Patil, 2023).

In sugarcane varietal improvement, the primary goal of breeders is to identify potential sugarcane clones with high yield and sugar content by screening existing germplasm and breeding materials. 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 per cent (CCS%), cane yield and commercial cane sugar yield among cultivated varieties and species clones (Govindaraj and Amalraj, 2022). Sustainable sugar productivity becomes a major concern due to adverse climatic conditions and the increasing cost of sugarcane cultivation. The cane industry demands high sugar producing varieties with other desirable agronomic traits (Pal et al., 2021). However, breeders face numerous challenges, including 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 recombinants and promising clones after the selection cycle (Creste et al., 2010). The screening of a large number of clones in replicated trails is highly laborious and resource demanding, which is practically not feasible. Typically, the seed of new entries are not enough for conducting replicated trials. In such conditions, the augmented design-II could be better option. It saves time and money without compromising on the precision of critical comparisons among treatments (Federer, 1956; Cyrilus et al., 2014).

The knowledge of trait associations in the breeding programme is essential for number of reasons. It enables the breeders to better understand genetic diversity in the breeding material by identifying traits with little or no breeding value (Kumar et al., 2018). The major challenge in sugarcane breeding is the use of yield per se as selection criteria for crop improvement, which is difficult due to the complexity of its nature as well as low heritability. As a result, realised gains for yield have not been very encouraging by direct selection for cane yield (Sanghera and Jamwal, 2019). Therefore, the great emphasis across all breeding programmes is to study the nature of relationships and trait associations between yield and other traits which are relatively less complex and have comparatively better heritability for use as indirect selection criteria for seeking improvement in yield (Sabitha et al., 2007). The success of a sugarcane breeding program highly depends on these genetic aspects, which rely partly on the recognition of several characters considered important in the selection. The identification of promising and productive segregants from diverse clones of sugarcane derived from different crosses is a cost effective and efficient approach. Therefore, the present study aims to identify promising sugarcane clones for various cane yield and its component traits in first clonal generations, with the goal of accelerating the varietal development programme.

2. MATERIALS AND METHODS

2.1 Planting material and Experimental design

The experimental material for the present study consisted of 150 diverse clones of sugarcane derived from twenty different crosses. These clones were selected in the seedling generation based on the productivity traits and the overall appearance of the cane type, including features like colour, detrashability and clump stand etc., compared to the popular commercial standards, during the 2020-21 cropping season and advanced to the first clonal generation. During the 2021-22 cropping season, the selected progenies underwent evaluation for cane yield and its component traits at the University of Agricultural Sciences, Dharwad, and the Agricultural Research Station, Sankeshwar (Peninsular Zone, 16°14′N/74°30′E), India in an augmented design-II (Federer and Searle, 1976), with a row spacing of 1.20 m apart. Each genotype was planted with seed rate of ten eye buds per meter in one row of 3.00 m length. The selected progenies were distributed across three blocks, and each blocks included 13 commercial checks, such as CoC 671, Co 09004, SNK 09211, Co 86032, Co 09232, SNK 09227, Co 09268, Co 088789, Co 07680, Co 08005, CoM 0265, SNK 09293 and MS 13081. The crop cultivation followed the recommended package of practices for the region. The details of the sugarcane clones derived from 20 different crosses in seedling nursery and checks are furnished in Table 1.

Table 1: List of number of selected clones from different cross combinations used under study with their parentage in the first clonal stage of sugarcane

Sl. No.	FC	Family name (Parentage)	NSE	NCS
1	**18F01**	CoVC 14062 × Co 89003	38	3
2	**18F02**	Co 86032 × CoVC 14061	117	37
3	**18F03**	CoH 119 × CoC 8001	1	1
4	**18F04**	Co 2000-10 × CoVC 14061	3	1
5	**18F08**	ISH 100 (GC)	4	1
6	**18F09**	CoM 6806 (GC)	389	25
7	**18F10**	Co 98006 (GC)	29	2
8	**18F11**	Co 99004 (GC)	63	3
9	**18F12**	CoJn 862072 (GC)	70	3
10	**18F14**	CoVC 14062 (GC)	257	19
11	**18F15**	CoC 90063 (PC)	2	1
12	**18F18**	Co 8371 (PC)	64	6
13	**18F19**	ISH 20 (GC)	25	3
14	**18F20**	Co 06034 (GC)	25	1
15	**18F24**	CP 52-1 (GC)	2	1
16	**18F26**	CoSnk 03632 (GC)	29	1
17	**18F27**	Co 11015 (GC)	118	21
18	**18F41**	Co 87015 (GC)	198	19
19	**18F42**	Co 95021 (GC)	28	1
20	**18F44**	SNK 049 (GC)	55	1
Total			**1517**	**150**

FC: Family code, NSE: Number of seedlings evaluated in seedling generation, NCE: Number of clones evaluated in clonal-I generation, PC: Poly cross, GC: General Collection (open pollinated cross)

2.2 Observations recorded

Data were recorded for the number of millable canes per plot (NMC/ plot) of each genotype at harvest. From each plot, three mother canes were randomly sampled, and their average measurements for cane girth (cm), millable cane height (cm) and single cane weight (kg) were recorded. Following the cane crushing process, juice was collected separately from each genotype and analysed for Brix per cent in juice (Brix%) and sucrose content in juice (Pol%) using a Brix hygrometer and a polariscope, respectively. The commercial cane sugar per cent (CCS%) was worked out from Pol% and Brix%, as per Meade and Chen (1977). Cane yield (CY) and commercial cane sugar 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.

2.3 Statistical analysis

The data were statistically analyzed, including analysis of variance (ANOVA), estimates of genetic variability parameters and the correlation coefficient matrix for cane yield and its component traits were statistically analyzed using the augmentedRCBD package in ‘R’ software (version R-4.2.1). Path coefficient analysis among the 150 clones of sugarcane was employed to determine the direct and indirect effects of different cane yield and its contributing traits using OPSTAT software. Further, mean values of different traits were compared with commercial standards at a 5% significance level (p=5%) using Microsoft Excel.

