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RESEARCH ARTICLE

Genetic variance and stability assessment of sugarcane (*Saccharum officinarum* L.) clones using the multi-trait stability index across diverse cropping seasons

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Abstract
The multi-trait stability index (MTSI) was employed in sugarcane (*Saccharum officinarum* L.) to identify superior clones that exhibit mean performance and stability across multiple trait combinations over crop seasons. Genetic variance analysis for thirteen yield and quality traits showed a significant effect ($p < 0.001$) for genotype, environment, and genotype-by-environment (G×E) interaction, except for stalk diameter over the crop seasons. Based on MTSI scores, two clones, 2017A 236 (G3) and 2017A 36 (G1) were identified as excellent variants with respect to mean performance and stability of cane yield and sugar quality traits across the three crop seasons. The MTSI index demonstrated selection differential for nine traits that exhibited positive selection gains, ranging from stalk length (5.21%) to number of tillers at 120 DAP (63.28%), while four traits showed negative gains for fiber (%) (-1.13%), brix (%) (-8.57%), jaggery yield (-14.32%) and stalk diameter (-23.69%). Correlation analysis showed a strong association among cane yield and yield-related traits across seasons, alongside high correlations observed among sucrose percent, brix percent and CCS percent over the crop seasons. The present results suggested that the selected clones are excellent candidates, showing superior performance for the evaluated traits across all crop seasons. Therefore, these promising clones hold potential for advancement in yield trials and inclusion in future breeding pipelines.
Keywords: ANOVA, best linear unbiased predictor, selection gain and MTSI.

Introduction
Sugarcane (*Saccharum officinarum* L.) is a C_4 crop and an allopolyploid species in the Poaceae family. It is the major source of sugar, jaggery, and bioethanol, playing a significant role in the agricultural industry worldwide. Sugarcane contributes to 80% of global sugar production and 20 to 25% of bioethanol production (Alarmelu and Kurup 2023). Brazil is the largest producer of sugarcane in the world, accounting for about 1.92 billion tonnes annually, which contributes to almost 38% of the world's sugar production. India ranks as the world's second-largest producer, following Brazil, with an average output of 421.02 million tonnes cultivated over 51.16 lakh hectares from 2018 to 2023. The states of Uttar Pradesh, Maharashtra, and Karnataka contribute to 80% of the national production, with an average yield of 82 tonnes per hectare. However, Andhra Pradesh has experienced a notable decline in sugarcane cultivation, with the area planted decreasing from 1.02 lakh hectares in 2018–19 to just 0.40 lakh hectares in 2023–24. Consequently, production has dropped from 8.09 million tonnes to 2.10 million tonnes. Currently, Andhra Pradesh ranks 11th in India, both in area and production, with an average yield of 76.78 t/ha, which is below the national average yield (E & S, DAC - *2nd Adv. Est.-2023-24). Evaluating clonal performance across crop cycles is essential for identifying stable and high-yielding genotypes with good ratoon ability, thereby supporting

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sustainable sugarcane improvement in the state (Tyagi et al. 2023).

Yield improvement in crop often influences other traits, sometimes resulting in undesirable changes when direct selection is focused on a single trait (Soni et al. 2024). Therefore, understanding the genetic interrelationships among yield, yield components, and quality traits is crucial. This knowledge helps plant breeders identify and combine target traits to develop superior clones (Shiri et al. 2024). To capture trait performance and yield expression across varying seasonal environments, researchers conduct multi-seasonal trials. In this context, the Multi-Trait Stability Index (MTSI) is a useful selection tool to identify clones that combine desirable stability with favorable genetic gains for most traits across multiple seasons (Sharifi et al. 2020). Cultivar selection is typically approached through either univariate or multivariate models, with the Best Linear Unbiased Prediction (BLUP) being a widely adopted multivariate method for estimating random effects in mixed models. However, its application in sugarcane remains limited, particularly for estimating genetic variance and heritability (Carvalho et al. 2020). Incorporating BLUP into selection strategies enhances the efficiency, adaptability, and stability of identifying superior clones.

