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Genetic Diversity Evaluation of Sugarcane Clones Using Multivariate Analysis

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ABSTRACT

The experiment was conducted during the 2022–2023 crop season (March, 2022 to May, 2023) at the Regional Agricultural Research Station (RARS), Anakapalle, Andhra Pradesh, to study the genetic variability among sugarcane (Saccharum spp.) clones for key agronomic and quality traits and to identify superior genotypes for breeding. A total of 130 sugarcane clones were evaluated using an augmented block design. Genetic variance analysis revealed significant variation for single cane weight, though other traits showed non-significant variance, possibly due to environmental consistency or design constraints. High genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for number of millable canes, single cane weight, Brix (%), and sucrose (%), while juice purity exhibited low variability. Stalk length and girth displayed moderate genetic variation. All traits showed high broad-sense heritability, with high genetic advance except for juice purity. Cluster analysis categorized the 132 clones into four groups, with Cluster 4 (69 clones) being the largest and Cluster 2 (7 clones) the smallest. Principal Component Analysis (PCA) retained the first three components (eigenvalues≥1), explaining 76.7% of total variation. PC1 (eigenvalue 2.494) accounted for 35.6% of variability, tied to juice quality traits. PC2 (eigenvalue 1.831) explained 26.2%, linked to stalk length and girth, while PC3 (eigenvalue 1.046) captured 14.9%, influenced by millable canes and stalk length. This study underscores PCA's value in identifying key traits for genetic variability, aiding breeding efforts. Future work should incorporate multi-location trials and molecular markers to enhance selection precision and identify stable, high-yielding clones.

KEYWORDS: Cluster analysis, genetic variation, principal component

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1. INTRODUCTION

Sugarcane, a member of the Poaceae family, is a vital crop known for its role in sugar production and bioenergy. It belongs to the Saccharum genus, which is closely related to other grasses like sorghum and maize (Jamoza et al., 2019; Karthik et al., 2025 and Venkatarayappa et al., 2025). The sugarcane genome is highly complex due to its polyploid nature, with most commercial varieties being octoploid or aneuploid, meaning they contain multiple sets of chromosomes derived from hybridization events between *Saccharum officinarum* and *Saccharum spontaneum* (Tolera et al., 2023; Iwuozor et al., 2023 and Mall et al., 2024). This polyploidy contributes to the crop's genetic diversity and adaptability but also complicates genome sequencing and breeding efforts. Sugarcane is cultivated globally, with major production in tropical and subtropical regions. Brazil leads the world in sugarcane cultivation, producing the largest quantity, followed by India, which is the second-largest producer (Tena et al., 2023; Maitah et al., 2024 and Chen et al., 2024).

In recent years, the global demand for sugar and biofuels has surged due to the increasing human population. In India, per capita sugar consumption has doubled from 10 kg in 2010 to 20 kg in 2025, making the country the fourth-largest sugar exporter, contributing 4.45% of global sugar exports (Ciric et al., 2024). However, India's sugar exports have declined in recent years, highlighting the need to enhance domestic production for self-sufficiency and increased export potential (Solomon et al., 2024). A significant challenge in India's sugar industry is the decline in sugarcane production and yield, with an average reduction of 10–15% from 2010 to 2025 (Supriya et al., 2024; Pathak et al., 2024 and Niranjan et al., 2024). One of the primary bottlenecks in sugarcane production is the lack of high-yielding and improved varieties. Enhancing sugarcane productivity and sugar output can be achieved through the development of superior cultivars and the adoption of efficient agronomic management practices.

