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Morphological characterization and quantitative genetic analysis of sugarcane (*Saccharum spp*) germplasm

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Abstract

The present study was conducted using 100 sugarcane genotypes in 2023-2024 in an Augmented Block Design-II at the Research farm, Main Sugarcane Research Centre, NAU, Navsari. The objective was to estimation of genetic parameters. Based on overall mean performance, genotype 2021 N 144 was identified as best clone exhibiting superior performance over the best standard for juice brix %, purity %, sucrose % and CCS %. Similarly, 2021 N 157 exhibited superior performance for number of tillers at 120 DAS, number of millable canes, stalk length and CCS (t/ha). Therefore, 2021 N 144 identified as best performer for juice quality characters and 2021 N 164 for cane yield contributing characters. Moderate variability, high heritability and moderate to high genetic advance as percent of mean were recorded for number of tillers at 120 DAS, number of shoots at 240 DAS, number of millable canes, stalk length, cane diameter, CCS %, CCS (t/ha), and cane yield.

Keywords: Saccharum, Genetic variability, Heritability, Genetic advance, Cane yield

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Introduction

Sugarcane is one of the important cash crops which is cultivated in tropical and sub-tropical regions of the world. It is valuable because it stores high concentration of sucrose in the stem and more recently for the production of an important renewable bio-fuel, ethanol (Sharma and Tamta, 2015) [1]. Globally, sugarcane is an important source of commercial sugar, accounting for almost two-thirds of worlds sugar production (Menossi *et al.*, 2008) [2]. India is the second largest producer of sugarcane and is the largest producer and consumer of sugar in the world. A significant portion of the canes are also crushed for the extraction of juice for domestic consumption, and about 10 % of the canes are used as seed for planting new crops (Viswanathan, 2012) [3].

The term *Saccharum* is derived from the Sanskrit word ‘sarkara’ or ‘sakkara,’ which means sugar, this transformed into ‘Sukkar’ in Arabic and ‘Sakharon’ in Greek. Sugarcane is a monocotyledon and belongs to the genus *Saccharum* of tribe Andropogoneae, sub-tribe Saccharineae in family Poaceae. The genus *Saccharum* consists of 6 to 37 species depending on taxonomic interpretation and the members are of tall grasses, native to warm temperate to tropical regions of South and South East Asia. Sugarcane has thick, jointed and fibrous stalks of 2 to 6 metres tall that store sugar. There are three cultivated species of sugarcane namely *Saccharum officinarum* (noble cane, 2n=80), *Saccharum barberi* (2n = 82-124), *Saccharum sinense* (2n = 111-120) and three wild species namely *Saccharum spontaneum* (2n = 40-128), *Saccharum robustum* (2n = 60-194) and *Saccharum edule* (2n = 60-80) (Gupta *et al.*, 2010). *Saccharum* species complex is widely cultivated in India after nobilization because of high sucrose content and adaptability to adverse environmental conditions.

Sugarcane contributes approximately 80% of the global sugar requirement; sugar beet meets the remainder. Brazil, India, Thailand, China, the USA, Mexico, Pakistan, Australia and Guatemala are the major sugarcane-producing countries (http://www.fao.org/faostat/en). The major sugarcane producing states in India are Uttar Pradesh, Maharashtra, Karnataka, Tamil Nadu, Bihar and Andhra Pradesh etc. It is the second most important agro-industrial crop in India, next only to cotton (Jayashree *et al.*, 2010) [5]. In India, sugarcane is grown in 5.2 Mha area, which is approximately 3.0% of the total cultivable area in the country, and it contributes 7.5% gross value of agricultural production (https://indiansugar.com/Statics.aspx).

With additional backcrossing with *Saccharum officinarum*, modern sugarcane hybrids they originated from interspecific crosses between the wild, thin-stalked, low-sugar *Saccharum spontaneum* and the thick-stalked, high-sugar *Saccharum officinarum*. In addition to improving the present farmed sugarcane hybrids' vigor, robustness, tillering, disease resistance, and environmental adaptability, this complicated hybridization process increased the genome's complexity beyond that of their ancestors. Hybrids might have between 100 and 130 chromosomes, depending on the particular cross. Depending on the specific cross, hybrids might have between 100 and 130 chromosomes. Around 70–80% of these chromosomes come from *S. officinarum*, 10–20% from *S. spontaneum*, and 10% are the product of interspecific recombination. (Bao *et al*. 2024) [6].