Edapho-climatic conditions play a crucial role in sugarcane cultivation and directly influence yield potential. Optimal growth and high yields in sugarcane require favorable temperatures (25–38°C) and adequate annual rainfall (around 1,600 mm) (Carvalho et al. 2020). As a heavy nutrient feeder, sugarcane extracts substantial amounts of both macro- and micronutrients from the soil. In Andhra Pradesh, variations in temperature and soil properties across different regions add complexity to sugarcane production. Seasonal impacts are also significant, particularly as farmers often prefer ratoon crops due to their lower cost and faster turnaround compared to fresh plantings. Therefore, it is essential to identify superior clones that combine high yield, good quality, and stability across both plant and ratoon crops. In this context, the present study was undertaken to evaluate ten sugarcane clones along with one standard check to identify high-yielding and stable clones across diverse crop seasons.

Materials and methods

Experimental materials and lay out

The experimental material consisted of ten mid-late maturing sugarcane clones (Table 1), which were evaluated along with one standard check variety, 87A 298 (Viswamitra). Field trials were conducted at the Regional Agricultural Research Station (RARS), Anakapalle, located at 17.6914° N latitude, 83.0041° E longitude, and an altitude of 26 meters above sea level. The study spanned three crop cycles; the first plant crop and ratoon crop during 2020–21 and 2021–22, respectively, and a second plant crop in 2021–22. The experiment was laid out in a randomized block design (RBD) with three replications. Each genotype was planted in plots comprising six rows, each six meters long, with a row-to-row spacing of 90 cm. Standard agronomic practices recommended for the region (Sugeerthi et al. 2018) were uniformly followed across all three seasons. Both plant crops were harvested at 12 months of age, during the second fortnight of December, while the ratoon crop was harvested at 10 months to maintain consistency in crop age and ensure precise, comparable data analysis.

Table 1. List of sugarcane clones used in this experiment

Code	Clones	Pedigree
G1	2017A36	CoA12321 X Co775
G2	2017A65	CoA12321 X Co775
G3	2017A236	CoA13327 X CoH15
G4	2017A253	CoT8201 X Co94008
G5	2017A340	Co0235GC
G6	2017A396	CoV89101 X CoT8201
G7	2017A408	CoV89101 X CoT8201
G8	2017A457	CoV89101 X CoT8201
G9	2017A405	CoV89101 X CoT8201
G10	2017A553	CoV89101 X ISH69
G11	87A298 (S)	Co 7704 X CoC 671

S = standard clone

Observations recorded

The study focused on 13 quantitative and quality traits of sugarcane, selected based on the descriptors and guidelines outlined by the PPV&FR Authority (2001) under distinctiveness, uniformity, and stability (DUS) criteria (Amalraj 2011). Observations included both yield and quality parameters. Yield-related traits recorded were, number of tillers (×1000/ha) at 120 and 240 days after planting (DAP), single cane weight (kg), cane yield (t/ha), number of millable canes (NMC, ‘000/ha), stalk length (cm), and stalk diameter (cm). Cane yield was estimated by harvesting the middle four rows of each plot, weighing the cane harvested on a plot basis, and then extrapolating the yield to a per-hectare basis. NMC was manually counted from the net plot area and expressed in thousands per hectare.

Stalk length and diameter were measured from ten randomly selected canes per clone, and average values were calculated. For quality traits, brix (%) and sucrose (%) were measured at the 10^{th} month of crop growth using five randomly selected canes per clone. Brix was measured using a refractometer, and sucrose was determined using a sucrolyser. Commercial Cane Sugar (CCS) yield (t/ha) was estimated using the formula: CCS yield = (Cane yield × CCS%) / 100, where CCS (%) was calculated using the formula: CCS%

= (Sucrose% × 1.022) – (Brix% × 0.292). Jaggery yield (t/ha) was computed using the formula: (Jaggery weight/Cane weight) × 100. Fiber content (%) was estimated by using the formula: Fiber (%) = (Weight of dry fiber / Weight of fresh cane) × 100 (Nair et al. 1999).

