

# ASSESSMENT OF GENETIC PARAMETERS AND TRAIT INTERRELATIONSHIPS IN EARLY MATURING SUGARCANE CLONES OVER THREE CROP CYCLES

D. ADILAKSHMI\*, P.V. PADMAVATHI and D. PURUSHOTAMA RAO

Department of Genetics and Plant Breeding, Regional Agricultural Research Station, Anakapalle, Acharya N.G. Ranga Agricultural University, Andhra Pradesh-531001, India

Date of Receipt : 28-10-2025

Date of Acceptance : 05-12-2025

## ABSTRACT

This study evaluated seven early maturing sugarcane clones across three crop cycles at the Regional Agricultural Research Station, Anakapalle, to estimate genetic variability, heritability, trait associations, and direct effects on key economic traits. The analysis of variance indicated significant effects of genotype, season and genotype  $\times$  season interactions for all traits under this study, except for number of millable canes, cane girth and single cane weight. Among ten sugarcane clones across three crop cycles, clone 2018A 133 showed the best overall performance for cane yield, sugar yield and millable canes, while 2018A 65 excelled in juice quality traits. The ratoon crop consistently exhibited higher genotypic coefficients of variation, broad-sense heritability, and genetic advance, especially for cane yield, commercial cane yield and number of millable canes, signifying their selection potential in later stages. Brix, Sucrose and CCS% demonstrated moderate to low GCV values over crop cycles, suggesting limited genetic variability. Cane yield and CCS yield both exhibited high heritability across the three crop cycles. Traits like Brix, CCS%, and Sucrose showed low to moderate heritability in the early crop cycles but exhibited substantial increase in later crop cycles. Traits such as cane yield, CCS yield, and number of millable canes had both high heritability and high genetic advance as a percentage of mean in the ratoon crop. In contrast, traits like single cane weight and cane girth showed inconsistent heritability and genetic advance across cycles, reflecting genetic instability. Juice quality traits (Brix, Sucrose, CCS%) showed increased heritability and genetic advance in the ratoon crop. Cane yield showed a strong positive correlation with CCS yield in all crop cycles. Juice quality traits such as Brix, Sucrose, and CCS% showed very strong positive correlations among themselves in all cycles. CCS yield exhibited significant positive correlations along with substantial direct effects in each season, highlighting their importance as key selection criteria in sugarcane breeding programs.

**Key words:** Genetic advance, Genetic correlation, Heritability and Path analysis

## INTRODUCTION

Sugarcane is cultivated extensively in the tropical and subtropical regions of India. It was

grown across 56.48 lakh hectares, producing an annual yield of 446.43 million tonnes in the country (E&S, DAC - \*2nd Adv. Est. - 2023).

---

\*Corresponding author email id: [d.adilakshmi@angrau.ac.in](mailto:d.adilakshmi@angrau.ac.in)

However, the area and production of sugarcane in Andhra Pradesh had been declining steadily since 2014–15. Over the past six years, there has been a drastic reduction in both the area under cultivation and production. Data from 2018–19 to 2023–24 indicated a drop in the area from 1.02 lakh hectares to 0.27 lakh hectares, representing a nearly 74% decline. Correspondingly, production fell from 8.09 million tonnes in 2018–19 to only 2.10 million tonnes in 2023–24 (E&S, DAC – \*2nd Adv. Est. – 2023-2). The long duration conventional sugarcane varieties posed challenges, particularly when early crushing schedules of sugar mills did not align with the maturity of the crop. This mismatch led to poor sugar recovery and economic losses for both farmers and millers (Tyagi *et al.*, 2023). To address these challenges, the introduction of early maturing sugarcane clones was proposed as a strategic solution.

Effective selection of cultivars within a plant population across diverse environments requires a thorough understanding of the genetic relationships among key traits. Insights into genetic and phenotypic variances, covariances and associated statistical parameters are essential for predicting the response to selection and for developing best selection strategies (Tolera *et al.*, 2024). Genetic parameters are population and environment specific, meaning they are influenced by the particular genotypes and environmental conditions under which they are estimated (Barreto *et al.*, 2021). Misleading conclusions can arise from unrepresentative sampling of genotypes or production environments, including variations across years and locations (Tolera *et al.*, 2023). Consequently, genetic correlations among sugarcane traits reported in other studies had limited applicability to multi-yield traits under the North Coastal Zone of Andhra Pradesh

over the crop cycles. Therefore, region-specific and cycle-wise genetic evaluations were essential to ensure accurate selection and genetic improvement of sugarcane cultivars in this agro-climatic zone.

The present study aimed to estimate the genetic correlations among key yield-related traits in sugarcane and to understand the nature of these correlations through path coefficient analysis. Additionally, the study sought to examine the influence of different crop cycles on the genetic relationships among sugarcane clones. The investigation was conducted using seven sugarcane clones evaluated under multi-yield trait trials across three cropping cycles at the Regional Agricultural Research Station, Anakapalle.

