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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND QUALITY ATTRIBUTES IN ADVANCED SUGARCANE (*Saccharum officinarum* L.) CLONES.

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ABSTRACT

A field evaluation was conducted during the *Rabi* season of 2024–25 to assess the genetic architecture, heritable components, and expected genetic gains among seventeen advanced sugarcane genotypes including three check varieties (Co 86032, Coc 671, and Co 9004) using a Randomized Block Design (RBD) with three replications. Analysis of variance (ANOVA) revealed highly significant differences among genotypes for all quantitative agronomic and juice quality attributes. Genotypic coefficient of variation (GCV) values were high for the number of millable canes (NMC), Commercial Cane Sugar (CCS) yield, and cane yield. High heritability (h^2) coupled with high genetic advance as a percentage of mean (GA) was recorded for NMC (h^2 =84.19 %, GA = 30.93%), CCS yield (h^2=70.93%, GA = 20.16%), and cane yield (h^2=59.37%, GA = 14.61%). This configuration demonstrates the predominance of additive gene action, proving that phenotypic selection for these characters will be highly rewarding. Advanced breeding clones CoM 19081 (134.56 t/ha) and CoR 19143 (130.58 t/ha) emerged as elite high-yielding entries, while Co 19014 generated the maximum sugar output (18.91 t/ha of CCS). The study suggests that selecting for high millable cane populations alongside optimal sucrose metrics is the most effective breeding strategy to maximize regional sugar productivity.

***Key words*:** Sugarcane, Genetic variability, Heritability, Genetic advance, Additive gene action, Quality traits.

Introduction

Sugarcane (*Saccharum officinarum* L.) is a paramount global agro-industrial cash crop, functioning as the foundational source for crystalline sugar extraction, animal feed components, and high-volume bio-ethanol production. To break current yield plateaus and support commercial processing facilities, modern crop improvement programs focus heavily on creating varieties that combine high agricultural tonnage with rapid sugar accumulation. However, because sugarcane features a complex inter-specific polyploid hybrid genome combined with a highly heterozygous clonal propagation network, direct phenotypic selection for ultimate economic yield is frequently inefficient (D'Hont *et al*., 1996; Elahi and Ashraf, 2001). Cane yield and commercial sugar yield are complex quantitative parameters controlled by polygenic structures that are highly sensitive to environmental fluctuations (Fisher, 1918; Jamil, 2026).

The efficiency of any crop breeding program depends directly on the nature and magnitude of genetic variability present within the working germplasm. Genetic variability acts as the primary prerequisite for selection; without significant heritable differences among breeding lines, selection protocols cannot succeed (Anbanandan and Eswaran, 2018; Ahmed *et al*., 2019). However, the total observable phenotypic variance within a trial population is a combined product of the true genotypic variance and environmental noise. To separate these components,

breeders use statistical parameters like the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), which provide a clear measure of absolute variability across traits across diverse field crops (Sahu *et al*., 2008; Upadhyay *et al*., 2009; Ali *et al*., 2021; Yadav and Sahu, 2022; Sahu *et al*., 2023; Belsariya *et al*., 2024; Chang, 2025).

While GCV measures the total extent of genetic variation present for a character, it does not determine the proportion of this variation that can be reliably transmitted from parent to offspring. This heritable component is quantified using broad-sense heritability (h^2). However, high heritability estimates do not always signify high genetic progress in subsequent generations unless the trait is governed primarily by additive gene action. Therefore, heritability estimates must be evaluated in tandem with Genetic Advance as a percentage of Mean (GA) to build an accurate selection model (Jogi *et al*., 2009; Sahu *et al*., 2013; Sahu *et al*., 2015; Toppo and Sahu, 2022; Bi, 2023; Harrison, 2024). Trait combinations displaying high heritability coupled with high genetic advance indicate the predominance of additive gene action, making them ideal targets for mass phenotypic selection. This investigation applies these genetic parameters to a diverse collection of fourteen elite genotypes and three checks evaluated under an Advanced Varietal Trial setup to isolate reliable selection criteria for sub-tropical sugarcane breeding.