3. RESULTS AND DISCUSSION

3.1 Analysis of variance

The analysis of variance revealed significant mean sum of squares for all traits across different sources of variation. The block effect (ignoring treatments) and the treatment effects (ignoring as well as eliminating blocks) were significant for all traits except for single cane weight (Table 2). Similarly, the effects due to checks and varieties were also significant for all traits. However, the block effects (eliminating treatments) were non-significant for all traits, indicating homogeneity of evaluation blocks. Similarly, the mean square due to checks v/s varieties was significant for all traits, indicating that the test entries were significantly different from checks. This effect has been widely studied by Sanghera and Jamwal, (2019); Somu and Nagaraj (2020); Khokhar et al., (2022), and it was reported that the augmented design is efficient in conducting large-scale sugarcane breeding experiments.

In the present study, 150 hybrid progenies along with 13 commercial standards were evaluated in an augmented design-II for cane yield and its component traits in first clonal generation. The mean values of number of millable canes per plot, cane girth (cm), millable cane height (cm), single cane weight, Brix%, Pol%, CCS%, CCS yield and cane yield were 28.85, 2.52 cm, 293.00 cm, 1.63 kg, 22.61%, 20.36%, 14.59%, 18.71 t/ha and 129.00 t/ha, with their respective range lied between 7.96 to 56.96, 1.97 to 3.44 cm, 195.53 to 369.27 cm, 0.72 to 2.74 kg, 17.58 to 26.06%, 13.45 to 24.09%, 9.09 to 17.79%, 4.46 to 32.78 t/ha and 33.13 to 226.63 t/ha (Table 3). To decipher the amount of existing variability in the present clones, range, mean, standard deviation, standard error and coefficient variation (CV) were calculated (Table 3). However, range is the crude method of estimation of variability, which indicates observed phenotypic variability only. It also showed the advisable range of co-efficient of variation for all the traits. Among the traits studied, the highest co-efficient of variation was observed for CCS yield (30.11%) and cane yield (29.15%). While low level of variation was observed for cane girth (8.10%), Brix% (5.84%) and Pol% (8.87%). The results are in accordance with the findings of Anna Durai et al., (2015); Somu and Nagaraj (2020).

Table 2: Analysis of variance for different cane yield and its component traits in first clonal generation of sugarcane

Source of variance	**Treatment (ignoring Blocks)**	**Treatment: Check**	**Treatment: Clones**	**Treatment: Clones vs. Check**	**Block (eliminating Treatments)**	**Error**	**Block (ignoring Treatments)**	**Treatment (eliminating Blocks)**	**Treatment: Check**	**Treatment: Test and Test vs. Check**	**Error**
d.f.	162	12	149	1	2	24	2	162	12	150	24
NMC/ plot	66.43**	83.76**	65.22**	38.54**	0.02^{NS}	1.91	430.87**	61.11**	83.76**	59.30**	1.91
CG (cm)	0.07**	0.15**	0.06**	0.31**	0.01^{NS}	0.01	0.11**	0.07**	0.15**	0.06**	0.01
CH (cm)	1798.37**	2860.02**	1260.32**	69228.43**	252.73^{NS}	91.05	1488.16**	1783.12**	2860.02**	1696.97**	91.05
SCW (kg)	0.13**	0.24**	0.12**	0.20*	0.10^{NS}	0.03	0.03^{NS}	0.13**	0.24**	0.12**	0.03
Brix %	2.51**	7.51**	2.06**	9.79**	0.47^{NS}	0.15	5.93**	2.44**	7.50**	2.04**	0.15
Pol %	3.71**	4.88**	3.62**	2.64**	0.17^{NS}	0.17	28.63**	3.36**	4.88**	3.23**	0.17
CCS %	2.55**	3.55**	2.49**	0.63**	0.03^{NS}	0.05	24.87**	2.25**	3.55**	2.14**	0.05
CY (t/ha)	1722.87**	3638.93**	1564.85**	2274.55**	7.25^{NS}	80.32	6617.61**	1641.26**	3638.93**	1481.44**	80.32
CCSY (t/ha)	38.62**	105.36**	33.31**	28.58**	1.01^{NS}	0.79	23.42**	38.34**	105.36**	32.98**	0.79

^{NS} P > 0.05; * P < = 0.05; ** P < = 0.01

NMC/ plot – Number of millable canes / plot, CH – Millable cane height (cm), CG – Cane girth (cm), SCW – Average single cane weight (kg), CB – Brix per cent (%), CP – Sucrose content (Pol%), CCS% – Commercial cane sugar per cent (%), CY - Cane yield (t/ha), CCSY - Commercial cane sugar yield (t/ha), d.f. – degrees of freedom

Table 3: Descriptive statistics of cane yield traits in 150 sugarcane clones at the first clonal stage

Variables	Mean	Std. Deviation	Min.	Max.	Std. Error	CV (%)
NMC/ plot	28.85	7.86	7.96	56.96	0.64	27.24
CG (cm)	2.52	0.20	1.97	3.44	0.02	8.10
CH (cm)	293.00	32.81	195.53	369.27	2.68	11.20
SCW (kg)	1.63	0.27	0.72	2.74	0.02	16.74
Brix%	22.61	1.32	17.58	26.06	0.11	5.84
Pol %	20.36	1.81	13.45	24.09	0.15	8.87
CCS %	14.59	1.53	9.09	17.79	0.13	10.47
CY (t/ha)	18.71	5.63	4.46	32.78	0.46	30.11
CCSY (t/ha)	129.00	37.60	33.13	226.63	3.07	29.15

NMC/ plot – Number of millable canes / plot, CH – Millable cane height (cm), CG – Cane girth (cm), SCW – Single cane weight (kg), CB – Brix per cent (%), CP – Sucrose content (Pol%), CCS% – Commercial cane sugar per cent (%), CY - Cane yield (t/ha), CCSY - Commercial cane sugar yield (t/ha)

Table 4: Estimates of genetic variability parameters for cane yield and its components traits in first clonal generation of sugarcane

Trait	Mean	σ^2_p	σ^2_g	σ^2_e	GCV	PCV	h^2_{BS}	GAM
NMC/ plot	28.76	65.22	63.31	1.91	27.67	28.08	97.07	56.24
CG (cm)	2.53	0.06	0.05	0.01	8.95	9.93	81.15	16.63
CH (cm)	289.23	1260.32	1169.27	91.05	11.82	12.27	92.78	23.49
SCW (kg)	1.62	0.12	0.09	0.03	18.83	21.60	75.99	33.86
Brix%	22.56	2.06	1.92	0.15	6.13	6.36	92.92	12.20
Pol %	20.33	3.62	3.45	0.17	9.13	9.36	95.30	18.40
CCS %	14.58	2.49	2.43	0.05	10.70	10.82	97.79	21.82
CY (t/ha)	128.31	1413.73	1333.42	80.32	28.46	29.30	94.87	57.02
CCSY (t/ha)	18.63	31.71	30.93	0.79	29.05	30.23	97.64	60.81