Materials and Methods

Total 100 genotypes were used in the study including 3 checks. The genotypes were of 2020 N series and from 2021 N series. Total 13 characters were studied. Ten plants from each plot were randomly selected for all the morphological observations except for character such as germination % at 45 DAS which were recorded from net area of the standing crop in all the accessions. All the remaining observations were recorded from plants in the field at an appropriate time. Quantitative parameters were recorded during the last week of December. The mean values of each observation obtained from the selected ten plants were used for statistical analysis. Seed yield was taken from the net plot area. The observations were recorded for 13 traits. Out of which six are agro-morphological *viz*., germination % at 45 DAS, number of tillers at 120 DAS, number of shoots at 240 DAS, single cane weight (kg), stalk length (cm), and cane diameter (cm). This study also included brix %, sucrose % and purity % which are quality parameters. Number of Millable Canes (N.M.C), C.C.S %, cane yield (t/ha) and CCS (t/ha) are the traits associated with yield.

Results and Discussion

To assess the performance and genetic diversity of sugarcane genotypes under evaluation, this design enabled efficient comparison among 97 unreplicated test entries using three replicated checks across six blocks. The analysis yielded insights into both raw trait performance and into stability and potential of genotypes for further selection. List of top performing genotypes over best check is given in Table 1. The mean values of 97 genotypes and 3 checks for various quantitative and qualitative traits in sugarcane is given in supplementary table. 1.

Germination % at 45 DAS

Germination % is the first observable trait reflecting early vigor. It was ranged from a minimum of 41.98% (2021 N 301) to a maximum of 65.59%, observed in 2020 N 107, 2020 N 164, and 2021 N 105. The best check variety was CoN 13072, and 13 test clones surpassed it in germination percentage, indicating better initial establishment.

Number of tillers at 120 DAS

In the present study, tiller count varied from a minimum of 87.47 (2021 N 103) to a maximum of 150.68 (2021 N 105 and 2021 N 189). Again, CoN 13072 was the best check, but only 6 clones performed better in tiller production a key yield determinant.

Number of shoots at 240 DAS

Number of shoots varied notably among the genotypes, ranging from 80.02 (2021 N 216) to 138.79 (2021 N 105 and 2021 N 189). With CoN 13072 as the standard check, 5 genotypes *viz*., 2020 N 164, 2021 N 10, 2021 N 105, 2021 N 140, and 2021 N 189 outperformed the superior check, reflecting sustained vegetative growth.

Number of millable canes

In this study, NMC values varied considerably among the genotypes, ranging from a minimum of 72.91 (observed in 2021 N 52 and 2021 N 60) to a maximum of 122.52 (recorded in 2021 N 105 and 2021 N 189). Higher NMC is desirable for achieving better yield per hectare, provided stalk quality is maintained. Ten genotypes exceeded the best check CoN 13072 for millable canes, an essential trait for harvestable yield.

Single cane weight (kg)

Single cane weight is a vital yield contributing trait, as it directly influences the total biomass and harvested tonnage per unit area. In this study, single cane weight values ranged from 0.74 kg (2021 N 115) to 1.34 kg (2021 N 49) The best performing check was Co 86032, and 33 genotypes recorded higher individual cane weight, showing great potential for biomass accumulation. The best five were 2020 N 164, 2020 N 44, 2021 N 114, 2021 N 44, and 2021 N 49. These genotypes are especially promising for selection, as increased single cane weight when combined with a high number of millable canes can significantly enhance total cane yield and commercial productivity.

Stalk length (cm)

Stalk length among the genotypes exhibited substantial variability, ranging from 147.05 cm (2021 N 97) to 257.05 cm (2021 N 98). Five genotypes surpassed CoN 13072, the best check variety for stalk length.

