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Assessment of Genetic Variability, Heritability and Genetic Advance for Enhancing Cane Yield and Quality Traits in Sugarcane (*Saccharum spp.* Complex)

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ABSTRACT

Background: Sugarcane is a vital sugar and bio-energy crop with rich in genetic diversity and holds immense potential for agricultural advancements. Leveraging this diversity, sugarcane breeding focuses on enhancing yield and sucrose quality, ensuring improved productivity and sustainability for both the sugar and bio-energy industries.

Methods: The experimental material consists of thirty sugarcane genotypes which were evaluated to assess genetic variability based on seventeen morphological and quality traits. The study was conducted using a randomized block design with three replications at the research farm of the Regional Research Station, Kaul, Kaithal, CCS Haryana Agricultural University, during the *spring* season of 2022-2023.

Result: The analysis of variance showed that the mean sum of squares due to genotypes was highly significant for all the characters studied, indicating adequate genetic variability in all thirty genotypes. Higher estimates of PCV than the corresponding GCV reveal that the environment has a minor influence on several traits. High heritability coupled with high genetic advance as a percent of the mean was observed for CCS (t/ha), cane yield, number of tillers at 120 DAP, number of shoots at 240 DAP and single cane weight. This underscores the importance of additive gene action, suggesting that selection for these characters would be effective for future breeding programs to improve yield and quality traits in sugarcane.

Key words: Cane yield, Genetic variability, Heritability, Sugar, Sugarcane.

INTRODUCTION

Sugarcane (*Saccharum officinarum* L.) is a tall, perennial C4 grass, native to warm temperate and tropical regions of India, South East Asia and New Guinea. Beyond its role in sugar production, sugarcane is a vital source of ethanol, fodder and electricity. Globally, the total sugarcane production is 1.92 billion metric tons with 26.08 million hectares an area of yield of 73.67 tons per hectare in 2022 (FAOSTAT, 2022). In India, sugarcane is grown on an area of 5.83 million hectares with a production of 494.22 million tons and an average productivity of 84.8 tons per hectare during 2022-23. In Haryana, sugarcane is grown on a 1.08 lakh hectare area with a production of 8.86 million tons and an average cane yield of 82.23 tons per hectare during 2022-23 (Anonymous, 2023; Hazarika *et al.,* 2025).

The sugar industry's efficiency is mostly determined by the availability of high-yielding and high-sugar cane types in sufficient quantities. The selection of ideal early and mid-late varieties has the potential to improve sugar recovery. The composition of varieties in the cane supply significantly impacts sugar recovery and any region's total sugar production (Singh *et al.,* 2019; Yadav *et al.,* 2025). Currently, the breeding of sugarcane varieties aims to improve, through the selection of clones that have high yield and high sucrose as well as drought tolerance, ratooning ability, disease and pest resistance and better adaptation. Within the crop improvement programs for genetic improvement of sugarcane, conventional breeding is still the main route for obtaining improved varieties (De Morais *et al.*, 2015; Mukesh *et. al.,* 2025) as compared to pulses (Mukesh *et al.,* 2024).

Hence, there is a need to develop new high-yielding cultivars that would boost cane yields. Genetic improvement for quantitative traits depends on the nature and amount of variability present in the genetic stock and the extent to which the desirable traits are heritable. Successful plant breeding relies heavily on genetic variability, which determines how often a population exhibits

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traits that differ from one another and allows breeders to improve the traits to generate new varieties (Tolera *et al.,* 2023). The variability may be due to environment or genotypes or interaction of both. The information about the extent of several genetic parameters *viz*., phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), broad sense heritability and genetic gain is necessary for successful genetic improvement of a genotype (Kishore *et al.,* 2015). Therefore, the present study aims to assess the extent of genetic variability, heritability and genetic advance for enhancing cane yield and quality traits in sugarcane clones.