Establishing a strong breeding program is crucial to sustaining high productivity levels by replacing aging cultivars, which gradually lose their resistance to biotic and abiotic stresses and exhibit reduced yield potential over time (Tabassum et al., 2023 and Xie et al., 2024). Genetic diversity plays a pivotal role in breeding programs, as it enables the selection of genetically diverse parents for hybridization, leading to superior recombinant varieties (Abu-Ellail et al., 2023). To assess genetic diversity in sugarcane, various approaches have been employed, including morphological trait analysis. Morphological traits have been instrumental in evaluating phenotypic diversity in crop improvement programs (Rakesh et al., 2023 and Li et al., 2024). Additionally, multivariate statistical tools, such as principal component analysis (PCA) and cluster analysis, are widely utilized for assessing genetic variability and determining genetic relationships among genotypes (Rao and Chaturvedi, 2022). These advanced techniques facilitate the identification of promising genetic resources for developing high-yielding, stress-tolerant sugarcane varieties.

Cluster analysis and principal component analysis (PCA) are widely used multivariate statistical techniques for evaluating genetic diversity and relationships among genotypes. Cluster analysis classifies individuals into distinct groups based on their genetic similarity, while PCA reduces dimensionality, identifying key traits that contribute to variation (Janrao et al., 2019). In the present study, 130 sugarcane clones were analyzed to assess the extent of genetic diversity and establish relationships among them using both quantitative and qualitative traits. Multivariate analysis provided valuable insights into the genetic structure of the population, facilitating the selection of diverse parental lines for breeding programs.

2. MATERIALS AND METHODS

The experiment was conducted during the 2022–2023 (March, 2022–May, 2023) crop season at the Regional Agricultural Research Station (RARS), Anakapalle, Andhra Pradesh. A total of 130 sugarcane clones (128 test entries and 2 checks; Table 1) were selected from the selection nursery and evaluated using an augmented block design with two standard checks. Three-budded sets were used for planting, with each genotype established in two rows, each measuring six meters in length and spaced 90 cm apart, 132 clones adjusted in two blocks. Standard agronomic practices were uniformly applied throughout the crop cycle. Stalk length (cm), stalk girth (cm), and single cane weight (kg) were measured from ten randomly selected samples clone^{-1}, and their averages were documented. For quality assessment, Brix (%) and sucrose (%) were estimated at the 10th month of crop growth using five randomly selected canes clone^{-1}. A Brix refractometer and a sucrolyser were employed for precise measurements. Juice purity was calculated using the formula: Juice purity (%)=(Sucrose (%)×100)/Brix (%) (Nair et al., 1999). The number of millable canes (NMC) was manually counted within the net plot area and expressed as thousands hectare^{-1} ('000ha^{-1}). The data analysis was conducted using R Studio. The 'augmentedRCBD' package was utilized for genetic variance and variability analysis. Clustering and principal component analyses (PCA) were performed using the "factoMineR" package (Le et al., 2008) and the "factoextra" package (Irnawati et al., 2021).