Statistical analysis

The data from plant and ratoon trials were recorded across three crop cycles for subjected to statistical analysis. Bartlett's test was performed to assess the homogeneity of error variances across the three experiments. This analysis was conducted using OPSTAT, open-source statistical software. The non-significant results of Bartlett's test for all traits confirmed the homogeneity of error variances, allowing the data from three crop cycles to be combined for further analysis. The combined analysis of variance, BLUPs-based genetic parameters, correlation, WAASBi index and multi-trait stability index were estimated by using 'metan' package (Olivoto and Lucio 2020) in R Studio (Posit Team 2022) running in R version 4.1. The WAASBi stands for Weighted Average of Absolute Scores of the *i*th genotype, and it's a stability index used to evaluate the genotype × environment interaction (GEI) in multi-environment trials (METs). It was proposed by Olivoto et al. (2019) as a part of mixed-model-based stability analysis. The WAASB index was calculated using the following formula:

$$\mathrm{WAASB_i} = \frac{\sum_{k=1}^{p} |IPCA_{ik} \times EP_k|}{\sum_{k=1}^{p} EP_k}$$

$$\mathrm{WAASBY_i} = \frac{\left\{W_{Y\times}\left[\left(\frac{GY_i}{GY_{max}}\right)\times 100\right]\right\} + \left[W_{S\times}\left(100 - \frac{WAASB_i}{WAASB_{min}}\right)\right]}{W_Y + W_S}$$

Where, WAASBi is the weighted average of absolute scores of the ith genotype and IPCAik is the score of that genotype in the kth interaction principal component axis.

Results and discussion

The development of highly stable clones is essential for general adoption of sugarcane cultivation. Genotype-by-environment interaction plays a central role in selecting candidate clones through multi-environment and multi-season trials. The joint analysis of seasonal variance for cane yield and quality traits across different crop seasons is presented in Table 2. The joint analysis of seasonal variance shows a significant effect ($p \leq 0.01$) of genotype (G), environment (E), and their interaction (GEI) for all traits under study, except stalk diameter, whereas single cane weight shows environmental effect is non-significant. The significant GEI effect indicates that the mean performance of the clones responded differently to variations in seasonal conditions, and this variance is valuable for studying phenotypic stability and adaptability across diverse crop

Table 2. Joint analysis of variance for 13 yield and quality traits in eleven sugarcane clones over three seasons

Source	Df	No. of shoots at 120 DAP (x 1000/ha)	No. of shoots at 240 DAP (x 1000/ha)	Stalk length (cm)	Stalk diameter (cm)	Single cane weight (kg)	No. of millable canes (000'/ha)	Cane yield (t/ha)	CCS yield (t/ha)	Jaggery yield (t/ha)	Brix (%)	Sucrose (%)	CCS (%)	Fiber (%)
ENV	2	11018.61*	3579.51*	343.5*	0.03	0.02	5814.35*	5928.35*	10.18*	19.15*	10.18*	11.33*	8.64*	423.62*
REP(ENV)	6	72.76	49.3	56.49	0.04	0.00	54.63	8.09	3.55	4.07	3.55	2.97	3.29	3.28
GEN	10	3380.14*	1634.03*	21327.23*	0.04	0.09*	1258.18*	1994.71*	4.26*	20.55*	4.26*	4.17*	2.81*	3.20*
GEN:ENV	20	868.01*	346.64*	2772.02*	0.04	0.02*	209.81*	454.84*	2.82*	11.85*	2.82*	2.03*	1.15*	12.90*
Residuals	60	0.32	0.39	0.25	0.05	0.00	0.46	0.09	0.07	0.07	0.07	0.06	0.05	0.05

*=P<0.05

cycles (Vinu et al. 2024). Similar findings reported by Durai et al. (2025) for single cane weight and stalk diameter, Adilakshmi et al. (2025) for cane yield and CCS yield and Tena et al. (2019) for sucrose, brix (%) and CCS(%).