NMC: Number of millable canes per plot, CG: Cane girth, CH: Millable cane height, SCW: Single cane weight, Brix%: Brix per cent, Pol%: Sucrose per cent in juice, CCS%: Commercial cane sugar per cent, CY: Cane yield, CCSY: Commercial cane sugar yield, σ^2_P: Phenotypic variance, σ^2_g: Genotypic variance, σ^2_e: Environmental variance, GCV: Genotypic coefficient of variation (%), PCV: Phenotypic coefficient of variation (%), h^2_{BS}: Heritability (Broad Sense, %): GAM: Genetic advance over mean (%)

3.2 Estimates of genetic variability for the first clonal generation of sugarcane

Variability is measured by estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (h^2_{BS}) and genetic advance as per cent of mean (GAM). These parameters help in selection for improvement of desired traits. Environment plays an important role in the expression of phenotype. The phenotypic variability which is observable includes both genotypic (heritable) and environmental variation (non-heritable). The estimates for PCV were higher than for GCV in all the traits studied, indicating greater influence of environment on genetic variation. The narrow difference between PCV and GCV were recorded for all the traits (Table 4). The highest phenotypic and genotypic coefficient of variation were observed for CCS yield (PCV = 30.23%, GCV = 29.05%) followed by cane yield per plot (PCV = 29.30%, GCV = 28.46%) and number of millable cane per plot (PCV = 28.08% and GCV = 27.67%). These findings were in accordance with Kumar et al., 2018; Sanghera and Jamwal (2019).

In the present experiment, high heritability estimates were recorded for all the traits except for single cane weight (75.99%) and cane girth (81.15%), which were found to be moderate values. This suggests that simple selection for these traits would be effective. Heritability estimates along with GAM is more useful than the heritability value alone in predicting the resultant effect for selecting the best genotypes [23]. Maximum genetic gain (as percent of mean) was observed for CCS yield (60.81%) followed by cane yield (57.02%) and NMC per plot (56.24%), indicating that there exist a scope to improve cane yield to a considerable extent by adopting suitable breeding procedures. Cane girth (16.63%), Brix% (12.20%) and Pol% (18.40%) had moderate GAM, suggesting a little scope in the improvement of these traits. Perusal of Table 5 revealed that cane yield has significant association with traits with number of millable canes per plot, millable cane height, single cane weight, CCS yield and CCS% these traits be given consideration while making indirect selection for cane yield. These findings were in accordance with Kumar et al., (2018); Tolera et al., (2023).

3.3 Correlation studies with cane yield and its component traits

The Pearson's correlation coefficients between different pairs of cane yield and its component traits were calculated to examine the relationships among the various traits studied. The correlation coefficient values are presented in Figure 1, revealing that cane yield is significantly positively related to CCS yield (0.93***), number of millable canes (0.72***), single cane weight (0.54**), millable cane height (0.39***) and cane girth (0.26***). This has significant implications for the selection of varieties to be used as parental material in crossing programs. The information above suggests that many characters influence cane yield, and the extent to which each character affects yield depends on the degree of association between that character and cane yield.

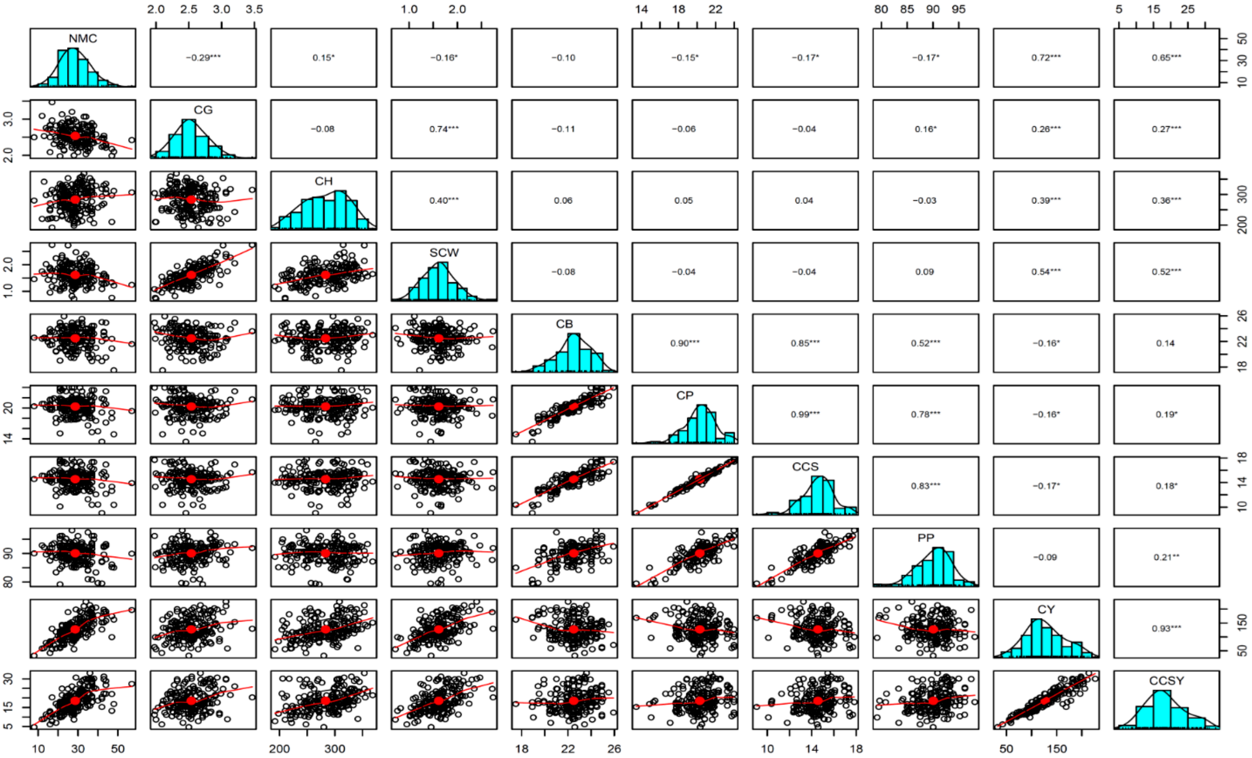
With regard to the quality traits in the present study, CCS yield was closely correlated ($P < 0.01$) with Brix%, Pol% and CCS%. The three sugar quality traits also had strong positive significant association with each other (Figure 1). This indicated that selection through Brix%, Pol% and CCS% would produce varieties with high levels of sugar recovery. In contrast, CCS% (-0.17*), Brix% (-0.16*) and Pol% (-0.16*) showed negatively significant to cane yield. These results are in accordance with the findings of Tena et al., (2016), who also reported significant correlation of cane yield with all other traits.