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

The genetic variance results for 130 clones are presented

Table 1: List of 130 genotypes used in this investigation

Code	Genotype	Code	Genotype	Code	Genotype	Code	Genotype	Code	Genotype	Code	Genotype
G1	CoA 08323	G23	Co 98061	G45	CoA 05321	G67	2010A 229	G89	CoA 95081	G111	CoA 96081
G2	2006A 64	G24	87A 380	G46	2003V 46	G68	CoC 13337	G90	98A 168	G112	CoA 87085
G3	CoA 7701	G25	2007A 177	G47	2000A 64	G69	2020A 93	G91	2017A 67	G113	72A 66
G4	2001A 70	G26	97A 53	G48	81A 99	G70	CoA 7601	G92	2009A 280	G114	2008A 160
G5	2009A 107	G27	2000A 56	G49	2006A 223	G71	CoA 11321	G93	2011A 11	G115	2016A 229
G6	2020A 70	G28	2009A 252	G50	Co 149	G72	CoA 13322	G94	Co 7219	G116	2016A 680
G7	CoA 7602	G29	85A 261	G51	74A 95	G73	CoA 13327	G95	96A 176	G117	93V 297
G8	CoA 11326	G30	2009A 55	G52	2020A 55	G74	ISH 37	G96	70A 5	G118	96A 3
G9	2009A 235	G31	2003A 255	G53	CoA 8402	G75	CoA 13324	G97	97A 44	G119	97R 401
G10	2004A 107	G32	Co6907	G54	93A 145	G76	2012A 222	G98	2012A 319	G120	2016A 503
G11	CoA 8401	G33	2011A 294	G55	CoA 13321	G77	Bo 91	G99	2012A 287	G121	2020A 11
G12	2011A 194	G34	Co6806	G56	Co 975	G78	CoC 99081	G100	2009A 269	G122	2012A 23
G13	2003A 51	G35	93V 66	G57	69A 591	G79	97A 28	G101	2006A 102	G123	2012A 270
G14	2011A 277	G36	2012A 49	G58	2004A 55	G80	2008A 56	G102	2009A 225	G124	Co 03-113
G15	99V 30	G37	2011A 260	G59	CooR 13346	G81	97A 85	G103	CoA 12322	G125	2008A 113
G16	89A 74	G38	2001A 63	G60	Co 7805	G82	Co 90068	G104	Co86032	G126	CoM 250
G17	CoA 93081	G39	2000A 225	G61	CoA 06321	G83	2012A 340	G105	2008A 66	G127	2000A 240
G18	84A 125	G40	CoA 90081	G62	2011A 67	G84	CoA 93082	G106	CoA 05322	G128	CoA 89085
G19	2012A 249	G41	Co 11015	G63	2005A 14	G85	Co 87634	G107	Co 86036	G129	87A 298 (check)
G20	2020A 82	G42	CoA 88081	G64	CoA 05323	G86	CoC 13339	G108	2012A 335	G130	83V 15 (check)
G21	2020A 148	G43	CoA 11325	G65	2005A 128	G87	CoA 1325	G109	Co 8371		
G22	2000A 226	G44	2020A 138	G66	2000A 213	G88	2004A 104	G110	98A 163		

in Table 2. The variance analysis revealed that all traits, except for single cane weight (SCW), exhibited non-significant variation across different sources of variation. The lack of significant variance in most traits suggests genetic uniformity among clones or the potential influence of environmental stabilization. However, the significant variation observed in SCW indicates potential genetic differentiation among clones for biomass-related traits. To improve the detection of genetic variance, future studies should incorporate replicated trials or multi-location testing. Dumont et al. (2022) highlighted that the Augmented RCBD design can sometimes obscure genetic variation due to its lack of replication for test clones, which may explain why only SCW exhibited significant variance while other traits were potentially influenced by environmental uniformity or measurement inconsistencies. Additionally, Hoarau et al. (2022) emphasized that variance in sugarcane trials is highly dependent on replication strategy and field layout, both of which can impact the statistical power to detect significant differences.

3.2. Genetic variability parameters

In the present study, the number of millable canes, single cane weight, brix (%), and sucrose (%) exhibited high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), indicating substantial genetic variability and the potential for effective selection. Stalk length and girth showed a moderate degree of genetic variability, suggesting a controlled influence of genetic factors. However, juice purity exhibited a low level of genetic variation, which may limit the effectiveness of selection for this trait. High broad-sense heritability was

Table 2: Analysis of variance for seven qualitative and quantitative traits of 130 sugarcane clones using an augmented design

Source	Df	Mean sum of squares						
		No. of millable canes	Stalk length (cm)	stalk girth (cm)	single cane weight	Brix (%)	Sucrose (%)	Juice purity (%)
Block (ignoring Treatments)	1	71.72	16042.48*	0.73*	2.62**	114.61*	113.13*	2.51
Treatment (eliminating Blocks)	129	512.41	1436.42	0.05	0.02**	44	43.7	1.71
Treatment: Check	1	103.02	855.56	0.2	0.01**	0.36	0.2	0.25
Treatment: Test and test vs. check	128	515.61	1440.95	0.05	0.02**	44.34	44.04	1.73
Treatment (Ignoring Blocks)	129	512.55	1560.69	0.06	0.04**	44.89	44.58	1.69
Treatment: Check	1	103.02	855.56	0.2	0.01**	0.36	0.2	0.25
Treatment: Test	127	512.1	1577.89	0.05	0.04**	45.59	45.28	1.71
Treatment: Test vs. check	1	978.67	81.6	0.11	0.02**	0.22	0.02	0.86
Block (Eliminating treatments)	1	54.02	10.56	0	0	0.04	0.12	5.29
Residuals	1	17.22	10.56	0	0	0.25	0.3	0.16