## MATERIAL AND METHODS

The experimental material comprised seven early maturing sugarcane clones, namely 2018A 133, 2018A 30, 2018A 31, 2018A 37, 2018A 65, 2018A 107 and 2018A 152, which were evaluated along with three standard checks: 87A 298, CoC 01061, and 2000A 128. The field experiments were conducted at the Regional Agricultural Research Station (RARS), Anakapalle, located at 17.6914° N latitude and 83.0041° E longitude, with an altitude of 26 meters above sea level. The study was carried out over three crop cycles, including the first plant and ratoon crops during 2022–23 and 2023–24, respectively, and a second plant crop during 2023–24. The experiment was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was grown in plots consisting of six rows, each six meters long, with a row-to-row spacing of 90 cm. Standard agronomic practices were uniformly followed throughout all three seasons, as recommended for the region (Sugeerthi *et al.*, 2018). Both the plant and ratoon crops were harvested at 10 months of age, specifically during the second fortnight of November, to maintain

uniformity in harvesting age for precise and comparable data analysis.

The present study recorded phenotypic data from nine quality and quantitative traits of sugarcane according to the guidelines provided by PPV & FR, 2001, under the DUS criteria. These traits included the number of millable canes (NMC) expressed in '000/ha, single cane weight (SCW) in kg, and cane yield (CY) in t/ha, it was measured on a per-plot basis and subsequently calculated per hectare. CCS yield (CCSY) was determined using the formula  $(\text{Cane yield} \times \text{CCS \%}) / 100$ . At the harvest stage, brix (%) (BP) and sucrose (%) (SP) were recorded using a Brix refractometer and a sucrolyser, respectively. The Commercial Cane Sugar percentage (CCSP) was calculated by the formula  $(\text{Sucrose \%} \times 1.022) - (\text{Brix \%} \times 0.292)$ . Cane length (cm) and girth (cm) recorded at harvest stage (Nair *et al.*, 1999).

Phenotypic data from both plant crops and ratoon crop were collected and analysed to assess genetic variability and trait associations. Bartlett's test was performed to evaluate the homogeneity of error variances across three crop cycles using Grapes statistical software. The non-significant results obtained from the three crop cycles indicated consistent error variance, allowing the data to be pooled for further analysis. All genetic analyses were performed using Grapes statistical software. Genotypic and phenotypic variations were calculated following the method described by Burton and De Vane (1953). Coefficients of variation were computed according to the guidelines of Singh and Chaudhary (1999). Broad-sense heritability was estimated using the formula provided by Allard (1960). Genetic advance was recorded following the approach of Johnson *et al.* (1955). Genotypic correlations were calculated using the method suggested by Al-Jibouri *et al.*

(1958) and were analyzed for direct and indirect effects based on the methodology of Dewey and Lu (1959).

## RESULTS AND DISCUSSION

### Analysis of variance and mean performance

Genetic analysis for cane yield and juice quality traits among ten early maturing sugarcane clones evaluated across three crop cycles is presented in Table 1. All traits exhibited statistically significant ( $P < 0.05$ ) differences for genotype, season, and genotype  $\times$  season interaction effects, except for number of millable canes, cane girth and single cane weight, which were non-significant for genotypic means. These results indicated the presence of considerable genetic variation among the clones, which is essential for effective selection and genetic improvement. Similar findings were reported by Shanmuganathan *et al.* (2015), who observed significant variation for cane yield and CCS yield. Yadawad *et al.* (2022) also reported significant genetic variability for sucrose content (%), Brix (%), and CCS (%). In contrast, Vinu *et al.* (2024) observed non-significant variation for number of millable canes and single cane weight across crop cycles, which support the current results. The detection of significant genotype  $\times$  season interaction further emphasized the importance of evaluating genotypes across multiple environments, as also highlighted by Milligan *et al.* (1990), to ensure stable performance and reliable selection of superior clones.

The mean performance of ten early maturing sugarcane clones over three crop cycles was illustrated in Table 2. The IIP crop recorded the highest millable cane population, showing improved establishment during the second crop cycle. Clones 2018A 133 and CoC 01061 showed superior stooling capacity ( $>115$  canes in IIP), suggesting good ratoon

vigor. Sucrose and Brix content increased notably in the ratoon crop, indicating enhanced sugar accumulation in later crop stages. CCS improved with successive crop cycles, aligning with sucrose trends. 2018A 65 had the highest ratoon CCS (14.60%), suggesting strong recovery potential for sugar yield. The clones 2018A 107 and 2018A 37 maintained relatively high SCW (>1.0 kg) in IP, beneficial for early yield. Yield dropped notably in the ratoon crop ("21.6%), showing moderate ratoon decline. 2018A 133 achieved the highest cane yield across all cycles (average H" 101 t/ha), marking it as a top-performing genotype. The study indicates clone 2018A 133 as the best performer for both cane and sugar yield stability across cycles, while 2018A 65 shows strong potential for sugar recovery. The ratoon decline is evident mainly due to reduced cane weight and population, despite improvements in juice quality.