3.4 Path coefficient analysis

3.4.1 Direct effects of different component traits on cane yield

Path analysis helps us in identifying the most important characters affecting directly and indirectly through other characters. In the present study, the path coefficient analysis was performed for cane yield as a dependent variate and such of the traits having high correlation with cane yield like NMC per plot, cane girth, millable cane height, single cane weight, Brix%, Pol%, CCS% and CCS yield as independent variables (Table 5). The results revealed that, among the cane traits studied, CCS yield (t/ha) had highest positive direct effect of 0.805 on cane yield followed by Pol per cent in juice (0.631), CCS% (0.286), number of millable canes (0.175) and single cane weight (0.159). Cane girth and cane height exhibited negative direct effects of -0.036 and -0.001, respectively. The results are in accordance with the findings of Marsi (2015); Tena et al., (2016); Ahmed et al., (2019); Somu et al., (2020).

Figure 1: Pearson's correlation matrix of 150 genotypes for cane yield and its components traits in first clonal generation of sugarcane.



NMC – Number of millable canes / plot, CH –Millable cane height (cm), CG –Cane girth (cm), SCW – Single cane weight (kg), CB – Brix per cent (%), CP – Sucrose content (Pol%), CCS% – Commercial cane sugar per cent (%), PP – Juice purity per cent (%),CY - Cane yield (t/ha), CCSY - Commercial cane sugar yield (t/ha)

3.4.2 Indirect effects of different component traits on cane yield

The relationship between CCS yield and cane yield was positive and significant (0.93***). This trait also exhibited the highest positive direct effect on cane yield (0.805). CCS yield registered positive and high indirect effect on cane yield through NMC per plot (0.506), single cane weight (0.407), cane height (0.361) and cane girth (0.207) (Table 5). Residual effect was found to be very low (0.00879) which indicated that almost all the cane yield traits were included.

Critical analysis of the results by path analysis revealed that the traits CCS yield, single cane weight, Pol% and NMC per plot exhibited high positive direct effects on cane yield and many traits also exhibited their indirect positive effects on cane yield via these traits indicating that these are the major contributing traits to cane yield in sugarcane. Hence, direct selection for CCS yield, Pol%, single cane weight and NMC per plot would be helpful for the improvement of cane yield in first clonal stage. These four traits showed significant positive correlation among themselves and with cane girth, millable cane height and CCS%, indicating that indirect selection based on these traits may be given importance in first clonal stage. Similar results of positive direct effect on cane yield were also reported by Ahmed et al., (2019); Somu et al., (2020).

Table 5: Direct (diagonal) and indirect effects of cane yield component traits on cane yield at phenotypic level in first clonal stage of sugarcane

	NMC/ P	CG	CH	SCW	CB	CP	CCS	CCSY
NMC/ P	**0.175**	0.011	0.000	-0.035	-0.015	0.122	-0.056	0.506
CG	-0.055	**-0.036**	0.000	0.123	-0.009	0.025	-0.006	0.207
CH	0.026	0.000	**-0.001**	0.068	0.009	-0.049	0.020	0.361
SCW	-0.038	-0.028	0.000	**0.159**	-0.006	0.012	-0.001	0.407
CB	-0.027	0.004	-0.001	-0.011	**0.094**	-0.586	0.256	0.114
CP	-0.034	0.001	-0.001	-0.003	0.088	**0.631**	0.285	0.145
CCS	-0.034	0.001	0.000	-0.001	0.084	-0.628	**0.286**	0.153
CCSY	0.110	-0.009	0.000	0.080	0.013	-0.114	0.054	**0.805**
CY	0.72***	0.26***	0.39***	0.54***	-0.16*	-0.16*	-0.17*	0.93***

Residual effect: 0.00879

NMC: Number of millable canes per plot, CG: Cane girth, CH: Millable cane height, SCW: Single cane weight, Brix%: Brix per cent, Pol%: Sucrose content in juice, CCS%: Commercial cane sugar per cent, CCSY: Commercial cane sugar yield, CY: Cane yield

3.5 Mean performance of 150 clones for cane yield and quality traits

Mean performance of hybrid progenies (clones) and standards for cane yield and its component traits are presented in Table 6. The number of clones (genotypes) that were significantly superior over the popular mid-late check, Co 86032 was 31 (cane yield), 65 (CCS yield), 34 (Brix per cent in juice), 42 (sucrose content in juice), 29 (CCS%), 31 (single cane weight), 17 (cane girth), 96 (millable cane height), 54 (number of millable canes per plot). Similarly, the number of genotypes that surpassed the popular early check, Co 09004 was 08 (cane yield), 03 (CCS yield), 11 (Brix per cent in juice), 09 (sucrose content in juice), 12 (CCS%), 16 (single cane weight), 06 (cane girth), 83 (millable cane height), 13 (number of millable canes per plot).