**, *= significant at (p=0.01) and (p=0.05)

observed for all traits, highlighting strong genetic control. However, heritability alone is not a sufficient criterion for selection; combining it with genetic advance (GA) allows for more precise selection of desirable traits (Singh et al., 2013). In this study, high heritability coupled with high genetic advance as a percentage of mean was observed for all traits except juice purity, reinforcing the potential for significant genetic gains through selection (Dumont et al., 2022). Genetic parameters of all traits were presented in Table 3. This finding aligns with previous studies indicating that traits with high heritability and genetic advance are more reliable for breeding programs focused on yield improvement (Esayas et al., 2021).

Table 3: Genetic parameters of yield and quality related traits in 130 sugarcane clones

Item	No. of millable canes	Stalk length (cm)	stalk girth (cm)	single cane weight	Brix (%)	Sucrose (%)	Juice purity (%)
Phenotypic variance	512.10	1577.89	0.05	0.04	45.59	45.28	1.71
Genotypic variance	494.88	1567.33	0.05	0.04	45.34	44.98	1.55
GCV	25.41	18.21	10.29	23.55	29.64	31.63	1.34
PCV	25.85	18.27	10.54	23.55	29.72	31.73	1.40
heritability broad sense (hBS)	96.64	99.33	95.39	100.00	99.45	99.33	90.65
Genetic advance	45.12	81.40	0.46	0.43	13.85	13.79	2.45
genetic advance as per cent of mean (GAM)	51.54	37.44	20.73	48.58	60.99	65.02	2.63
CV	4.73	1.50	2.26	0.22	2.20	2.59	0.43
Mean	87.54	217.39	2.21	0.89	22.72	21.21	93.17

3.3. Cluster analysis

Cluster analysis was conducted using the UPGMA technique based on the Euclidean distance matrix. The optimal number of clusters was determined using the K-means method and is presented in Figure 1. accordingly, cluster analysis effectively grouped the 130 sugarcane clones into four distinct clusters (Figure 2 and Table 4) based on seven quantitative and qualitative traits, with all of these