### Genetic Variability Analysis

The genetic variance components for cane yield and juice quality traits among ten sugarcane clones over three crop cycles were summarized in Table 3. In this study, the phenotypic coefficient of variation (PCV) consistently exceeded the genotypic coefficient of variation (GCV) for all traits. The ratoon crop (RA) exhibited higher GCV values for most economic traits, except for cane length and girth, suggesting a greater potential for genetic gain in later cycles. Thus, selection was recommended to prioritize ratoon crop performance due to its pronounced genetic variability (Tena *et al.* 2016).

Cane yield, commercial cane yield, and single cane weight exhibited moderately to high GCV and PCV across all crop cycles, with the highest values observed in the ratoon crop, indicating greater genetic variability and selection potential at later stages. Particularly, cane yield and commercial cane yield showed

GCV values of 21.20 and 20.24, respectively, suggesting strong prospects for genetic improvement. These results were in alignment with the findings of Tena *et al.* (2023), who reported increased genetic advance in older crop cycles. In contrast, single cane weight displayed erratic behavior, especially in the second plant stage, where a high PCV (26.01) and low GCV (2.07) indicated a strong environmental influence. Brix, Sucrose, and CCS% demonstrated moderate to low GCV values over crop cycles, suggesting limited genetic variability. Cane length and girth showed very high GCV and PCV in the second plant stage, suggesting that these traits were more influenced by genotype  $\times$  crop interactions. These observations were consistent with Milligan *et al.* (1990), who highlighted strong genotype  $\times$  crop and location interactions for stalk traits such as length and girth.

The heritability estimates across crop cycles revealed valuable insights for sugarcane improvement. In the present study, most traits showed higher heritability (CY: 90.28%, NMC: 89.18%, CCS Yield: 84.61%, and Sucrose: 80.39%) in the ratoon crop, suggesting that genetic factors played a more significant role in later crop cycles. These findings aligned with those of Abu-Ellail *et al.* (2017), who reported increased heritability and genetic gain in older ratoon crops due to reduced environmental variance and improved genotype differentiation. Cane yield and CCS yield both maintained high heritability across all stages, indicating strong selection potential for yield improvement throughout the crop cycle. Traits like Brix, CCS%, and Sucrose showed low to moderate heritability in the early crop cycles but exhibited substantial increases in later cycles. This trend indicated environmental sensitivity in the early stages but greater genetic determination as the crop matured. Milligan *et al.* (1990) observed similar increases in genetic parameters in

**Table 1. Combined pooled analysis of variance for nine characters in ten sugarcane genotypes across three seasons**

Source	Df	NMC		BP		SP		CCS (%)		SCW		CCSY		CL		CG		CY	
		Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)	Mean Sq (>F)	Pr (>F)
Location	2	4221	0	17	0	2365	0	9	0	2742	0	147	0	3822	0	440	0	440	0
Treatment	9	57	0	2	0	8	0	2	0	26	0	14	0	61	0	21	0	21	0
Replication with in location	6	1	1	0	1	1	0	0	0	3	0	1	0	3	0	2	0	2	0
Location x Treatment	18	29	0	2	0	6	0	2	0	14	0	10	0	29	0	11	0	11	0
Error	54	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1

NMC= Number of millable canes ('000/ha), BP= Brix (%), SP= Sucrose (%), CCS (%)= Commercial cane sugar, SCW= Single cane weight (kg), CCSY= Commercial cane sugar yield (t/ha), CL= Cane length (cm), CG=Cane girth (cm) and CY= Cane yield (t/ha).