MATERIALS AND METHODS

The experiment was conducted at the research farm of CCS Haryana Agricultural University, RRS, Kaul, Kaithal during the *spring* season 2022-23 having an altitude of 230.7 m above mean sea level, 29°85'N longitude and 76°66'E latitude and located at the Agro-climatic Zone-VI of India. The experiment material consists of thirty sugarcane clones comprising 27 advanced generation clones and 3 standard checks were evaluated by planting in a randomized block design with three replications. The details of genotypes are given in Table 1. Each genotype was grown in 4 rows of 6 m length with row-to-row spacing of 0.75 m. Seventeen Morphological and yield characters were *viz*. number of tillers (thousand/ha) at 120 days after planting, number of shoots (thousand/ha) at 240 days after planting, cane yield (t/ha) at harvest, number of millable canes (thousand/ha) at harvest, stalk length (cm) at harvest, stalk diameter (cm) at harvest and single cane weight (kg) at harvest. The data of morphological traits was recorded from five randomly tagged plants of each genotype. Yield and its associated characters were first recorded on a per-plot basis and then conversion formula was used to calculate it for per hectare basis. Quality traits namely brix %, pol %, purity % and CCS % were observed after the 8^{th} and 10^{th} month of planting while CCS (t/ha) and extraction % were studied at harvest. Analysis of variance was estimated according to Fisher (1925) to test the variations among genotypes by using F-test. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated using the formulae provided by Burton and DeVane (1953). Heritability in broad sense and genetic advance was computed with the formula given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The analysis of variance for different morphological and quality traits revealed that the mean sum of square due to genotypes was highly significant for all the seventeen characters namely numbers of tillers at 120 DAP (‘000/ha), number of shoots at 240 DAP (‘000/ha), stalk length (cm), stalk diameter (cm), number of millable canes at harvest (‘000/ha), single cane weight (Kg), cane yield (t/ha), CCS (t/ha), Brix % at 8^{th} month, pol % at 8^{th} month, purity % at 8^{th} month, CCS % at 8^{th} month, brix % at 10^{th} month, pol % at 10^{th} month, purity % at 10^{th} month, CCS % at 10TH month and extraction % as shown in Table 2. It implied that there was abundance of genetic variability in all thirty genotypes studied. Similar results had been observed by earlier workers namely Sharma *et al.* (2023); Hardeep *et al.* (2023); Patra *et al.* (2022); Kumar *et al.* (2021); Singh *et al.* (2020); Kumar *et al.* (2018) and Hiremath and Nagaraja (2016).

The estimated values of mean, range, variability, heritability (h^2), genetic advance and genetic advance as percent of mean for morphological and quality traits were illustrated in Table 3. The present study illustrated a large range of phenotypic variability and very significant differences among genotypes for all parameters under consideration, as illustrated by the graph in Fig 1. This suggested that there was significant amount of genetic variation present in the material and there is good scope for development of numerous morphological and qualitative attributes, including cane yield, if judicious selection pressure is applied to the genetic material. The present investigation is in accordance with Hardeep *et al.* (2023); Sharma *et al.* (2023); Tena *et al.* (2023); Tolera *et al.* (2023);

Table 1: List of advanced-generation clones/varieties of sugarcane.

Entry no.	Parentage
S10-31	CoH 119 × Co 86011
S12-38	CoH 119 GC
S14-105	Co 89003 × Co 775
S14-178	Co 89003 × CoPant 97222
S15-1743	Co 86011 GC
S15-1745	Co 86011 GC
S15-1765	Co 86011 GC
S15-1805	CoH 99 GC
S15-197	CoS 510 GC
S15-2975	CoH 92 GC
S15-3017	CoH 92 GC
S15-350	Co 98010 × Co 1148
S15-352	Co 98010 × Co 1148
S15-365	Co 98010 × Co 1148
S15-377	Co 98010 × Co 1148
S15-98	CoH 119 GC
S16-123	CoH 56 GC
S16-168	CoH 104 × Co 755
S16-174	CoH 104 × Co 755
S16-246	CoS 8436 × Co 89003
S16-249	CoS 8436 × Co 89003
S16-77	CoH 92 GC
S15-1763	Co 86011 GC
S15-2314	CoJ 82315 GC
S15-2387	CoJ 82315 GC
S16-266	CoS 8436 × Co 89003 GC
S16-369	CoVc 89101 PC
Standard checks	Co 0238
	Co 05009
	CoJ 64

Table 2: Analysis of variance for yield and quality characters in sugarcane clones.