Table 6: Mean performance of 163 genotypes (150 clones & 13 check varieties) for cane yield and its components traits in first clonal generation of sugarcane

S. No.	clones	FC	NMC/P	CG	CH	SCW	CB	CP	CCS	CCSY	CY
1	SNK 180011	**18F01**	32.9*	3.0*	302.3*	2.2*	22.6	19.9	14.1	29.4*	206.7*
2	SNK 180018	**18F01**	36.8*	2.7	310.0*	1.9*	23.0	20.1	14.2	28.5*	199.7*
3	SNK 180028	**18F01**	33.9*	3.0*	306.9*	2.2*	22.1	19.0	13.3	29.8*	221.7*
4	SNK 180064	**18F02**	30.9	2.6	333.2*	1.9*	22.6	19.6	13.9	23.7*	169.9*
5	SNK 180090	**18F02**	33.9*	2.4	330.1*	1.5	22.1	19.2	13.6	18.2	134.2
6	SNK 180122	**18F02**	43.6*	2.3	303.8*	1.5	19.8	17.3	12.3	22.1*	179.7*
7	SNK 180058	**18F02**	25.1	2.7	280.6	1.7	22.1	19.9	14.3	16.8	117.9
8	SNK 180082	**18F02**	30.0	2.5	333.2*	1.9*	22.6	19.4	13.6	22.3*	163.3*
9	SNK 180111	**18F02**	24.1	2.7	271.4	1.6	20.7	17.8	12.5	13.4	107.5
10	SNK 180061	**18F02**	41.6*	2.5	316.2*	1.2	24.9*	21.8*	15.5	19.5*	126.7
11	SNK 181265	**18F02**	19.3	2.4	226.6	1.2	20.7	17.3	11.9	7.2	62.1
12	SNK 180053	**18F02**	41.6*	2.3	293.0*	1.4	22.1	19.2	13.6	20.5*	150.7
13	SNK 181267	**18F02**	29.0	2.6	331.6*	2.0*	23.9*	21.2	15.1	24.6*	162.9
14	SNK 180124	**18F02**	34.8*	2.2	300.7*	1.4	23.9*	20.2	14.0	18.6	132.4
15	SNK 180113	**18F02**	31.9*	2.3	337.8*	1.6	25.3*	22.2*	15.8*	22.8*	144.2
16	SNK 180041	**18F02**	30.0	2.4	337.8*	1.5	23.9*	20.9	14.8	18.6	126.0
17	SNK	**18F0**	33.9*	2.2	302.3	1.5	23.9	20.7	14.6	19.2*	131.8

	180118	**2**			*		*				
18	SNK 180121	**18F02**	27.1	2.3	313.1*	1.4	24.4*	21.8*	15.6*	15.4	99.3
19	SNK 180073	**18F02**	31.9*	2.5	314.6*	1.7	24.4*	22.2*	16.1*	23.9*	148.1
20	SNK 180080	**18F02**	34.8*	2.7	319.3*	1.9*	20.7	16.8	11.4	22.1*	193.2*
21	SNK 181271	**18F02**	21.2	2.6	293.0*	1.7	21.2	17.9	12.5	12.5	101.1
22	SNK 180065	**18F02**	38.7*	2.6	325.4*	1.8	21.2	17.7	12.2	24.7*	201.9*
23	SNK 180123	**18F02**	34.8*	2.6	310.0*	1.9*	22.6	19.9	14.1	26.0*	183.3*
24	SNK 180051	**18F02**	20.2	2.6	319.3*	1.8	23.9*	21.4*	15.3	15.9	104.7
25	SNK 180054	**18F02**	34.8*	2.4	320.8*	1.6	23.9*	20.7	14.6	22.4*	153.4
26	SNK 180112	**18F02**	25.1	2.7	294.5*	1.7	23.9*	21.2	15.1	18.1	120.8
27	SNK 180070	**18F02**	42.6*	2.5	271.4	1.6	23.5	21.7*	15.8*	29.6*	186.8*
28	SNK 180089	**18F02**	28.0	2.5	269.8	1.5	23.5	21.4*	15.5*	18.3	118.5
29	SNK 180037	**18F02**	25.1	2.5	322.4*	1.7	23.0	21.2	15.5*	18.5	120.3
30	SNK 180087	**18F02**	29.0	2.3	305.4*	1.3	22.6	19.4	13.6	12.9	95.7
31	SNK 181268	**18F02**	32.9*	2.4	369.3*	1.7	23.0	20.1	14.2	21.4*	149.9
32	SNK 180067	**18F02**	22.2	2.7	323.9*	1.9*	22.6	20.4	14.7	18.0	123.1
33	SNK 181257	**18F02**	36.8*	2.5	248.2	1.4	23.5	21.2	15.3	20.9*	137.1
34	SNK 181272	**18F02**	34.8*	2.8*	303.8*	1.9*	21.2	20.5	15.2	29.7*	193.5*
35	SNK 180106	**18F02**	26.1	2.5	242.0	1.7	23.0	20.8	15.0	17.9	120.3
36	SNK 180110	**18F02**	33.9*	2.1	288.4*	1.2	23.5	21.2	15.3	15.0	99.5
37	SNK 181255	**18F02**	47.5*	2.2	310.0*	1.3	17.9	15.2	10.5	16.9	160.4
38	SNK	**18F0**	23.2	2.5	299.2	1.6	23.9	21.2	15.1	15.1	101.2

	181269	**2**			*		*				
39	SNK 180031	**18F02**	21.2	2.7	272.9	1.7	19.3	15.3	10.3	10.0	98.1
40	SNK 180116	**18F02**	23.2	2.5	293.0*	1.7	23.0	20.1	14.2	15.1	106.7
41	SNK 180230	**18F09**	30.9	2.4	234.3	1.4	22.1	19.0	13.3	15.3	115.0
42	SNK 180449	**18F09**	36.8*	2.6	320.8*	1.7	19.3	15.6	10.5	17.8	168.7*
43	SNK 181311	**18F09**	39.7*	2.4	259.3	1.6	19.7	15.7	10.6	18.6	175.5*
44	SNK 180349	**18F09**	41.6*	2.5	266.7	1.5	19.3	13.8	9.2	15.4	166.6*
45	SNK 180319	**18F09**	34.8*	2.4	296.7*	1.5	22.9	19.4	13.5	19.5*	144.8
47	SNK 180218	**18F09**	46.5*	2.1	215.8	1.0	22.5	19.2	13.4	13.4	100.4
46	SNK 181281	**18F09**	42.6*	2.3	271.4	1.4	22.9	20.6	14.7	22.3*	150.7
48	SNK 180249	**18F09**	19.3	2.8*	265.2	2.1*	22.5	20.1	14.4	17.0	118.7