**Table 2a. Mean performance of ten clones over three crop cycles among nine agronomic traits**

Clone	NMC			Brix (%)			Sucrose (%)			CCS (%)		
	IP	IIP	Ratoon	IP	IIP	Ratoon	IP	IIP	Ratoon	IP	IIP	Ratoon
2018A 133	109.57	118.29	108.33	17.73	16.97	19.30	16.25	15.97	17.27	11.43	11.36	12.01
2018A 30	76.85	100.71	100.52	18.83	19.20	17.23	16.73	18.27	16.68	11.60	13.06	12.01
2018A 31	92.08	102.63	78.70	17.79	18.40	18.80	15.61	17.09	17.73	10.76	12.09	12.63
2018A 37	88.58	93.21	83.95	18.53	16.83	19.90	16.89	15.25	18.83	11.84	10.67	13.43
2018A 65	87.14	96.53	100.31	18.58	18.60	21.40	17.87	17.39	20.40	12.84	12.34	14.60
2018A 107	67.28	101.31	98.36	18.83	18.08	19.80	16.37	16.97	18.20	11.24	12.06	12.82
2018A 152	84.98	100.54	99.28	17.34	17.50	18.80	16.00	16.23	17.10	11.29	11.48	11.98
87A 298	95.37	88.35	88.89	18.65	17.30	19.97	17.00	16.07	18.69	11.93	11.37	13.27
CoC 01061	96.09	118.75	93.42	19.66	17.73	19.60	17.59	16.21	17.76	12.23	11.39	12.42
2000A 128	84.67	81.33	66.15	19.35	18.60	19.33	18.36	16.90	17.35	13.11	11.85	12.09
Mean	88.26	100.16	91.79	18.53	17.92	19.41	16.87	16.64	18.00	11.83	11.77	12.73

older crops, emphasizing the need to evaluate advanced stages for juice quality traits. Single cane weight exhibited very high heritability in the first plant crop (91.43%) and the ratoon crop (85.81%) but showed almost negligible heritability in the second plant crop (0.63%), implying that environmental influence or inconsistency in expression strongly affected this trait during the second plant stage, as also discussed by Milligan *et al.* (1990) regarding the instability of stalk weight across cycles. Overall, the results suggested that ratoon crops offered a more reliable stage for the selection of key economic traits, while traits with fluctuating heritability required stage-specific breeding strategies.

Cane yield, commercial cane yield, and number of millable canes exhibited high heritability in the ratoon crop (90.28%, 84.61%, and 89.18%, respectively) along with high GAM values (41.49%, 38.35%, and 26.12%, respectively). These results indicated strong additive gene effects and suggested that direct phenotypic selection in the ratoon phase would be highly effective, as also emphasized by Jeena (2023), who reported greater selection efficiency in older crop stages due to increased genetic expression. Brix, Sucrose, and CCS% showed low to moderate heritability and genetic advance in the first and second plant crops, but exhibited substantial increases in the ratoon crop, where Brix reached 44.66% heritability and 6.35% GAM, and Sucrose reached 80.39% heritability and 10.71% GAM. This trend aligned with the findings of Abu-Ellail *et al.* (2022), who noted that environmental variation strongly affected juice quality traits in early crops, while ratoon crops provided more stable expression and better genetic differentiation.

Cane length demonstrated extremely high heritability (96.10%) and genetic advance (100.52) in the second plant crop, with GAM peaking at 45.98%, indicating strong selection

potential at this stage. However, in the ratoon crop, although heritability remained high (92.93%), GAM dropped to 22.08%, likely due to a decline in mean values or increased environmental effects, as also noted by Saadan *et al.* (2025) in ratooning studies. Cane girth showed good potential in the second plant crop (81.38% heritability and 34.72% GAM) but dropped significantly in the ratoon crop (37.92% heritability and 12.34% GAM), suggesting instability and environmental sensitivity of this trait in later cycles. Single cane weight exhibited practically zero genetic advance and GAM in the second plant crop, reflecting poor genetic expression during this stage, potentially due to stress or environmental interactions, a phenomenon also reported by Milligan *et al.* (1990) in their studies on ratoon performance.

The results indicate that ratoon crops are most suitable for effective selection, particularly for yield traits like cane yield, CCS yield, and number of millable canes, due to high heritability and high genetic advance. Juice quality traits become more responsive to selection in later cycles, suggesting that early selection may be inefficient. Morphological traits like cane length and girth require crop-specific selection strategies and erratic traits like single cane weight must be interpreted cautiously.

### **Correlation Studies**

Trait correlation analysis provided insights into the direction and strength of associations between traits, which was crucial for indirect selection in sugarcane breeding. The present study assessed genetic correlations among key agronomic and juice quality traits across three crop cycles, as presented in Table 4. The findings revealed both consistent and cycle-specific relationships, reflecting the dynamics of trait expression over time.