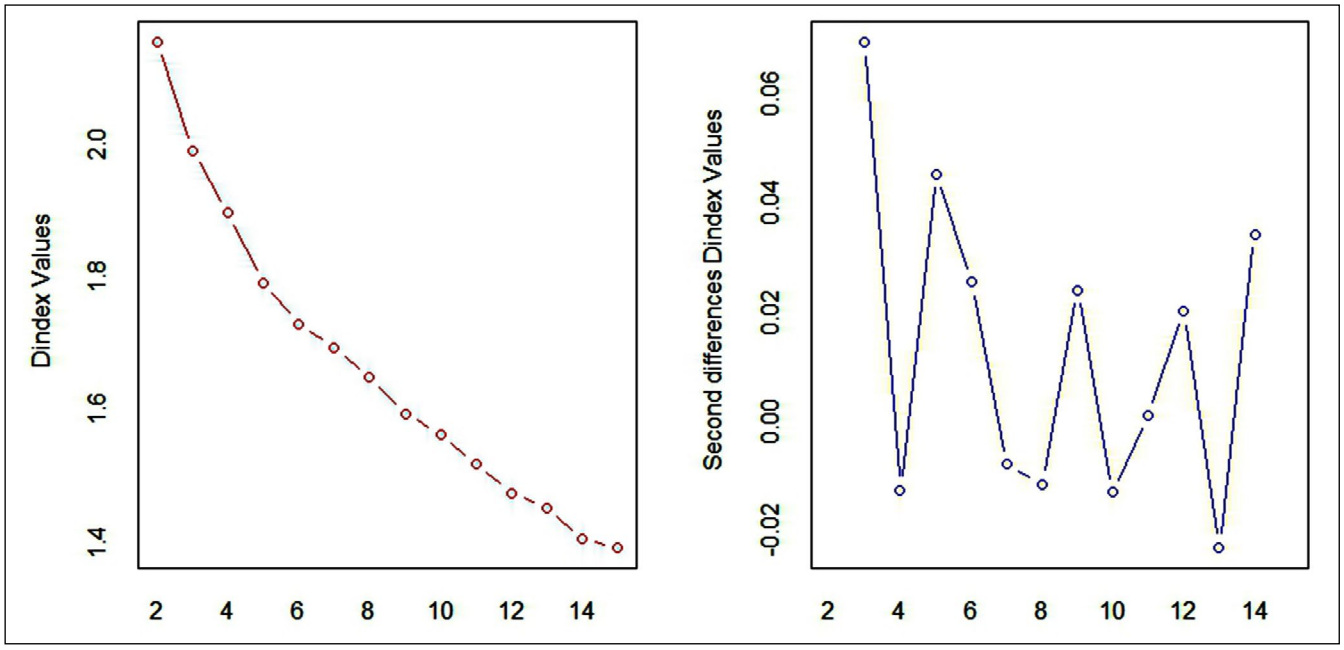

Figure 1: Graphical representation of the Dindex indicating the optimal number of clusters for 130 sugarcane genotypes: (a) Dindex values and (b) second difference of Dindex values

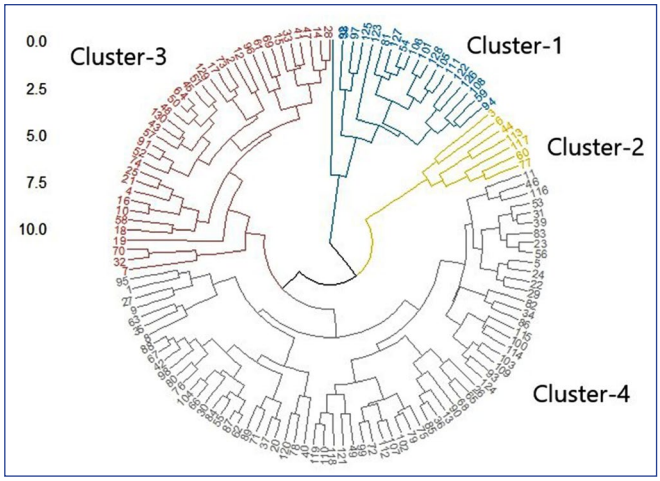

Figure 2: Dendrogram of 130 sugarcane genotypes illustrating genetic similarity based on UPGMA cluster analysis

clusters further dividing into sub-clusters. The clustering pattern demonstrated high homogeneity within clusters and high heterogeneity between clusters, indicating strong genetic relationships among genotypes. This clustering approach helps in identifying genetically similar clones for targeted breeding programs. Similar studies in sugarcane have reported comparable findings. For instance, in Ethiopia, Esayas et al. (2021) grouped 400 genotypes into 19 main clusters and a singleton using 21 quantitative traits, highlighting the genetic diversity in sugarcane populations. In another study, 135 F1 sugarcane hybrids were grouped into three clusters using 11 attributes, further supporting the use of clustering techniques for assessing genetic diversity in sugarcane (Tiwari et al., 2020). These findings align with the