Characters	Source of variation		
	Replication	Treatment	Error
Degree of freedom	2	29	58
Cane yield (t/ha)	322.031	661.950**	78.100
CCS (t/ha)	4.000	10.845**	1.154
CCS % (10 m)	0.352	1.093**	0.099
Pol % (10 m)	0.443	1.922**	0.162
Brix % (10 m)	0.092	1.730**	0.147
Purity % (10 m)	2.857	3.665**	0.683
Extraction % (10 m)	7.931	14.134**	5.872
NMC at harvest (‘000/ha)	351.763	414.915**	65.737
Stalk length (cm)	246.650	457.508**	77.620
Stalk diameter (cm)	0.014	0.139**	0.025
Single cane weight (kg)	0.000	0.045**	0.004
CCS % (8 m)	0.022	0.804**	0.061
Pol % (8 m)	0.028	1.430**	0.106
Brix % (8 m)	0.006	1.397**	0.123
Purity % (8 m)	0.271	4.045**	0.729
Number of shoots (‘000/ha) 240 DAP	734.481	629.732**	87.082
Number of tillers (‘000/ha) 120 DAP	1452.560	1339.249**	235.998

** = Significant at 1% level.

CCS = Commercial cane sugar; NMC = Number of millable canes; DAP = Days after planting; m = Month.

Table 3: Genetic parameters of seventeen characters for morphological and quality characters in sugarcane clones.

Characters	Mean	Range		Coefficient of variation		Heritability (%)	Genetic advance (%)	Genetic advance as per cent of mean (%)
		Maximum	Minimum	GCV (%)	PCV (%)			
Cane yield (t/ha)	87.84	114.52	52.95	15.88	18.80	71.36	24.27	27.63
CCS (t/ha)	9.94	14.24	5.50	18.07	21.05	73.67	3.17	31.95
CCS % (10 m)	12.14	13.18	10.68	4.73	5.39	77.06	1.04	8.57
Pol % (10 m)	17.45	18.83	15.63	4.38	4.95	78.41	1.39	8.00
Brix % (10 m)	19.50	20.83	18.13	3.72	4.21	78.23	1.32	6.78
Purity % (10 m)	89.52	91.01	86.08	1.11	1.44	59.25	1.58	1.76
Extraction % (10 m)	58.64	63.15	53.99	2.83	5.00	31.92	1.93	3.29
NMC at harvest (‘000/ha)	90.97	118	58	11.85	14.83	63.90	17.76	19.52
Stalk length (cm)	264.82	297.96	179.86	8.09	8.75	85.56	40.86	15.43
Stalk diameter (cm)	2.54	2.96	1.96	7.63	9.87	59.78	0.30	12.15
Single cane weight (kg)	1.01	1.21	0.62	11.50	13.08	77.31	0.21	20.84
CCS % (8 m)	11.12	12.01	9.87	4.47	4.99	80.10	0.91	8.24
Pol % (8 m)	16.13	17.33	14.57	4.11	4.58	80.64	1.22	7.61
Brix % (8 m)	18.39	19.73	17.03	3.54	4.02	77.55	1.18	6.42
Purity % (8 m)	87.71	89.84	84.88	1.19	1.54	60.25	1.68	1.91
Number of shoots at 240 DAP (‘000/ha)	108.31	146	74	12.41	15.11	67.50	22.76	21.01
Number of tillers at 120 DAP (‘000/ha)	143.50	201	89	13.36	17.12	60.91	30.83	21.48

CCS = Commercial cane sugar; NMC = Number of millable canes; DAP = Days after planting; m = Month; GCV = Genotypic coefficient of variation; PCV = Phenotypic coefficient of variation.