ASSESSMENT OF GENETIC PARAMETERS IN EARLY MATURING SUGARCANE CLONES

**Table 2b. Mean performance of ten clones over three crop cycles among nine agronomic traits**

Clone	SCW (kg)			CCSY (t/ha)			Cane length (cm)			Cane girth (cm)			Cane yield (t/ha)		
	IP	IIP	Ratoon	IP	IIP	Ratoon	IP	IIP	Ratoon	IP	IIP	Ratoon	IP	IIP	Ratoon
2018A 133	0.99	0.76	0.87	13.55	10.23	11.33	205.00	305.00	195.67	1.37	2.13	2.00	118.45	90.15	94.38
2018A 30	0.98	0.92	0.80	8.71	12.11	9.64	152.67	241.67	208.00	2.20	2.33	2.13	75.43	93.00	80.44
2018A 31	1.02	1.11	0.79	8.29	13.83	7.85	157.00	305.00	209.67	2.13	2.02	2.20	77.32	114.35	62.20
2018A 37	1.05	1.04	0.88	11.94	10.42	9.88	266.33	271.67	245.33	2.47	2.68	2.47	100.70	97.05	73.37
2018A 65	1.08	0.94	0.72	12.56	11.20	10.57	150.33	215.00	190.33	2.17	2.39	2.40	98.15	90.49	72.36
2018A 107	1.17	0.91	0.66	9.57	11.12	8.29	253.67	280.00	202.00	2.57	2.21	1.73	85.12	92.47	64.65
2018A 152	0.94	0.91	0.90	9.07	10.52	10.67	259.00	271.67	242.00	2.17	2.41	2.20	80.55	91.60	89.03
87A 298	1.03	0.77	0.70	10.38	7.66	8.27	258.33	287.67	183.67	2.23	2.45	2.20	87.03	67.69	62.30
CoC.01061	0.61	0.65	0.62	9.79	8.77	7.22	212.00	291.67	181.00	1.37	1.86	1.67	80.08	77.00	58.10
2000A 128	1.12	0.98	0.66	10.97	9.44	5.30	272.00	295.33	233.00	2.13	2.20	2.17	83.70	79.94	43.84
Mean	1.00	0.90	0.76	10.48	10.53	8.90	218.63	276.47	209.07	2.08	2.27	2.12	88.65	89.37	70.07

Cane yield showed a strong positive correlation with CCS yield in all crop cycles, particularly in the ratoon crop ( $r = 0.948^{**}$ ), indicating that selection for CCS yield would simultaneously improve cane yield. In the first plant and ratoon crops, cane yield was also positively correlated with single cane weight ( $r = 0.755^{**}$  in the first plant and  $0.804^{**}$  in the ratoon), confirming the significant role of this trait in determining yield. These results were consistent with the findings of Reddy *et al.*, (2024), who identified stalk weight and number as primary determinants of yield. Number of millable canes and cane yield showed a strong positive correlation in the second plant ( $r = 0.646^{**}$ ) and ratoon crops ( $r = 0.809^{**}$ ), supporting indirect selection through number of millable canes, especially in the later stages. However, in the first plant crop, the number of millable canes showed a significant negative correlation with single cane weight ( $r = -0.555^*$ ) and cane girth ( $r = -0.724^{**}$ ), suggesting a trade-off between the number and size of canes a trend also observed in ratooning studies by Tabassum *et al.* (2023).

Juice quality traits such as Brix, Sucrose, and CCS% showed very strong positive correlations among themselves in all crop cycles. This reflected their shared biochemical basis and suggested that selection for one was likely to improve the others. However, Brix and the number of millable canes were negatively correlated in the second plant and ratoon crops, reflecting a dilution effect, where an increased number of canes might reduce overall juice concentration. The correlation between CCS percentage and cane yield in the first plant crop was positive and significant ( $r = 0.360^*$ ), suggesting that sucrose-based yield gains could be realized in later cycles. Single cane weight showed a strong positive correlation with cane girth in all crop cycles, while it was negatively correlated with the number of millable canes, highlighting the inverse

relationship between cane number and cane size. Cane length and cane yield showed a weak to moderate correlation, suggesting that gains in cane length might not directly translate into higher yield unless supported by improvements in weight or juice traits. Cane girth and cane yield were mostly uncorrelated, except for a weak negative correlation in the second plant crop ( $r = -0.351^*$ ), possibly due to competition or lodging effects.

### Path coefficient analysis

The results of the genotypic path coefficient analysis, presented in Table 5, revealed that cane yield exerted the strongest positive direct effect on Brix percentage and CCS yield across all crop cycles. CCS yield exhibited significant positive correlations along with substantial direct effects in each season, highlighting its importance as a key selection criterion in sugarcane breeding programs. Cane length and single cane weight showed positive direct effects on cane yield across the first and second plant crops. The number of millable canes also exhibited a positive direct effect on cane yield in the first plant and ratoon crops. Tena *et al.* (2023) reported similar findings for cane yield and CCS yield. Abu-Ellail *et al.* (2017) reported comparable results for the number of millable canes, and Reddy *et al.* (2024) observed similar effects for single cane weight.