Analysis of genetic parameters derived from BLUP

In the current study, the likelihood ratio test was applied and which indicates that all cane yield and quality attributes demonstrated significant ($p \leq 0.01$) effects for genotype, environment, and the interaction between genotype and environment, except stalk diameter (Supplementary Table S1). The characters of stalk length, number of millable canes, and number of shoots at 240DAP had a high genotypic effect, contributing significantly to the phenotypic variance, while remaining traits exhibit higher GEI variance than genotypic and residual variance (Fig. 1); hence, GEI variance is considered an important component of the phenotypic variance. These findings suggest that there is a better potential for selection gains across most of the investigated traits, as well as a deeper understanding of how these agronomic traits respond to seasonal impacts. BLUP-based variance components for cane yield and quality attributes across three growing seasons are presented in Table 3. BLUPs for cane yield identified clone 2017A236 as having the highest predicted mean across three seasons (Figs. 2a and 2b).

All yield-related traits exhibit moderate heritability ($h^2_{bs} >$ 0.30), while sugar-quality traits exhibit low heritability. The fiber quality percentage did not respond to the heritability due to it being fully exploited by residual variance. Similar results were reported by de Souza et al. 2019 in sorghum. Stalk length expressed higher phenotypic variance due to the environment effect. Similar reports are provided for plant height (Olivoto and Nardino 2020) in wheat. Selection accuracy was higher for all traits, except brix and fiber percentage. Which indicates experimental design was consistent. Stalk length has been recorded as the highest genotypic coefficient of variation. All characters exhibit a higher range of GEI effects. The findings were supported

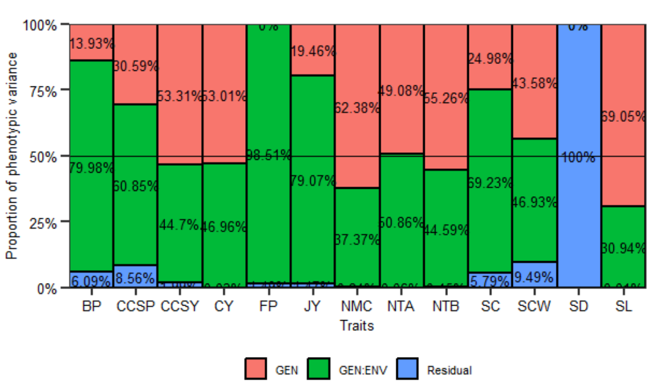


Fig. 1. Proportion of phenotypic variance for 13cane yield and quality traits over crop seasons

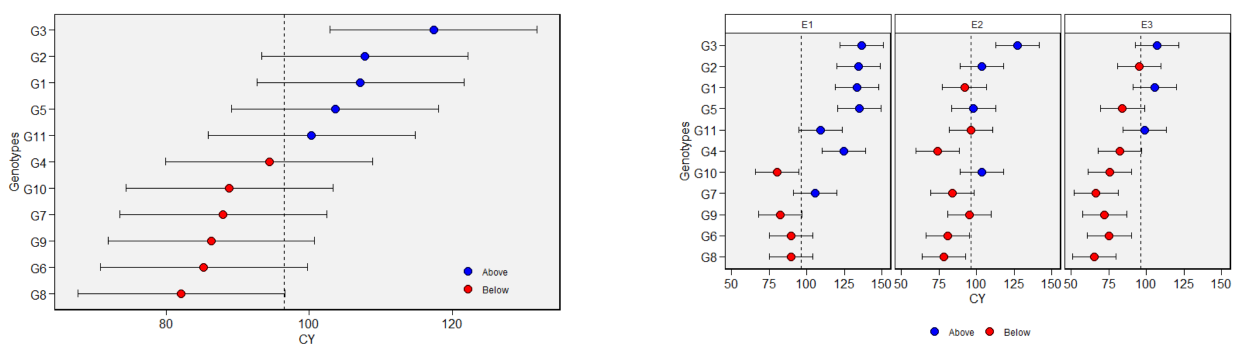
Table 3. BLUP-Based Variance Components for 13 cane yield and quality traits over the crop seasons