Table 4: List of clones grouping into four clusters

Cluster 1	18	G92, G38, G97, G123, G125, G126, G81, G101, G128, G105, G111, G54, G127, G108, G106, G94, G59, G122
Cluster 2	7	G3, G6, G114, G113, G117, G77, G60
Cluster 3	36	G7, G32, G70, G19, G18, G58, G10, G16, G4, G21, G25, G74, G52, G91, G57, G43, G130, G48, G50, G64, G45, G51, G129, G17, G73, G2, G12, G96, G61, G69, G15, G33, G41, G47, G14, G28
Cluster 4	69	G95, G1, G27, G9, G63, G35, G8, G88, G67, G42, G98, G80, G76, G104, G66,G30, G84, G55, G87, G62, G89, G71, G37, G20, G120, G78, G40, G119, G110, G118, G121, G49, G99, G72, G112, G107, G102, G79, G75, G85, G36, G13,G90, G68, G65, G26, G124, G93, G109, G103, G114, G100, G115, G86, G34, G82, G29, G22, G24, G5, G56, G23, G83, G39, G31, G53, G116, G46, G11,G44

current study, demonstrating the utility of cluster analysis in categorizing genotypes for efficient breeding strategies.

The clustering analysis revealed distinct genetic groupings among the 130 sugarcane clones, with Cluster 1 (Figure 2) containing 18 genotypes, Cluster 2 (Figure 2) comprising seven genotypes, Cluster 3 (Figure 2) including 36 genotypes, and Cluster 4 (Figure 2) being the largest, with

69 genotypes. The significant variation in cluster sizes indicates varying degrees of genetic similarity, with Cluster 4 potentially encompassing more genetically diverse clones. Similar clustering patterns have been reported in previous sugarcane studies. Singh et al. (2013) used cluster analysis to classify 150 sugarcane clones into five major clusters, with some clusters having a larger number of genotypes due to shared genetic backgrounds. These findings reinforce the efficiency of hierarchical clustering in distinguishing genetic relationships among sugarcane clones, which is crucial for breeding and conservation strategies.

The cluster means of seven traits are presented in Table 5 and cluster distances were presented in Table 6. The clustering analysis of sugarcane genotypes revealed distinct variations in performance across clusters based on the cluster means and divergence pattern. Cluster 4, with the highest number of millable canes (91.59), exhibits superior tillering ability, making it ideal for higher cane yield. Cluster 2 stands out for its tallest stalks (256.74 cm), which can contribute to increased biomass yield but may require better lodging resistance, and it also has the thickest stems (2.41 cm), enhancing juice content and

Table 5: Mean trait values for each cluster

Cluster	No. of millable canes	Stalk length (cm)	stalk girth (cm)	single cane weight	Brix (%)	sucrose (%)	Juice purity (%)
Cluster 1	85.76	183.77	2.01	0.67	19.63	18.14	92.32
Cluster 2	64.03	256.74	2.41	0.96	19.37	17.79	91.81
Cluster 3	84.29	236.24	2.22	1.04	23.16	21.75	93.97
Cluster 4	91.59	212.06	2.23	0.86	22.6	21.06	93.13

Table 6: Intra and inter-cluster distances (Average euclidean distance between clusters)

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	51.78	95.09	68.84	53.95
Cluster 2		80.52	69.62	81.96
Cluster 3			51.76	55.39
Cluster 4				48.02

structural sturdiness. Cluster 3, with the highest single cane weight (1.04 kg), suggests better juice content and overall yield cane^{-1}. For sugar accumulation, Cluster 3 leads with the highest Brix percentage (23.16%) and sucrose content (21.75%), making it the best for sugar production. Additionally, its highest juice purity (93.97%) enhances sugar extraction efficiency, reinforcing its suitability for commercial sugar production. In conclusion, if the objective is high sugar yield, Cluster 3 is the most suitable choice due to its superior sugar traits. If taller and sturdier plants are preferred, Cluster 2 is ideal, though it shows greater intra-cluster variation. For high tillering and uniform yield, Cluster 4 is the best option, with its strong tillering ability and stable cane production.