Materials and Methods

The field experiment was conducted at the experimental research farm of Sant Kabir College of Agriculture and Research Station, Indira Gandhi Krishi Vishwavidyalaya, Kawardha (Kabirdham) (C.G.), India, during the *Rabi* cultivation window of 2024–25. The genetic material evaluated consisted of fourteen advanced clonal entries tested against three standard checks (Co 86032, Coc 671 and Co 9004). The trial was conducted in a Randomized Block Design (RBD) with three replications. Each genotype was allocated a net plot size of 36 m^2 with a standardized row spacing of 1.2 meters. The genotypes were planted in the first week of February by adopting all recommended agronomical practices. Two-to-three budded setts with an overlapping arrangement were planted in a single-row system. The yield performance and other yield-attributing characters were observed at the time of maturity (James, 1971).

Observations were systematically recorded for nine critical growths, yield and bio-chemical attributes. The number of millable canes (NMC '000/ha) and cane yield (t/ha) were logged on a plot scale at maturity. Structural stalk dimensions, including cane height (cm) at maturity, single cane weight (SCW, kg) and cane girth (stalk diameter, cm) were measured from five randomly selected canes per genotype per replication. At harvest, representative stalk samples were crushed through a commercial trial mill to perform juice analytics. Brix (%) was recorded using a Brix hydrometer, while sucrose % was evaluated using a polarimeter. Juice Purity % was calculated using the formula (Sucrose % / Brix %) × 100. The total Commercial Cane Sugar yield (CCS t/ha) was derived using the formula (Cane yield (t/ha) × CCS%)/ 100 (Kang *et al*., 1989). Statistical analysis of variance (ANOVA) was executed according to Panse and Sukhatme (1967). Genotypic and phenotypic coefficients of variation (GCV and PCV) were estimated using the formulas described by Burton (1952). Heritability (h^2) was computed following Burton and De Vane (1953) and the expected genetic advance under selection alongside genetic advance as a percentage of mean (GA) was worked out using the statistical procedures outlined by Johnson *et al*., (1955).

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance revealed highly significant differences ($p < 0.01$) among the seventeen sugarcane genotypes for all evaluated agronomic, morphological and chemical processing attributes (including NMC, cane height, single cane weight, cane girth, cane yield, CCS yield, Brix % and Sucrose %). This confirms the presence of substantial genetic diversity within the testing matrix, matching the findings of Sharma *et al*., (2022) and Joshi *et al*., (2026) in quantitative trait evaluation trials. The calculated F-values for genotypes significantly exceeded critical table limits, demonstrating that the observed performance differences are driven by true genetic variation rather than random environmental factors.

Table 1: Analysis of Variance (ANOVA) for Yield, Stalk and Juice Quality Traits.

Source of Variation	df	NMC ('000/ha)	Height (cm)	SCW (kg)	Girth (cm)	Cane Yield (t/ha)	CCS Yield (t/ha)	Brix %	Sucrose %
Replications	2	48.20	42.15	0.01	0.04	18.85	0.85	0.14	0.05
Genotypes	16	255.26**	636.76**	0.02**	0.06**	226.34**	5.79**	4.46**	4.59**
Error	32	48.61	63.14	0.002	0.01	42.05	0.70	0.16	0.15
(* Significant at 5%; ** Significant at 1% level).									

Table 2: Mean Phenotypic Performance Profiles of Sugarcane Clones.

Genotype Entry	NMC ('000/ha)	Height (cm)	SCW (kg)	Girth (cm)	Cane Yield (t/ha)	CCS Yield (t/ha)	Brix %	Sucrose %	Purity %
Co 19002	51.53	273.67	1.76	8.55	98.83	12.89	20.16	18.52	91.87
Co 19004	56.81	302.33	1.85	7.31	92.32	12.63	21.96	19.66	89.53
Co 19005	55.14	297.89	1.74	7.84	106.54	15.08	22.52	20.28	90.05
Co 19008	50.28	294.22	2.52	9.28	101.70	14.62	22.10	20.38	92.22
Co 19009	47.78	306.67	2.12	8.23	100.19	14.95	22.79	21.11	92.63
Co 19014	85.83	298.33	1.61	7.42	127.22	18.91	22.49	20.97	93.24
CoM 19081	66.53	329.78	1.62	7.34	134.56	17.81	21.59	19.12	88.56
CoT 19366	41.81	300.33	1.77	8.07	98.36	14.97	23.80	21.69	91.13
CoT 19367	49.17	283.16	1.43	7.88	92.49	14.10	23.29	21.57	92.61
CoR 19141	61.81	280.69	1.61	8.05	118.90	16.71	23.19	20.38	87.88
CoR 19143	62.36	308.44	1.75	7.67	130.58	18.47	23.23	20.48	87.78
CoT 18366	36.81	269.33	1.81	8.36	73.74	11.37	22.23	21.44	92.29
CoT 18368	64.58	284.56	1.66	7.88	120.31	17.80	22.82	21.00	92.02
CoT 18369	46.39	298.67	2.00	8.62	95.62	14.81	24.23	22.08	91.13
Co 86032 (Check)	46.67	307.78	1.81	8.34	107.79	15.70	21.71	20.45	89.09
Coc 671 (Check)	51.67	304.22	2.00	9.17	120.09	16.79	21.54	19.83	90.14
Co 09004 (Check)	42.78	306.67	1.75	8.24	103.29	14.76	22.22	20.33	86.99