Parameters	No. of shoots at 120 DAP (x 1000/ha)	No. of shoots at 240 DAP (x 1000/ha)	No. of millable canes (000'/ha)	Stalk length (cm)	Stalk diameter (cm)	Single cane weight (kg)	Cane yield (t/ha)	CCS yield (t/ha)	Jaggery yield (t/ha)	Brix (%)	Sucrose (%)	CCS (%)	Fiber (%)
Phenotypic variance	568.67	258.85	186.73	2985.83	0.05	0.02	322.77	5.40	4.97	1.15	0.95	0.60	3.26
Heritability	0.49	0.55	0.62	0.69	0.00	0.44	0.53	0.53	0.19	0.14	0.25	0.31	0.00
GEIr^2	0.51	0.45	0.37	0.31	0.00	0.47	0.47	0.45	0.79	0.80	0.69	0.61	0.99
h^{2}mg	0.74	0.79	0.83	0.87	0.00	0.72	0.77	0.78	0.42	0.34	0.51	0.59	0.00
Accuracy	0.86	0.89	0.91	0.93	0.00	0.85	0.88	0.88	0.65	0.58	0.72	0.77	0.00
rge	1.00	1.00	0.99	1.00	0.00	0.83	1.00	0.96	0.98	0.93	0.92	0.88	0.99
CVg	14.10	11.57	11.49	15.94	0.00	8.85	13.56	14.34	9.29	2.17	2.87	3.58	0.00
CVr	0.47	0.60	0.72	0.17	8.41	4.13	0.32	2.77	2.55	1.43	1.38	1.89	1.78
CV ratio	29.75	19.22	15.98	91.57	0.00	2.14	42.87	5.18	3.64	1.51	2.08	1.89	0.00

Heritability = Broad-sense heritability BLUP basis; GEIr^2= Coefficient of determination for the genotype-vs-environment interaction effects; h^2 mg = Heritability on the mean basis; Accuracy = Selective accuracy; rge = Genotype X environment correlation; CVg = Genotypic coefficient of variation; CVr = Residual coefficient of variation; CV = Ratio between genotypic and residual coefficient of variation.

Table 4. Factor analysis using MTSI method for 13 cane yield and quality traits over the crop seasons

S.No	VAR	FA1	FA2	FA3	FA4	Communality	Uniquenesses
1	No. of shoots at 120 DAP (x 1000/ha)	0.69	0.06	-0.11	0.53	0.77	0.23
2	No. of shoots at 240 DAP (x 1000/ha)	0.96	0.16	0.11	0.17	0.98	0.02
3	No. of millable canes (000'/ha)	0.9	0.29	-0.07	0.05	0.91	0.09
4	Cane yield (t/ha)	0.9	-0.18	-0.21	-0.19	0.92	0.08
5	CCS yield (t/ha)	0.82	-0.23	-0.13	-0.27	0.81	0.19
6	Jaggery yield (t/ha)	0.39	-0.23	-0.66	-0.04	0.64	0.36
7	Brix (%)	-0.14	0.87	-0.04	-0.3	0.87	0.13
8	Sucrose (%)	0.18	0.97	-0.07	-0.05	0.98	0.02
9	CCS (%)	0.11	0.94	-0.14	-0.02	0.91	0.09
10	Fiber (%)	-0.02	-0.25	0.15	0.84	0.8	0.2
11	Stalk length (cm)	0.27	-0.24	0.85	-0.06	0.86	0.14
12	Stalk diameter (cm)	-0.22	-0.12	0.75	0.28	0.7	0.3
13	Single cane weight (kg)	0.23	-0.57	-0.33	-0.42	0.66	0.34
Eigenvalues		4.3	3.3	2.1	1.1		
Variance (%)		32.8	25.6	16.2	8.7		
Cum. variance (%)		32.8	58.3	74.5	83.2		



a) b)

Fig. 2. a) BLUP mean values of eleven clones for cane yield over crop seasons and b) BLUP values for cane yield in first, second plant crops and ratoon crop

by the results reported in different crops by Munda et al. (2023) in Curcuma; Koundinya et al. (2021) in cassava, and Taleghani et al. (2023) in sugarbeet.