### CONCLUSION

This study highlights significant genetic variability, heritability, and trait interrelationships among ten early maturing sugarcane clones evaluated across three crop cycles. The analysis of variance suggesting that selection across seasons is necessary for stable trait expression. These findings emphasize that the ratoon crop is the most reliable stage for selection in early maturing sugarcane due to higher heritability, stronger genetic correlations, and better trait stability. Traits such as cane

**Table 3. Genetic parameters of yield and quality related traits in ten sugarcane clones over three seasons**

Response Variable	GCV			PCV			Heritability			Gen-Advance			Gen-Adv % Means		
	IP	IIP	RA	IP	IIP	RA	IP	IIP	RA	IP	IIP	RA	IP	IIP	RA
Number of millable canes ('000/ha)	11.20	12.87	13.43	12.66	13.11	14.22	78.35	96.25	89.18	20.46	22.95	23.98	20.43	26.00	26.12
Brix (%)	3.11	3.08	4.61	6.15	5.20	6.90	25.60	35.02	44.66	0.58	0.70	1.23	3.24	3.75	6.35
Sucrose (%)	4.00	4.47	5.80	6.95	6.25	6.47	33.18	51.02	80.39	0.79	1.11	1.93	4.75	6.57	10.71
Commercial cane sugar (%)	4.33	5.52	6.27	7.61	7.36	7.24	32.39	56.11	74.95	0.60	1.01	1.42	5.08	8.51	11.19
Single cane weight (kg)	15.18	2.07	12.92	15.87	26.01	13.95	91.43	0.63	85.81	0.27	0.00	0.19	29.90	0.34	24.66
Commercial cane sugar yield (t/ha)	15.63	14.91	20.24	17.81	19.63	22.00	77.06	57.66	84.61	2.98	2.45	3.41	28.27	23.32	38.35
Cane length (cm)	8.62	22.77	11.12	13.17	23.23	11.54	42.85	96.10	92.93	32.15	100.52	46.17	11.63	45.98	22.08
Cane girth (cm)	9.06	18.68	9.73	12.59	20.71	15.79	51.78	81.38	37.92	0.31	0.72	0.26	13.40	34.72	12.34
Cane yield (t/ha)	13.44	12.92	21.20	15.28	18.63	22.31	77.32	48.09	90.28	21.75	16.36	29.07	24.34	18.45	41.49

IP= first plant crop, IIP= second plant crop, RA= ratoon crop

Table 4. Genotypic correlations for each season across nine agronomic and quality traits

Traits	Crop cycle	NMC	BP	SC	CCSP	SCW	CCY	CL	CG	CY
<b>NMC</b>	IP	1	-0.228	-0.016	0.049	-0.555*	0.114	0.284	-0.724**	0.117
	IIP	1	-0.364*	-0.054	0.029	-0.969**	0.555*	-0.102	-0.794**	0.646**
	RA	1	-0.035	-0.013	-0.007	0.309	0.800**	-0.408*	-0.36*	0.809**
<b>BP</b>	IP		1	0.999**	0.989**	0.473*	0.634**	-0.929**	-0.393*	0.37*
	IIP		1	0.753**	0.633**	-0.991**	-0.128	0.176	0.003	-0.41*
	RA		1	0.999**	0.986**	-0.404*	0.043	-0.333	0.03	-0.293
<b>SP</b>	IP			1	0.996**	0.293	0.612**	-0.946**	-0.32	0.359*
	IIP			1	0.986**	-0.859**	0.439*	0.184	-0.041	0.100
	RA			1	0.998**	-0.231	0.129	-0.278	0.506*	-0.194
<b>CCSP</b>	IP				1	0.24	0.613**	-0.964**	-0.301	0.360*
	IIP				1	-0.37*	0.549*	0.171	-0.05	0.221
	RA				1	-0.177	0.157	-0.261	0.667**	-0.164
<b>SCW</b>	IP					1	0.714**	-0.178	0.418*	0.755**
	IIP					1	-0.956**	0.958**	0.993**	-0.936**
	RA					1	0.755**	0.567*	0.641**	0.804**
<b>CCY</b>	IP						1	-0.28	-0.123	0.946**
	IIP						1	0.106	-0.301	0.937**
	RA						1	0.026	0.387*	0.948**
<b>CL</b>	IP							1	-0.526*	-0.032
	IIP							1	0.263	0.064
	RA							1	0.606**	0.096
<b>CG</b>	IP								1	-0.028
	IIP								1	-0.351*
	RA								1	0.157
<b>CY</b>	IP									1
	IIP									1
	RA									1

IP= First plant, IIP= Second plant, RA=Ratoon. NMC= Number of millable canes ('000/ha), BP= Brix (%), SP= Sucrose (%), CCS (%)= Commercial cane sugar, SCW= Single cane weight (kg), CCY= Commercial cane sugar yield (t/ha), CL= Cane length (cm), CG=Cane girth (cm) and CY= Cane yield (t/ha).