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S. No.	**clones**	**FC**	**NMC/P**	**CG**	**CH**	**SCW**	**CB**	**CP**	**CCS**	**CCSY**	**CY**
49	SNK 180220	**18F09**	32.9*	2.5	339.3*	1.7	22.9	20.8	15.0	23.3*	154.9
50	SNK 180252	**18F09**	30.0	2.4	287.1*	1.6	20.6	18.2	12.9	17.1	132.4
51	SNK 180294	**18F09**	28.0	2.4	250.9	1.4	21.0	17.9	12.4	12.9	104.4
52	SNK 180364	**18F09**	27.1	2.3	328.1*	1.7	20.6	18.2	12.9	16.3	126.6
53	SNK 180219	**18F09**	33.9*	2.6	262.0	1.4	21.5	19.4	14.0	17.9	128.1
54	SNK 180328	**18F09**	35.8*	2.4	256.7	1.6	21.5	19.2	13.7	21.7*	157.5
55	SNK 180341	**18F09**	27.1	2.9*	256.4	1.3	21.0	18.4	13.0	12.2	94.5
56	SNK 180175	**18F09**	24.1	2.5	263.2	2.0*	22.9	20.7	14.9	21.0*	140.1
57	SNK	**18F0**	30.9	2.6	234.2	1.3	21.9	19.6	14.0	15.0	107.8

	180265	**9**									
58	SNK 180435	**18F09**	22.2	2.6	233.9	1.5	22.4	19.8	14.1	12.8	91.7
59	SNK 180308	**18F09**	29.0	2.4	227.1	1.3	23.3	21.6*	15.7*	14.8	94.9
60	SNK 180288	**18F09**	46.5*	2.3	294.4*	1.4	21.0	18.1	12.7	22.0*	172.3*
61	SNK 180467	**18F09**	35.8*	2.3	308.0*	1.3	21.0	18.1	12.7	15.9	125.5
62	SNK 180442	**18F09**	36.8*	2.4	333.7*	1.9*	22.4	20.6	14.9	29.5*	196.6*
63	SNK 180318	**18F09**	23.2	2.6	317.3*	1.9*	21.9	19.6	14.0	17.3	123.1
64	SNK 180339	**18F09**	30.0	2.4	271.6	1.3	20.6	18.0	12.7	13.3	105.1
65	SNK 180172	**18F09**	19.3	2.5	286.7*	1.7	20.6	18.2	12.9	11.9	92.7
66	SNK 180519	**18F11**	24.1	2.5	308.6*	1.7	24.3*	23.1*	17.0*	18.9*	111.3
67	SNK 180537	**18F11**	29.0	2.3	297.2*	1.5	21.0	17.9	12.4	15.2	122.0
68	SNK 180536	**18F11**	31.9*	2.4	289.5*	1.5	21.9	19.4	13.8	18.1	130.8
69	SNK 180634	**18F12**	22.2	2.5	309.6*	1.7	22.9	21.2	15.4*	15.7	102.5
70	SNK 180625	**18F12**	32.9*	2.5	318.8*	1.7	21.0	18.1	12.7	19.2*	150.7
71	SNK 180582	**18F12**	23.2	2.5	317.3*	1.9*	22.4	20.8	15.1	18.7	123.9
72	SNK 180775	**18F14**	26.1	2.5	291.0*	1.6	22.5	21.0	15.3	17.4	113.9
73	SNK 180664	**18F14**	29.0	2.9*	312.7*	2.3*	22.9	21.2	15.4*	30.4*	195.3*
74	SNK 180674	**18F14**	30.9	2.5	348.2*	1.7	21.9	19.6	14.0	20.2*	143.6
75	SNK 180800	**18F14**	21.2	2.6	329.3*	1.9*	23.3	21.8*	15.9*	18.1	113.5
76	SNK 180784	**18F14**	36.8*	2.5	237.0	1.2	24.3*	23.3*	17.3*	20.2*	117.0
77	SNK 180705	**18F14**	36.8*	2.5	295.7*	1.7	21.9	19.6	14.0	24.7*	174.8*
78	SNK	**18F1**	32.9*	2.8	300.3	1.8	22.9	21.2	15.4	26.2*	169.0*

	180731	**4**		*	*				*		
79	SNK 180665	**18F14**	16.4	2.8*	298.8*	1.8	22.9	20.7	14.9	12.3	83.6
80	SNK 180702	**18F14**	29.0	2.7	269.4	1.6	20.6	17.9	12.6	16.6	131.4
81	SNK 180796	**18F14**	43.6*	2.3	312.7*	1.4	24.7*	23.1*	16.9*	26.6*	156.6
82	SNK 180662	**18F14**	42.6*	2.6	325.0*	1.7	23.3	21.6*	15.7*	30.9*	194.9*
83	SNK 180693	**18F14**	28.0	2.6	316.7*	1.6	23.8*	21.8*	15.8*	18.8*	119.7
84	SNK 180732	**18F14**	21.2	2.7	278.7	1.7	23.3	21.6*	15.6*	15.9	102.4
85	SNK 180730	**18F14**	27.1	2.4	249.6	1.4	24.3*	23.8*	17.8*	17.9	101.4
86	SNK 180768	**18F14**	22.2	2.6	308.0*	1.7	22.4	20.5	14.8	15.2	102.9
87	SNK 180774	**18F14**	43.6*	2.4	329.6*	1.6	22.4	20.7	15.1	28.7*	188.4*
88	SNK 180792	**18F14**	30.9	2.7	247.2	2.1*	21.9	19.9	14.3	27.3*	189.2*
89	SNK 180716	**18F14**	21.2	2.8*	278.0	1.9*	22.4	20.8	15.1	17.0	112.6
90	SNK 180795	**18F14**	33.9*	2.5	240.0	1.3	23.8*	21.6*	15.5*	17.8	115.0
91	SNK 180823	**18F18**	27.1	2.5	308.9*	1.6	21.9	20.4	14.8	17.5	118.3
92	SNK 180875	**18F18**	23.2	2.5	290.7*	1.5	21.9	19.6	14.0	13.7	98.4
93	SNK 180878	**18F18**	36.8*	2.5	338.3*	1.8	22.9	21.2	15.4*	28.2*	181.6*
94	SNK 180876	**18F18**	12.5	3.0*	223.1	1.7	22.4	20.8	15.1	9.1	61.7
95	SNK 180847	**18F18**	33.9*	2.4	298.8*	1.4	21.5	19.4	14.0	18.0	128.4
96	SNK 180832	**18F18**	21.2	2.1	301.2*	1.2	24.7*	23.8*	17.6*	11.4	66.3
97	SNK 180922	**18F19**	24.1	2.6	297.2*	1.6	20.6	18.2	12.9	13.6	106.2
98	SNK 180899	**18F19**	24.1	2.7	326.6*	2.0*	21.9	20.1	14.5	21.0*	143.5
99	SNK	**18F1**	21.2	2.4	297.2	1.6	24.3	23.1	17.0	16.0	95.0