Cane diameter (cm)

In this study, the narrowest cane is 2021 N 165 with the diameter of 1.77 cm. The widest cane was observed in genotype 2020 N 77, which stood out significantly with a diameter of 4.66 cm. The narrow gap between genotypes also indicates strong genetic control and limited environmental interference. Thirty-one genotypes had a larger average diameter than the best check Co 86032, which is vital for cane volume and juice content.

Brix %

Brix values ranged from 15.18 % in 2021 N 169 to 26.11 % in 2021 N 41. A total of 25 genotypes showed superior brix values compared to CoN 13072, reflecting higher sugar concentration. Best performing clones were 2020 N 102, 2021 N 41, 2021 N 52, 2021 N 55, and 2021 N 68.

Sucrose %

In the present study, sucrose % varied from 14.25 % (2020 N 2) to 21.89 % (2021 N 144), with a mean value of 18.66 % and a coefficient of variation of 2.57%. Twenty-four test entries surpassed the sucrose content of CoN 13072.

Purity %

Purity ranged from 80.23 % (2021 N 41) to 99.58 % (2021 N 101), with a mean of 93.86 % and a CV of 2.03%, suggesting high trait stability and minimal environmental influence. High purity is critical for efficient sugar recovery and processing economy, as it signifies a lower proportion of non-sugar impurities in the juice. With a remarkable 50 genotypes outperforming CoN 13072 which is the best check in juice purity, this trait showed strong improvement potential.

C.C.S %

In the present evaluation, CCS % ranged from 9.64 % (2021 N 230) to 16.24 % (2021 N 105), A total of 27 test clones recorded higher CCS% than CoN 13072, pointing to genetic enhancement in sugar recovery.

CCS (t/ha)

Commercial cane sugar (t/ha) is a vital economic trait that directly reflects the total sugar yield obtained per unit area. In the present study, commercial cane sugar (t/ha) ranged from 7.26 t/ha (2021 N 216) to 20.63 t/ha (2021 N 105). Eight clones surpassed CoN 13072 in CCS (t/ha).

Cane yield (t/ha)

In the present study, cane yield showed a wide range from 67.58 t/ha (2021 N 115) to 143.16 t/ha (2020 N 164). Eighteen test entries outperformed the check CoN 13072 in total cane yield, a key productivity indicator.

Estimation of Genetic Variability, Heritability and Genetic Advance

A critical persual of PCV and GCV indicated that, PCV estimates were higher than GCV for all the characters and the closeness between GCV and PCV values for almost all the characters except stalk length and CCS (t/ha) indicated that these characters are less influenced by the environment. Moderate values of both PCV and GCV were observed for all the traits except for germination at 45 DAS, single cane weight, brix, per cent and purity percent. Moderate PCV and low GCV was recorded for sucrose per cent. Lower values of PCV and GCV of these traits indicates the presence of limited amount of genetic variability for these traits in the population.

The high heritability in broad sense with high genetic advance was recorded for cane yield, CCS (t/ha), and cane diameter. It indicated that most likely these characters are governed by the additive gene effects and selection for these characters will be effective for improvement in successive generations. As heritability in broad sense is high it also indicated that these characters are least influenced by the environmental effects. Moderate GCV, PCV along with high h^2b and GAM were recorded for cane yield, CCS (t/ha), and cane diameter indicates wider range of variability in the material and importance of additive gene action in the inheritance of these characters in sugarcane. Moderate estimates of GCV and PCV coupled with high estimates of heritability in broad sense and moderate genetic advance over mean recorded for number of tillers, number of shoots, number of millable canes, stalk length, and CCS per cent also indicated the importance of additive gene action in the inheritance of this character. These characters can be improved through simple selection. All the remaining traits have low to moderate PCV, GCV coupled with high heritability yet moderate genetic advance as percent of mean. Therefore, it is needed to go for indirect selection through more heritable and variable correlated traits and further hybridization to create the variability for these characters. Measures of variability parameters for different characters in sugarcane are given in table 2.