Patra *et al.* (2022); Kumar *et al.* (2021); Singh *et al.* (2020); Kumar *et al.* (2018) and Patil and Patel (2017).

According to Burton and DeVane (1953), a more accurate index for estimating the genetic variability of various traits. Examination of the data for the genotypic and phenotypic coefficient of variation revealed that CCS (t/ha) character exhibited (18.07%) moderate GCV and (21.05%) high PCV. The results for the coefficient of variation conform CCS (t/ha) were reported earlier by Sharma *et al.* (2023), Patra *et al.* (2022) and Béhou and Péné (2020). However, moderate estimates of variation were observed for the majority of morphological characters *viz*., cane yield (t/ha), number of millable canes at harvest, single cane weight, number of shoots at 240 days and number of tillers at 120 days. This indicated the presence of wide genetic variability and the possibility of genetic improvement through direct selection of these traits. These results were in agreement with the results of Hardeep *et al.* (2023); Singh *et al.* (2020), Kumar *et al.* (2018) and Mehareb *et al.* (2017). Purity % at 10th month recorded lowest values of GCV (1.11%) and PCV (1.44%) among morphological characters. Singh *et al.* (2020) and Kumari *et al.* (2020) also observed the lower estimate of genotypic and phenotypic coefficient of variation among morphological characters for Purity % at 10th month.

Lower values (<10%) of GCV and PCV were estimated for CCS % at 8th month, pol % at 8th month, brix % at 8th month, purity % at 8th month, stalk diameter, stalk length, CCS % at 10th month, pol % at 10th month, brix % at 10th month, purity % at 10th month and extraction %. These lower estimates imply that these features might slightly improve through direct selection. The present investigation are in accordance with Hardeep *et al.* (2023); Kumari *et al.* (2020); Ahmed *et al.* (2019); Kumar *et al.* (2018) and Agrawal and Kumar (2017).

The statistical analysis of data from seventeen characters under research revealed that the phenotypic coefficient of variance is higher than the genotypic coefficient, showing that variation is caused not only by genotypes but also by influences from the environment. The narrow difference between GCV and PCV levels demonstrated that genetic variables play a stronger influence in character expression than environmental ones. This is in consonance with earlier studies of Hardeep *et al.* (2023); Patra *et al.* (2022); Singh *et al.* (2020); Kumari *et al.* (2020); Kumar *et al.* (2018); Hiremath and Nagaraja (2016).

Measures of variability such as mean, range and coefficient of variation reflect mainly the extent of variability, not the proportion of variability that is heritable. To determine the heritability of each and every character, one must first understand the heritable portion of the variability. Knowing which traits are heritable is useful for breeders since it reveals how much improvement can be accomplished through selection for that specific feature. The heritability of any character of interest impacts the success of selection to improve it.

In the present investigation high heritability estimates were recorded for majority of morphological characters *viz*., stalk length (85.56%), single cane weight (77.31%), CCS (t/ha) (73.67%), cane yield (71.36%), number of shoots at 240 DAP (67.50%), number of millable canes at harvest (63.90%) and number of tillers at 120 DAP (60.91%). Among the quality characters highest broad sense heritability was recorded for pol % at 8th month (80.64%) followed by CCS % at 8th month (80.10%), pol % at 10th month (78.41%), brix % at 10th month (78.23%), brix % at 10th month (77.55%), CCS % at 10th month (77.06%) and purity % at 8th month (60.25 %). Purity % at 10th month (59.25%) and Extraction % at harvest (31.92%) showed moderate estimate of heritability. Hardeep *et al.* (2023), Patra *et al.* (2022) and Kumari *et al.* (2020) reported similar results as observed in this investigation. Kumari *et al.* (2020) also obtained high heritability values for pol % in juice at 12th month, CCS % at 12th month, brix % at 12th month, brix at 10th month stage, single cane weight, pol % in juice at 10th month, cane height