Table 5. Genotypic path coefficient analysis of cane yield and quality components for each crop season across nine agronomic and quality traits

	Crop cycle	NMC	BP	SC	CCSP	SCW	CCY	CL	CG	gen_corr with main variable
<b>NMC</b>	IP	<b>0.202</b>	-0.008	0.004	-0.001	-0.147	0.102	0.004	-0.039	0.117
	IIP	<b>-0.042</b>	-0.005	0.008	-0.008	-0.003	0.644	-0.003	0.054	0.646
	RA	<b>0.022</b>	-0.003	0.005	0.000	-0.002	0.785	0.005	-0.005	0.809
<b>BP</b>	IP	-0.046	<b>0.037</b>	-0.259	-0.024	0.125	0.571	-0.014	-0.021	0.370
	IIP	0.015	<b>0.013</b>	-0.112	-0.179	-0.003	-0.148	0.005	0.000	-0.410
	RA	-0.001	<b>0.085</b>	-0.371	-0.055	0.002	0.043	0.004	0.000	-0.293
<b>SP</b>	IP	-0.003	0.038	<b>-0.251</b>	-0.022	0.078	0.551	-0.014	-0.017	0.359
	IIP	0.002	0.01	<b>-0.149</b>	-0.279	-0.001	0.509	0.005	0.003	0.100
	RA	0.00	0.086	<b>-0.365</b>	-0.053	0.001	0.127	0.004	0.007	-0.194
<b>CCSP</b>	IP	0.01	0.039	-0.251	<b>-0.022</b>	0.064	0.552	-0.014	-0.016	0.360
	IIP	-0.001	0.008	-0.147	<b>-0.283</b>	0.000	0.637	0.005	0.003	0.221
	RA	0.00	0.088	-0.365	<b>-0.053</b>	0.001	0.154	0.003	0.009	-0.164
<b>SCW</b>	IP	-0.112	0.018	-0.073	-0.005	<b>0.265</b>	0.643	-0.003	0.022	0.755
	IIP	0.101	-0.033	0.128	0.105	<b>0.001</b>	-1.109	0.025	-0.311	-1.093
	RA	0.007	-0.034	0.084	0.009	<b>-0.005</b>	0.741	-0.007	0.008	0.804
<b>CCY</b>	IP	0.023	0.024	-0.153	-0.014	0.189	<b>0.901</b>	-0.004	-0.007	0.959
	IIP	-0.023	-0.002	-0.066	-0.155	-0.001	<b>1.16</b>	0.003	0.021	0.937
	RA	0.018	0.004	-0.047	-0.008	-0.004	<b>0.982</b>	0.000	0.005	0.948
<b>CL</b>	IP	0.057	-0.034	0.237	0.022	-0.047	-0.253	<b>0.015</b>	-0.028	-0.032
	IIP	0.004	0.002	-0.027	-0.048	0.001	0.124	<b>0.026</b>	-0.018	0.064
	RA	-0.009	-0.028	0.101	0.014	-0.003	0.026	<b>-0.013</b>	0.008	0.096
<b>CG</b>	IP	-0.146	-0.015	0.08	0.007	0.111	-0.111	-0.008	<b>0.054</b>	-0.028
	IIP	0.033	0	0.006	0.014	0.005	-0.349	0.007	<b>-0.068</b>	-0.351
	RA	-0.008	0.003	-0.185	-0.035	-0.003	0.38	-0.008	<b>0.013</b>	0.157

IP= First plant, IIP= Second plant, RA=Ratoon. NMC= Number of millable canes ('000/ha), BP= Brix (%), SP= Sucrose (%), CCS (%), CCSP= Commercial cane sugar, SCW= Single cane weight (kg), CCY= Commercial cane sugar yield (t/ha), CL= Cane length (cm), CG=Cane girth (cm) and CY= Cane yield (t/ha). Residual effect: IP-0.001, IIP-0.0009 & RA-0.0002.

yield, CCS yield, number of millable canes, and single cane weight emerged as primary targets for selection, particularly in the ratoon crop. Juice quality traits are best selected in advanced cycles due to reduced environmental interference. Meanwhile, traits like single cane weight and cane girth, which display inconsistent behavior, require stage-specific selection strategies or further environmental stabilization.