Correlations

The Pearson correlation matrix for 13 yield and quality traits of sugarcane is presented in Fig. 3. The t-test revealed 31 significant positive correlations and 11 significant negative correlations among the traits, with significance levels of $p < 0.05$, $p < 0.01$, and $p < 0.001$. High correlations ($|r| > 0.66$) were observed for the following trait pairs: no. of shoot at 120 DAP– no. of shoot at 240 DAP, no. of shoot at 120DAP–no. of millable canes, no. of shoot at 240 DAP–no. of millable canes, no. of shoot at 240DAP–cane yield, no. of shoot at 240DAP–CCS yield, no. of millable canes–cane yield, no. of millable canes–CCS (%), cane yield–CCS yield, Brix (%)–Sucrose (%), Brix (%)–CCS(%), and sucrose (%)– CCS(%). These strong correlations suggest that the associated traits may form a common cluster. Negative correlations, although weaker, were observed between Brix (%) and yield traits (no. of shoots at 120 DAP and 240 DAP, no. of millable canes and cane yield), as well as between fiber (%) and sugar quality traits (sucrose (%), Brix (%), and CCS (%)). The present study demonstrated a strong association among cane yield and yield-related traits across seasons, alongside high correlations that were observed among sucrose (%), Brix (%), and CCS (%) over the crop seasons. These strong inter-trait associations enhance the precision of selection strategies. Case studies were reported about the correlations

Table 5. Evaluation of selection differential for13 cane yield and quality traits over the crop seasons

S.No	VAR	Factor	Xo	Xs	SD	SD (%)	Sense
1	No. of shoots at 120 DAP (x 1000/ha)	FA 1	48.3	78.87	30.57	63.28	increase
2	No. of shoots at 240 DAP (x 1000/ha)	FA 1	45.83	73.13	27.3	59.56	increase
3	No. of millable canes (000'/ha)	FA 1	53.91	85.56	31.65	58.71	increase
4	Cane yield (t/ha)	FA 1	51.31	77.32	26.01	50.69	increase
5	CCS yield (t/ha)	FA 1	46.31	66.31	20	43.18	increase
6	Brix (%)	FA 2	54.98	50.27	-4.71	-8.57	Decrease
7	Sucrose (%)	FA 2	51.29	58.56	7.27	14.18	increase
8	CCS (%)	FA 2	47.3	54.84	7.54	15.93	increase
9	Single cane weight (kg)	FA 2	49.64	54.06	4.42	8.91	increase
10	Jaggery yield (t/ha)	FA 3	42.99	36.84	-6.16	-14.32	Decrease
11	Stalk length (cm)	FA 3	52.78	55.53	2.75	5.21	increase
12	Stalk diameter (cm)	FA 3	60.06	45.83	-14.23	-23.69	Decrease
13	Fiber (%)	FA 4	43.15	42.66	-0.49	-1.13	Decrease
	variable	min	mean	max	sum		
	SD (%)	-23.686	20.917	63.278	271.932		

Xo = mean for WAASBY index of the original population; Xs = mean for WAASBY index of the selected genotypes; SD and SD perc, The selection differential and selection differential in percentage

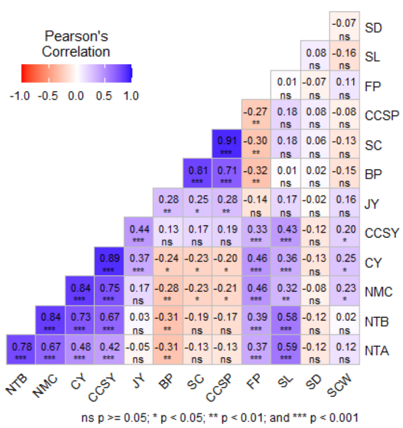


Fig. 3. Pearson's phenotypic correlations among 13 yield and quality traits among eleven clones

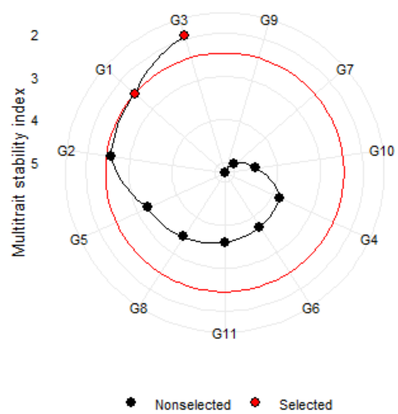


Fig. 4. Ranking of eleven clones in ascending order based on MTSI index

estimated over crops that were generally consistent with those observed within individual crops. Similar reports were given by Alam et al. (2024) in sweet potato and by Carvalho et al. (2020) in sugarcane.