	180912	**9**			*		*	*	*		

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S. No.	**clones**	**FC**	**NMC/P**	**CG**	**CH**	**SCW**	**CB**	**CP**	**CCS**	**CCSY**	**CY**
100	SNK181091	**18F26**	30.9	2.4	320.4*	1.7	23.8*	21.8*	15.8*	23.2*	146.6
101	SNK 181120	**18F27**	27.1	2.5	332.7*	1.8	23.8*	22.0*	16.0*	22.8*	142.4
102	SNK 181139	**18F27**	21.2	2.3	251.1	1.2	24.7*	23.6*	17.4*	10.6	63.1
103	SNK 181165	**18F27**	37.8*	2.4	301.5*	1.4	24.3*	23.3*	17.3*	25.3*	146.2
104	SNK 181220	**18F27**	23.2	2.5	306.7*	1.7	21.5	20.2	14.7	16.0	109.1
105	SNK 181127	**18F27**	18.3	2.3	308.3*	1.5	23.4	21.9*	15.9*	11.4	73.3
106	SNK 181110	**18F27**	22.2	2.8*	330.8*	2.2*	24.3*	23.3*	17.3*	24.8*	143.2
107	SNK 181160	**18F27**	30.9	2.3	346.9*	1.5	23.9*	23.7*	17.3*	22.1*	127.8
108	SNK 181148	**18F27**	28.0	2.4	277.4	1.5	24.4*	23.8*	17.3*	19.0*	110.6
109	SNK 181199	**18F27**	31.9*	2.3	356.8*	1.6	24.7*	23.1*	16.9*	23.3*	138.2
110	SNK 181174	**18F27**	27.1	2.4	294.4*	1.5	23.4	21.6*	15.7*	16.9	108.3
111	SNK 181106	**18F27**	23.2	2.2	299.0*	1.2	25.7*	23.8*	17.3*	12.5	74.0
112	SNK 181219	**18F27**	31.9*	2.3	336.1*	1.5	23.4	21.6*	15.7*	19.6*	124.9
113	SNK 181179	**18F27**	22.2	3.0*	318.5*	2.1*	23.8*	21.6*	15.5*	21.5*	138.3
114	SNK 181145	**18F27**	31.9*	2.8*	272.7	2.0*	22.4	21.0	15.4*	28.7*	185.6*
115	SNK 181203	**18F27**	29.0	2.5	303.0*	1.6	22.4	20.6	14.9	19.2*	129.2
116	SNK 181118	**18F27**	30.9	2.5	305.2*	1.7	23.4	21.6*	15.7*	22.7*	144.2
117	SNK 181112	**18F27**	29.0	2.7	274.3	1.8	22.0	20.1	14.5	21.0*	144.3
118	SNK 181149	**18F27**	25.1	2.5	267.2	1.4	22.9	21.2	15.4*	14.1	92.4

119	SNK 181143	**18F27**	24.1	2.8*	275.2	1.7	24.3*	23.1*	17.0*	20.1*	118.6
120	SNK 181126	**18F27**	35.8*	2.6	351.5*	2.0*	23.5	21.4*	15.4*	32.7*	210.2*
121	SNK 181190	**18F27**	57.0*	2.4	308.3*	1.3	21.7	19.5	13.9	27.2*	193.9*
122	SNK 181397	**18F41**	25.1	2.9*	351.5*	2.5*	21.2	18.6	13.1	24.6*	186.5*
123	SNK 181446	**18F41**	34.8*	2.2	257.0	1.2	22.6	20.6	14.8	16.0	108.9
124	SNK 181393	**18F41**	21.2	2.7	320.6*	2.0*	22.6	20.3	14.6	17.6	121.3
125	SNK 181396	**18F41**	30.9	2.6	317.5*	1.9*	22.1	20.1	14.5	24.0*	165.0*
126	SNK 181352	**18F41**	36.8*	2.6	308.3*	1.8	22.1	20.6	15.0	27.4*	181.3*
127	SNK 181452	**18F41**	17.3	3.4*	316.0*	2.7*	23.5	21.6*	15.6*	20.3*	129.7
128	SNK 181402	**18F41**	31.9*	2.7	267.2	1.8	22.1	20.4	14.7	24.6*	166.1*
129	SNK 181479	**18F41**	22.2	2.5	325.3*	1.8	21.2	18.1	12.6	14.1	112.2
130	SNK 181480	**18F41**	22.2	2.3	275.8	1.4	23.5	21.6*	15.6*	12.5	81.5
131	SNK 181476	**18F41**	13.4	2.5	340.7*	1.7	22.6	20.8	15.0	9.2	63.3
132	SNK 181410	**18F41**	24.1	2.6	260.4	1.7	23.1	21.2	15.4	17.7	115.6
133	SNK 181366	**18F41**	23.2	2.7	271.2	1.8	21.7	19.5	13.9	16.1	116.4
134	SNK 181518	**18F41**	17.3	2.6	201.7	1.3	22.1	19.7	14.0	8.1	59.5
135	SNK 181498	**18F41**	28.0	2.1	218.7	0.9	24.0*	21.6*	15.4*	8.9	59.6
136	SNK 181444	**18F41**	8.6	2.5	283.6*	1.5	22.6	20.3	14.6	5.1	37.3
137	SNK 181365	**18F41**	22.2	2.4	235.7	1.3	22.4	20.1	14.4	10.3	73.2
138	SNK 181499	**18F41**	22.2	2.6	284.5*	1.7	22.0	19.2	13.5	14.4	107.1
139	SNK180068	**18F41**	22.2	2.7	292.8*	1.9*	22.0	19.9	14.3	17.0	119.7