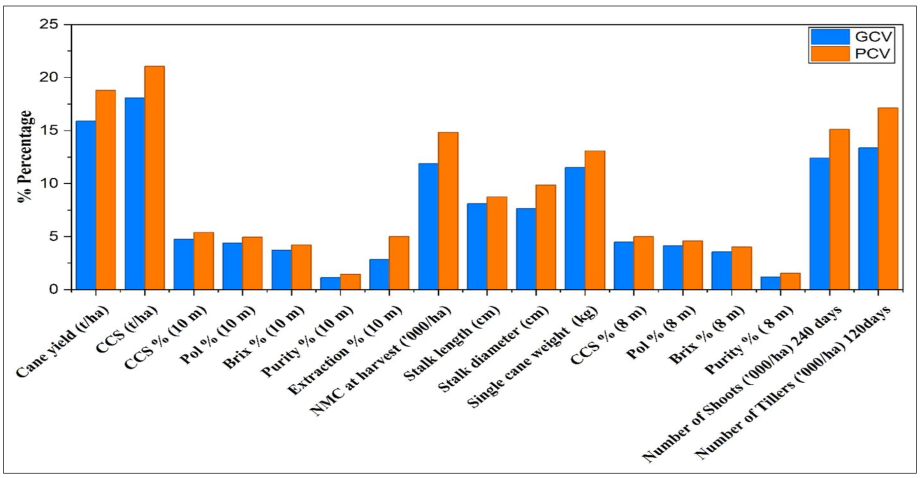

Fig 1: GCV and PCV for morphological and quality traits of sugarcane clones.

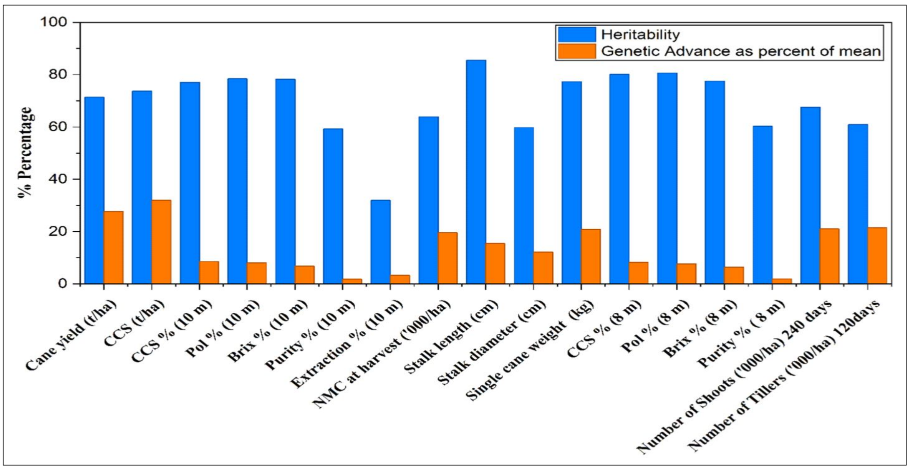

Fig 2: Heritability and Genetic Advance as per cent of mean for morphological and quality traits of sugarcane clones.

at harvest, cane diameter at harvest, cane yield, CCS % at 10th month, purity % at 10th month stage, number of milliable canes at harvest among the twenty characters. In contrary to present study Kumar *et al.* (2018) reported high broad sense heritability estimates for cane diameter, single cane weight, millable cane at harvest, extraction %, brix %, pol %, CCS % at 10th month, sugar yield and cane yield at harvest whereas, for purity % at 8th and 10th month they reported low estimates of heritability.