Loadings factor delineation

The results of the factor analysis using the Weighted Average of Absolute Scores from BLUP for Yield (WAASBY) index for 13 yield and quality traits across eleven clones are summarized in Table 4, which includes eigenvalues and explained variance. Four principal components were retained, with these components accounting for a cumulative variance of 83.23% (Table 4 and Supplementary Fig. 1). After applying varimax rotation, the average communality (h) was found to be 0.83, with a maximum of 0.98 for sucrose (%) and a minimum of 0.64 for jaggery yield. The WAASBY values for each yield and quality attribute were organized into the four factors. FA1 is associated with yield-related traits (no. of shoots at 120DAP and 240DAP, no. of millable canes, cane yield, and CCS yield). FA2 relates to sugar quality characteristics (Brix (%), sucrose (%), CCS (%), and single cane weight). FA3 includes traits related to plant features (stalk length, stalk diameter, and jaggery yield). FA4 is associated with fiber (%). Similar studies reported by Olivoto et al. (2021) in maize, Adilakshmi et al. (2025) in sugarcane and Palaniyappan et al. (2025) in fodder maize.

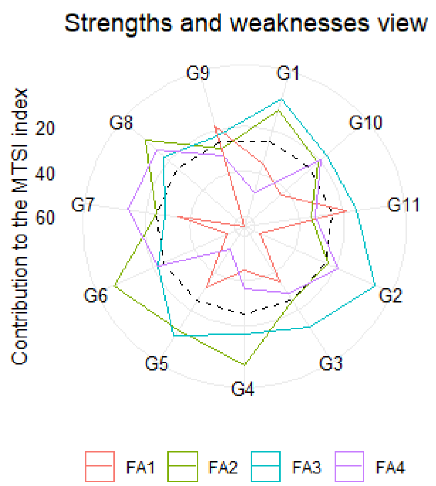


Fig. 5. The strengths and weaknesses view of eleven clones for 13 yield and quality traits

Multi-trait stability index clonal selection

The ranking of the eleven clones based on their MTSI scores is presented in Figure 4 and Supplementary Table S2. Two clones, viz., 2017A236 (G3) (MTSI= 1.926) and 2017A36 (G1) (MTSI= 2.451), were selected as stable performance clones in terms of multi-trait combination over the three seasons, assuming at 15% selection intensity.

The WAASBY index provides the selection differential for all investigated traits, and these are presented in Table 5. A desired positive selection differential (SD) was observed for nine traits out of thirteen traits and range from stalk length: 5.21% to no. of shoots at (120DAP): 63.28%. Brix percentage (-8.57%), jaggery yield (-14.32%), stalk diameter (-23.96), and fiber percentage (-1.13) were exhibited negative selection differentials. Positive selection differential represents those traits with stable performance across seasons, while negative selection differential demonstrates those traits with greater stability rather than base population (Olivoto et al. 2021). Studies conducted earlier in other crops by Khandelwal et al. (2024) in pearl millet, Patel et al. (2023) in sweet corn and Kumar et al. (2025) in cumin also supported the present findings.

The strengths-weaknesses view of eleven clones

Figure 5 illustrates the strength-weakness view of all clones based on the MTSI (Multi-trait Stability Index) index. Each factor contributing to the MTSI index was categorized into two groups: factors that contributed the least were presented at the edge of the plot, while highly significant contributing factors were shown in the center. The dashed line represents the theoretical value if all factors contributed equally. The clones 2017A236 (G3) and 2017A36 (G1) exhibit lower WAASB values for 13 yield-quality traits across four factors, indicating that these clones are considered stable. Standard clone 87A298 (G11) shows lower WAASB values for yield-related traits (cane yield, no. of shoots at 120DAP and 240DAP) in FA1. In FA2, 2017A553 (G10) demonstrates lower WAASB values for quality traits (Brix (%), sucrose (%), and CCS (%)). Meanwhile, 2017A405 (G9) displays strengths related to FA3 and FA4 (SL, SD, and stalk length, stalk diameter and fiber (%)). These findings underscore the potential of the MTSI index as a powerful tool for selecting elite sugarcane clones that combine superior yield, quality traits, and stability across diverse cropping environments, making them valuable candidates for future breeding programs.