140	SNK 181720	**18F41**	16.4	2.2	253.6	1.1	23.4	20.5	14.5	6.4	46.8
141	SNK 181543	**18F42**	16.4	2.5	257.9	1.6	22.9	20.1	14.2	10.3	73.9
142	SNK 181591	**18F44**	21.2	2.5	265.9	1.7	22.4	20.1	14.4	14.2	99.4
143	SNK 181227	**18F03**	14.4	2.7	300.2*	1.9*	22.4	20.1	14.4	11.5	81.3
144	SNK 181230	**18F04**	16.4	2.7	275.2	1.8	23.8*	21.6*	15.5*	13.2	86.3
145	SNK 180129	**18F08**	22.2	2.6	266.9	1.8	22.9	21.2	15.4*	16.9	110.4
146	SNK 180509	**18F09**	27.1	2.5	280.5	1.7	22.9	20.8	14.9	19.1*	128.3
147	SNK 180506	**18F09**	25.1	2.5	258.8	1.6	22.9	21.2	15.4*	16.9	110.1
148	SNK 180805	**18F15**	36.8*	2.7	280.5	1.7	23.4	21.4*	15.4*	27.8*	178.7*
149	SNK 180949	**18F20**	29.0	2.4	284.5*	1.4	23.4	21.6*	15.7*	16.2	103.9
150	SNK 180954	**18F24**	27.1	3.1*	249.0	2.0*	24.7*	23.1*	16.9*	25.9*	153.1

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	Standards	**Code**	**NMC/P**	**CG**	**CH**	**SCW**	**CB**	**CP**	**CCS**	**CCSY**	**CY**
Commercial standards											
	CoC 671	C1	30.0	2.8	208.5	1.6	24.7	20.9	14.8	21.1	137.0
	Co 09004	C2	37.0	2.7	219.8	1.6	23.5	22.3	16.4	26.0	172.7
	SNK 09211	C3	28.7	2.5	257.2	1.5	24.4	22.0	16.0	17.8	108.9
	Co 86032	C4	27.3	2.5	256.8	1.4	22.6	20.2	14.8	14.5	140.7
	Co 09232	C5	28.5	2.2	254.7	1.2	21.8	20.5	15.3	15.3	98.3
	SNK 09227	C6	28.5	2.4	228.5	1.4	22.1	20.1	14.1	15.6	112.1
	SNK 09268	C7	27.5	2.6	314.7	1.7	20.3	18.7	13.5	17.0	126.6
	SNK 08789	C8	22.5	2.3	249.2	1.4	21.3	20.0	14.6	12.1	84.4
	SNK 07680	C9	27.5	2.5	234.0	1.1	22.5	19.9	14.4	11.5	84.4
	VSI 12121	C10	36.0	2.8	253.7	1.9	19.8	18.5	12.8	27.7	182.9
	CoM 265	C11	16.0	2.8	221.0	1.6	21.6	20.0	14.5	11.6	77.4
	SNK 09293	C12	26.5	2.8	249.8	1.8	19.6	17.8	12.8	17.3	180.1
	MS 13081	C13	25.5	2.9	291.7	2.1	22.5	20.5	14.8	21.3	146.6
	CD @ 5%		3.4	0.3	23.6	0.4	0.9	1.0	0.6	4.2	22.2
	CV		4.83	4.29	3.37	10.65	1.70	2.0	1.6	4.8	7.0

*Significantly superior over popular check variety, Co 86032
FC: Family code, NMC/P: Number of millable canes per plot, CG: Cane girth, CH: Millable cane height, SCW: Single cane weight, CB: Brix per cent in juice, CP: Sucrose per cent in juice, CCS: Commercial cane sugar per cent, CY - Cane yield (t/ha), CCSY - Commercial cane sugar yield (t/ha), CD: Critical difference, CV: Coefficient of variation.

03.5.1 Cane and sugar productivity

The pre-selected clonal population from ground nursery exhibited wide range of cane productivity in comparisons with commercial standards. Among 150 clones, three clones, SNK 180028 (221.7 t/ha), SNK 181126 (210.2 t/ha), and SNK 180011 (206.7 t/ha) recorded significantly superior for cane yield over best cane yielding standard, VSI 12121 (Table 6). The significantly higher cane yield in three most promising progenies was due to their continuous vegetative growth and dry matter accumulation even beyond flowering period (November and December). These three genotypes recorded 31-37% superiority over popular commercial standard, Co 86032, indicating their great promise as improved commercial varieties with desirable feature. The performance of genotypes for commercial cane sugar yield (CCS) also shown similar trend where in three promising genotypes recorded 49-56% superiority over most popular commercial standard, Co 86032 (Table 6). Hence these genotypes hold great promise as commercial varieties in the region. The results are in accordance with the findings of Patil et al., (2015); Sanghera and Jamwal (2019).

Most of the clones had higher number of millable canes per plot than most popular standard, Co 09004, but seven genotypes, such as SNK 181190, SNK 181255, SNK 180288, SNK 180218, SNK 180774, SNK 180796 and SNK 180122, recorded significantly greater number of millable canes per plot (Table 6). SNK 181452 (Co 87015, GC) and SNK 180954 (CP 52-1, GC) had significantly the highest means of cane girth (3.40 and 3.10 cm, respectively) for the best standard, Co 09004 (2.70 cm). Among various juice quality parameters, the sucrose per cent in juice is an important and deciding trait for commercial acceptability in sugar industry. Six genotypes like SNK 181106, SNK 180730, SNK 180832, SNK 181148, SNK 181160 and SNK 181139 recorded superior sucrose content in juice (Pol%) over best commercial standard, Co 09004 but the cane productivity is significantly inferior (Table 6). Among 150 genotypes, the clones SNK 180070, SNK 180662, SNK 181126 and SNK 180805 recorded significant superiority over Co 86032 in both for cane and sugar productivity with higher sucrose content in juice.

4. CONCLUSIONS

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. Five genotypes, such as SNK 180011 (CoVC 14062 × Co 89003), SNK 180028 (CoVC 14062 × Co 89003), SNK 180070 (Co 86032 × CoVC 14061), SNK 180662 (CoVC 14062, GC) and SNK 181126 (Co 11015, GC) were found to be the most promising for commercial cultivation and suitably be exploited for sustaining and improving cane and sugar productivity in the region. The clones identified as promising for both cane yield and juice quality traits need to be further tested in advanced yield trials. Additionally, their parentage can be considered as proven parents for intensifying further improvement to realize the expected genetic gain in sugarcane breeding.

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