Evaluation of Clonal Performance Profiles

The performance evaluations across the genotypes highlighted several promising elite entries that outclassed the standard commercial check varieties. Advanced clone CoM 19081 recorded the highest cane yield of 134.56 t/ha and maximum stalk height of 329.78 cm, with single cane weight of 1.62 kg, girth of 7.34 cm, NMC of 66.53 '000/ha and CCS yield of 17.81 t/ha. Entry CoR 19143 also showed strong performance, yielding 130.58 t/ha with cane height of 308.44 cm, SCW of 1.75 kg, girth of 7.67 cm, NMC of 62.36 '000/ha and CCS yield of 18.47 t/ha, outyielding the commercial checks Co 86032 (107.79 t/ha), Coc 671 (120.09 t/ha) and Co 09004 (103.29 t/ha).

Clone Co 19014 produced the highest number of millable canes (85.83 '000/ha), driving its final cane yield to 127.22 t/ha, which compensated for its smaller stalk girth (7.42 cm) and single cane weight (1.61 kg). Regarding industrial quality parameters, advanced entry CoT 18369 excelled in sucrose accumulation metrics, recording the highest values for juice Brix (24.23%), Sucrose (22.08%), and Purity (91.13%), yielding 95.62 t/ha of cane and 14.81 t/ha of CCS. However, when evaluating total commercial sugar output per hectare, Co 19014 showed the highest final sugar productivity (18.91 t/ha of CCS), followed closely by CoR 19143 (18.47 t/ha) and CoM 19081 (17.81 t/ha). Check entries recorded CCS yields of 15.70 t/ha (Co 86032), 16.79 t/ha (Coc 671) and 14.76 t/ha (Co 09004). This demonstrates that absolute field biomass combined with high stalk density is a major driver of total sugar output per unit area in this group of genotypes.

Genetic Variability, Heritability, and Expected Genetic Advance

The metrics tracking phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) displayed specific patterns across traits. PCV values were slightly higher than corresponding GCV indicators for all attributes, implying that the influence of local environmental variations was minimal. This pattern establishes that selection protocols built upon structural phenotypes will remain highly reliable. Wide gaps for GCV estimates were recorded, spanning from 1.21% for juice Purity % up to 16.36% for total millable cane count, indicating considerable variability in the breeding stocks.

The highest GCV estimates were obtained for the number of millable canes (16.36% GCV, 17.83% PCV), Commercial Cane Sugar yield (11.62% GCV, 13.80% PCV), single cane weight (9.53% GCV, 11.32% PCV) and cane yield (9.20% GCV, 11.95% PCV) (Gowda *et*

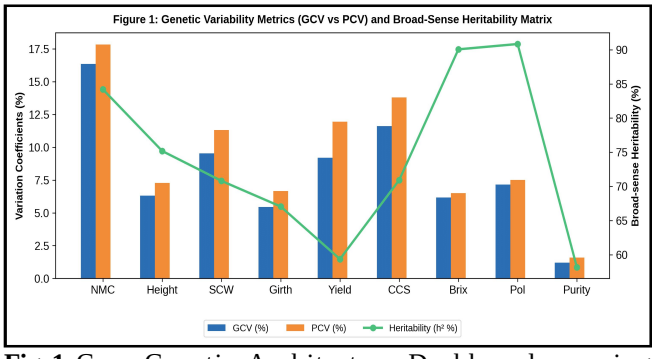


Fig. 1: Core Genetic Architecture Dashboard mapping structural metrics and heritable variation boundaries across lines.

Table 3: Genetic Parameter Matrix for Agro-Industrial Sugarcane Characters.