The primary objective of plant breeding is to enhance desirable traits by utilizing phenotyping among genetic strains. This is crucial for identifying and quantifying the behavioral aspect of agronomic and quality traits over the crop seasons or growing environments on the phenotype. Correlation and MTSI methodology are used to predict the genetic relation and stability of the adaptable traits over crop seasons on specific sugarcane clones. In this current study, the characters viz., number of shoots at 120 DAP, no. of shoots at 240 DAP, no. of millable canes and Brix (%) were found to be more stable across crop seasons. The clones 2017A236 (G3) and 2017A36 (G1) exhibited equal weights (~60%) of mean performance and stability for both yield and sugar quality traits. Hence, these genotypes are considered near ideotypes.

Supplementary material

Supplementary TablesS1 and S2 and Supplementary Figure 1 are provided, which can be accessed at www.isgpb.org

Authors' contribution

Conceptualization of research (PVP); Designing of the experiments (ADL); Contribution of experimental materials (CMR); Execution of field/lab experiments and data collection (DPR); Analysis of data and interpretation (DPR); Preparation of the manuscript (DPR).

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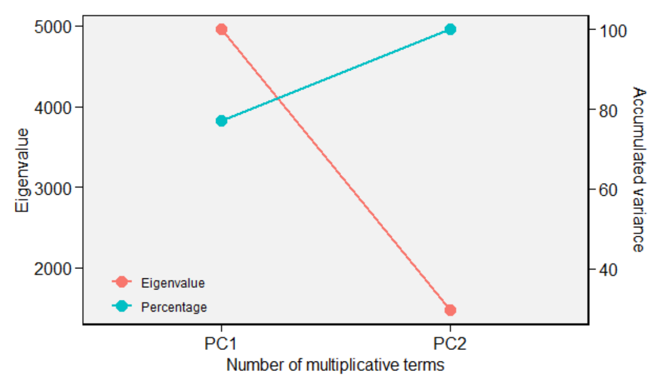
Supplementary Table S1. Likelihood Ratio Test (LRT) for 13 yield and quality traits among eleven cones over three crop cycles

```
----------------------------------------------------------------------
P-values for Likelihood Ratio Test of the analyzed traits
----------------------------------------------------------------------
   model     NTA     NTB     NMC     CY    CCSY     JY      BP      SC
COMPLETE       NA       NA       NA       NA       NA       NA       NA       NA
     GEN 9.83e-03 3.25e-03 6.96e-04 5.00e-03 4.15e-03 3.03e-01 4.43e-01 1.76e-01
 GEN:ENV 3.10e-81 1.35e-66 6.05e-58 1.02e-88 1.27e-33 1.46e-44 3.25e-27 3.91e-26
    CCSP       FP     SL SD      SCW
      NA       NA       NA NA       NA
9.18e-02 1.00e+00 1.21e-04  1 1.48e-02
2.29e-20 1.02e-49 1.23e-99  1 1.14e-16
----------------------------------------------------------------------
Variables with non-significant GxE interaction
SD
----------------------------------------------------------------------
The following traits had p-value for GE interaction = 1
SD
WAASBY value for these traits is based on mean performance only (PctResp)
----------------------------------------------------------------------
```

Supplementary Table S2. MTSI score for eleven clones over crop seasons

S. No.	Genotype	MTSI
1	G3	1.926
2	G1	2.452
3	G2	2.554
4	G5	3.247
5	G8	3.446
6	G11	3.603
7	G6	3.720
8	G4	3.811
9	G10	4.509
10	G7	4.940
11	G9	5.229



Supplementary Fig. 1, Eigenvalues plot for accumulated variance among eleven clones