## REFERENCES

- Abu-Elail, F.F., El-Taib, A.B and Masri, M.I. 2017. Broad-sense heritability, genetic correlation and genetic variability of sugarcane yield components at first selection stage. *Journal of Sugarcane Research*, 7(1): 27–34.
- Abu-Elail, F.F., Gadallah, A.F.I and El-Gamal, I.S.H. 2020. Genetic variance and performance of five sugarcane varieties for physiological, yield and quality traits influenced by various harvest age. *Journal of Plant Production*, 11(5): 429–438.
- Al-Jibouri, H., Miller, P.A and Robinson, H.F. 1958. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agronomy Journal*, 50(10): 633–636.
- Allard, R.W. 1961. Principles of plant breeding. *Soil Science*, 91(6): 414.
- Barreto, F.Z., Balsalobre, T.W.A., Chapola, R.G., Garcia, A.A.F., Souza, A.P., Hoffmann, H.P and Carneiro, M.S. 2021. Genetic variability, correlation among agronomic traits, and genetic progress in a sugarcane diversity panel. *Agriculture*, 11(6): 533.
- Burton, G.W and De Vane, E. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*). *Agronomy Journal*, 45: 478–481.
- Dewey, D.R and Lu, K. 1959. A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, 51(9): 515–518.
- Directorate of Economics and Statistics (E&S), Department of Agriculture and Cooperation (DAC), Ministry of Agriculture, Government of India. 2024. The Second Advance Estimates of production of Foodgrains, Oilseeds and Other Commercial Crops for the year 2023–24.
- Jeena, A.S. 2023. Estimation of genetic variability, character association and path coefficient using sugarcane segregating population. *Electronic Journal of Plant Breeding*, 14(2): 665–674.
- Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47: 314–318.
- Milligan, S.B., Gravois, K.A., Bischoff, K.P and Martin, F.A. 1990. Crop effects on genetic relationships among sugarcane traits. *Crop Science*, 30(4): 927–931.
- Nair, N.V., Nagarajan, R., Mathew, M.D and Sreenivasan, T.V. 1999. Components of yield and quality in intraspecific hybrids of *Saccharum officinarum* L. selected for ancillary uses. *Sugar Tech*, 1: 124–127.
- Reddy, G.E., Rakesh, G., Saicharan, M., Swapna, N., Swathi, Y., Naik, B.B and Sridhar, M. 2024. Correlation among yield, quality and mechanization amicable traits in sugarcane clones. *Journal of Experimental Agriculture International*, 46(10): 585–592.
- Saadani, A.S.A., Abazied, S.R and Abu-Elail, F.F.B. 2025. Assessment the correlation and heritability of promising sugarcane varieties for yield and quality attributes affected by pre-harvest irrigation

- withholding periods. *Journal of Plant Production*, 217–224.
- Shanmuganathan, M., Annadurai, K., Nageswari, R and Asokhan, M. 2015. Evaluation of sugarcane clones for quantitative yield and quality characters in AICRP trials for early season. *Electronic Journal of Plant Breeding*, 6(1): 292–297.
- Singh, R.K and Chaudhary, B.D. 1999. *Biometrical Genetics Analysis*. Kalyani Publishers.
- Sugeerthi, S., Jayachandran, M and Chinnusamy, C. 2018. Effect of planting materials and integrated nutrient management on yield of sugarcane seed crop. *Madras Agricultural Journal*, 105.
- Tabassum, Jeena, A.S and Rohit. 2023. Estimation of genetic variability, character association and path coefficient using sugarcane segregating population. *Electronic Journal of Plant Breeding*, 14(2): 665–674.
- Tena, E., Mekbib, F and Ayana, A. 2016. Heritability and correlation among sugarcane (*Saccharum* spp.) yield and some agronomic and sugar quality traits in Ethiopia. *American Journal of Plant Sciences*, 7(10): 1453–1477.
- Tena, E., Tadesse, F., Million, F and Tesfaye, D. 2023. Phenotypic diversity, heritability, and association of characters in sugarcane genotypes at Metehara Sugar Estate, Ethiopia. *Journal of Crop Improvement*, 37(6): 874–897.
- Tolera, B., Gedebo, A and Tena, E. 2023. Variability, heritability and genetic advance in sugarcane (*Saccharum* spp. hybrid) genotypes. *Cogent Food & Agriculture*. 9(1): 2194482.
- Tolera, B., Gedebo, A and Tena, E. 2024. Genetic variability, character association and path analysis in sugarcane genotypes. *Archives of Agronomy and Soil Science*, 70(1): 1–15.
- Tyagi, S., Chandra, S and Tyagi, G. 2023. Statistical modelling and forecasting annual sugarcane production in India: Using various time series models. *Annals of Applied Biology*, 182(3): 371–380.
- Vinu, V., Alarmelu, S., Elayaraja, K., Appunu, C., Hemaprabha, G., Parthiban, S and Varatharaj, M.K.C. 2024. Multi-environment analysis of yield and quality traits in sugarcane (*Saccharum* sp.) through AMMI and GGE biplot analysis. *Sugar Tech*, 1–19.
- Yadawad, A., Kongawad, B.Y., Kadlag, A.D and Veena, B. 2022. Evaluation of advanced sugarcane clones for cane yield and quality traits in plant and ratoon crops. *Electronic Journal of Plant Breeding*, 13(4): 1250–1259.

Adilakshmi, D., Padmavathi, P.V. and Rao, D.P. 2025. Assessment of genetic parameters and trait interrelationships in early maturing sugarcane clones over three crop cycles. *The Journal of Research ANGRAU*, 53 (4): 01-13.