Table 1: List of top performing genotypes over best check on basis of mean value

Characters	Best check	Five top performing genotypees
Germination % at 45 DAS	CoN 13072	2020 N 164, 2021 N 107, 2021 N 166, 2021 N 304, 2021 N 105
Number of tillers at 120 DAS	CoN 13072	2020 N 164, 2021 N 101, 2021 N 105, 2021 N 149,2021 N 189
Number of shoots at 240 DAS	CoN 13072	2020 N 164, 2021 N 10, 2021 N 105, 2021 N 140, 2021 N189
Number of millable canes	CoN 13072	2020 N164, 2021 N 105, 2021 N 169, 2021 N 189, 2021 N 149
Single cane weight (kg)	Co 86032	2020 N 164, 2020 N 44, 2021 N 114, 2021 N 44, 2021 N 49
Stalk length (cm)	CoN 13072	2020 N 158, 2021 N 15, 2021 N 230, 2021 N 93, 2021 N 98
Cane diameter (cm)	Co 86032	2020 N 65, 2020 N 77, 2021 N 49, 2021 N 66, 2021 N 68
Brix %	CoN 13072	2020 N 102, 2021 N 41, 2021 N 52, 2021 N 55, 2021 N68
Sucrose %	CoN 13072	2021 N 105, 2021 N 144, 2021 N 165, 2021 N 55
Purity %	CoN 13072	2020 N 140, 2021 N 101, 2021 N 105, 2021 N 106, 2021 N 115
C.C.S %	CoN 13072	2020 N 80, 2021 N 105, 2021 N 112, 2021 N 144, 2021 N 167
CCS (t/ha)	CoN 13072	2020 N 140, 2020 N 164, 2021 N 105, 2021 N 114, 2021 N 189
Cane Yield (t/ha)	CoN 13072	2020 N 107, 2020 N 164, 2021 N 105, 2021 N 114, 2021 N 189

Table 2: Measures of variability parameters for different characters in sugarcane

Characters	σ_p^2	σ_g^2	GCV (%)	PCV (%)	h_{bs}^2 (%)	GA	GAM
Germination % at 45 DAS	19.56	18.43	7.85	8.09	94.2	8.59	15.71
Number of tillers at 120 DAS	187.94	142.21	10.37	11.92	75.67	21.4	18.61
Number of shoots at 240 DAS	146.26	117.07	10.58	11.82	80.04	19.97	19.52
Number of millable canes	114.77	91.44	10.43	11.68	79.67	17.61	19.2
Single cane weight (kg)	0.01	0.01	6.87	7.8	77.65	0.13	12.49
Stalk length (cm)	662.7	485.85	10.85	12.67	73.31	38.94	19.17
Cane diameter (cm)	0.12	0.12	13.99	14.09	98.51	0.7	28.64
Brix %	3.44	3.08	8.84	9.33	89.71	3.43	17.26
Sucrose %	3.7	3.48	9.99	10.32	93.84	3.73	19.97
Purity %	14.57	10.95	3.53	4.07	75.14	5.92	6.3

C.C.S %	2.21	1.83	10.2	11.21	82.77	2.54	19.14
CCS (t/ha)	5.37	4.15	16.06	18.27	77.29	3.69	29.13
Cane Yield (t/ha)	169.52	127.18	11.81	13.64	75.02	20.15	21.11

Conclusion

Based on overall mean performance, genotype 2021 N 144 was identified as best clone exhibiting superior performance over the best standard for juice brix %, purity %, sucrose % and CCS %. Similarly, 2021 N 164 exhibited superior performance for number of tillers at 120 DAS, number of millable canes, stalk length and CCS (t/ha). Therefore, 2021 N 144 identified as best performer for juice quality characters and 2021 N 157 for cane yield contributing characters. The estimates of variability parameters revealed moderate GCV, PCV along with high h^2_{bs} and GAM were recorded for cane yield, CCS (t/ha), and cane diameter indicates wider range of variability in the material and importance of additive gene action in the inheritance of these characters in sugarcane. Moderate estimates of GCV and PCV coupled with high estimates of heritability in broad sense and moderate genetic advance as percent of mean recorded for number of tillers at 120 DAS, number of shoots, number of millable canes, stalk length, and CCS % also indicated the importance of additive gene action in the inheritance of this character.

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