Genetic advance refers to the accumulation of genes towards under selection pressure and it is expressed as genetic advance as percentage of the mean. The high genetic advance as percent of mean was recorded for CCS (t/ha) (31.95%) followed by cane yield (27.63%), number of tillers at 120 DAP (21.48%), numbers of shoots at 240 DAP (21.01%) and single cane weight (20.84%). The moderate values were observed for number of millable canes at harvest (19.52%), stalk length (15.43%) and stalk diameter (12.15%). These results were in agreement with the findings of Hardeep *et al.* (2023); Singh *et al.* (2020); Ahmed *et al.* (2019) and Kumar *et al.* (2018). Agarwal and Kumar (2017) obtained similar result for CCS (t/ha), cane yield, number of tillers at 120 DAP and number of shoots at 240 DAP. Tabassum *et al.* (2023) also reported high genetic advance as percent of mean for cane yield, CCS yield, number of tillers, number of millable canes and single cane weight. Patil and Patel (2017) also reported that number of millable canes at harvest, stalk length and stalk diameter possess moderate genetic advance as per cent of mean.

According to Johnson *et al.* (1955), heritability estimates combined with expected to genetic gain will be more beneficial in predicting the outcome of picking the best genotypes through selection. The high genetic advance coupled with high heritability revealed the most efficient state for selection. High heritability coupled with high genetic advance as percent of mean was recorded for CCS (t/ha) (73.67% and 31.95%) followed by cane yield (71.36% and 27.63%), number of tillers at 120 DAP (60.91% and 21.48%), numbers of shoots at 240 DAP (67.50% and 21.01%) and single cane weight (77.31% and 20.84%) as shown in graph (Fig 2) suggesting that these characters are governed by additive gene action and selection for these characters will be effective for further improvement in cane yield. In contract with present study Hardeep *et al.* (2023) observed high broad sense heritability with high genetic advance for number of tillers at 120 DAP, number of shoots at 240 DAP, single cane weight, cane length, cane yield and CCS (t/ha). High heritability with high genetic advance as per cent of mean was recorded for cane yield, CCS yield, number of tillers, number of millable canes and single cane weight was observed by Tabassum *et al.* (2023).

Two traits *viz*., number of millable canes at harvest (63.90% and 19.52%) and stalk length (85.56% and 15.43%) in current investigation showed high heritability in association with moderate genetic advance as percent of mean respectively. It indicates that non-additive gene expression governs these characters and careful selection is necessary to achieve the desired improvements in these characters. These results are in conformity with the findings of Kumar *et al.* (2018) for number of millable canes at harvest and stalk length. Negi *et al.* (2017) obtained similar result for cane height and Kumari *et al.* (2020) for number of millable canes at harvest.

The current findings provide significant insights into the genetic diversity of sugarcane germplasm. Based on the experiment, it can be concluded that CCS (t/ha), cane yield, number of tillers at 120 DAP, number of shoots at 240 DAP and single cane weight demonstrate the importance of additive gene action. Selection for these traits will be effective in future breeding programs aimed at improving sugarcane yield and quality traits.

CONCLUSION

The present investigation revealed considerable genetic variability among thirty sugarcane genotypes for all morphological and quality traits studied. Higher estimates of PCV over GCV indicated marginal environmental influence on trait expression. High heritability coupled with high genetic advance as percent of mean was recorded for CCS (t/ha), cane yield, number of tillers at 120 DAP, number of shoots at 240 DAP and single cane weight, confirming the predominance of additive gene action for these traits. This suggests that direct selection for these characters would be rewarding in future breeding programs. Number of millable canes and stalk length exhibited high heritability with moderate genetic advance, indicating non-additive gene action and the need for cautious selection. The superior genotypes identified in this study can be effectively utilized in hybridization and selection programs aimed at improving cane yield and sucrose recovery under Haryana agroclimatic conditions.

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Conflict of interest

No conflicting interests are disclosed by the authors.

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