Measured Trait Profile	Genotypic Var (σ^2g)	Phenotypic Var (σ^2g)	GCV (%)	PCV (%)	Heritability (h^2 %)	Genetic Advance (GA)	GA (%)
NMC ('000/ha)	68.88	117.49	16.36	17.83	84.19	46.85	30.93
Height (cm)	191.21	254.35	6.32	7.29	75.18	24.70	11.29
Single Cane Wt. (kg)	0.007	0.010	9.53	11.32	70.81	0.14	16.52
Cane Girth (cm)	0.016	0.024	5.45	6.66	67.06	0.23	9.19
Cane Yield (t/ha)	61.43	103.48	9.20	11.95	59.37	12.44	14.61
CCS Yield (t/ha)	1.70	2.40	11.62	13.80	70.93	2.26	20.16
Brix %	1.43	1.59	6.17	6.50	90.06	2.34	12.06
Sucrose %	1.48	1.63	7.16	7.51	90.84	2.39	14.06
Purity %	0.82	0.91	1.21	1.59	58.17	1.67	1.91

al., 2016; Hiremath and Nagaraja, 2016; Sahu and Tiwari, 2019; Sahu, 2021; Sahu *et al*., 2025; Sahu *et al*., 2026). Moderate to lower GCV values were observed for sucrose % (7.16% GCV, 7.51% PCV), cane height (6.32% GCV, 7.29% PCV), Brix % (6.17% GCV, 6.50% PCV) and cane girth (5.45% GCV, 6.66% PCV). These numbers reflect strong underlying genetic potential, confirming clear opportunities for directional crop improvement through selection. Conversely, juice Purity % showed a very narrow GCV value (1.21% GCV, 1.59% PCV), demonstrating a highly conserved parameter within this trial group, consistent with findings by Somu *et al*., (2020), Sharma *et al*., (2022), and Mishra *et al*., (2025).

Heritability metrics spanned from a baseline of 58.17% for juice Purity % up to a peak of 90.84% for Sucrose %. Outstanding heritability values were identified across the majority of agronomic components: Sucrose % (90.84%), Brix % (90.06%), number of millable canes (84.19%), mature stalk height (75.18%), Commercial Cane Sugar yield (70.93%), single cane weight (70.81%) and cane girth (67.06%). Cane yield also showed a high heritability value of 59.37%. These results show that a major portion of the observed variation is driven by genetic factors, indicating that selecting for these characters based on phenotypic expression will be effective.

Importantly, high heritability values coupled with high genetic advance as a percentage of mean (GA) respectively; were recorded for number of millable canes (h^2 = 84.19%, GA = 46.85, GA % = 30.93%), Commercial Cane Sugar yield (h^2 = 70.93%, GA = 2.26, GA % = 20.16%), and single cane weight (h^2 = 70.81%, GA = 0.14, GA % = 16.52%). Cane yield also followed this trend with high heritability and moderate-to-high genetic gains h^2 = 59.37%, GA = 12.44, GA % = 14.61%), alongside sucrose % (h^2 = 90.84%, GA = 2.39, GA % = 14.06%), Brix % (h^2 = 90.06%, GA = 2.34, GA % = 12.06%), cane height (h^2 = 75.18%, GA = 24.70, GA % = 11.29%), cane girth (h^2 = 67.06%, GA = 0.23, GA % = 9.19%) and Purity % (h^2 = 58.17%, GA = 1.67, GA % = 1.91%). This combination indicates that primary yield components and sugar yield attributes are governed predominantly by additive gene action, making them ideal targets for directional phenotypic selection (Agrawal and Kumar, 2017; Sahu *et al*., 2025; Sahu *et al*., 2026).

Conclusion

This quantitative genetic evaluation demonstrates that the number of millable canes, Commercial Cane Sugar yield, and single cane weight are governed primarily by additive gene action, as shown by their high heritability values coupled with high genetic advance. Consequently, direct mass selection based on these parameters will be highly effective for increasing sugarcane yield and total sugar yield per hectare. Advanced clonal entries CoM 19081 and CoR 19143 displayed excellent genetic potential, outperforming regional standard checks in both field yield and sugar production. Modern sugarcane breeding programs should focus selection indices on optimizing millable cane numbers while maintaining optimal single stalk weight and sucrose accumulation profiles to maximize economic returns per unit area.

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