Clustering analysis revealed variations in intra-cluster and inter-cluster distances among the four identified clusters. Despite having the largest number of genotypes (69), Cluster 4 exhibited the lowest intra-cluster distance (48.02), indicating that the genotypes within this cluster are highly similar. In contrast, Cluster 2 displayed the highest intra-cluster distance (80.52), suggesting greater variability among its genotypes, even though it consists of only seven members. This disparity implies that Cluster 2 contains genotypes with a wider spread in trait values, making them more heterogeneous. The inter-cluster distances further illustrate the genetic divergence between clusters. The highest inter-cluster distance was observed between Cluster 1 and Cluster 2 (95.09), indicating a significant difference in genotypic composition between these groups. On the other hand, the lowest inter-cluster distance was between Cluster 3 and Cluster 4 (55.39), suggesting a closer genetic relationship between these two clusters.

The identification of top-performing sugarcane genotypes was based on a composite score, which was derived from seven traits combination. The composite score was calculated using Min-Max normalization, ensuring that all traits contributed equally to the ranking. Based on this approach, the top 10% genotypes identified were G58, G4, G21, G18, G7, G1, G40, G34, G25, G8, G61, G29, and G19 (Table 8). Among these, Cluster 3 housed 8 out of 13 (61.5%) of the top genotypes, indicating its strong genetic background for multi-trait performance. Cluster 4 contained 5 genotypes (38.5%), reinforcing its superiority, particularly for yield-related traits. Notably, Clusters 1 and 2 did not have any genotypes in the top 10%, suggesting their relatively weaker overall performance. Key insights from this analysis indicate that Cluster 3 is the most promising cluster for multi-trait improvement, making it a valuable breeding resource. The highest-ranked genotypes, including G58, G4, G21, G18, and G7, can serve as elite lines for future selection. Additionally, crosses between Cluster 3 and Cluster 4 could lead to high heterotic

combinations, effectively integrating the genetic strengths of both clusters to develop superior hybrids.

3.4. Principal component analysis

Principal Component Analysis (PCA) is a robust multivariate technique widely used to identify the most influential traits contributing to genetic variability within sugarcane populations. In the present study, seven principal components (PCs) were extracted, corresponding to the number of evaluated traits. However, only the first three principal components (PC1–PC3) were retained for further interpretation based on the Kaiser criterion, as they exhibited eigenvalues greater than 1, indicating that they explained more variance than individual traits (Meharebet al., 2023). Together, these three components accounted for 76.7% of the total variation, signifying their substantial role in characterizing the genetic diversity of the population (Table 7, Figure 3). These findings align with previous reports by Alemu et al., (2022) and Tesfa et al. (2024), which also identified four main components contributing 75.63% and 71.44% of the variation, respectively.

Table 7: Eigenvalues of seven principal compounds

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigen-values	2.494	1.831	1.046	0.735	0.485	0.408	0
Propor-tion	0.356	0.262	0.149	0.105	0.069	0.058	0
Cumu-lative propor-tion	0.356	0.618	0.767	0.872	0.942	1	1

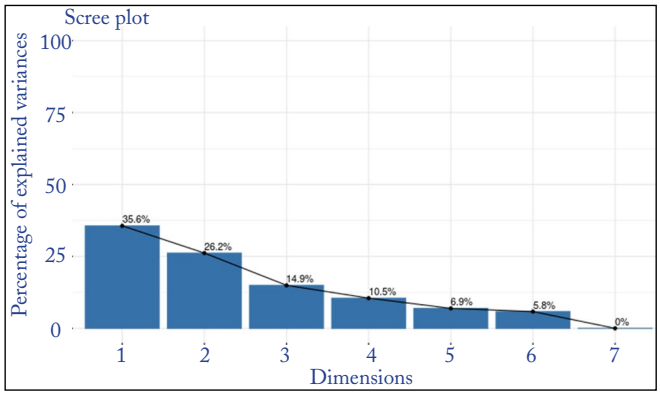

Figure 3:Screen plot constructed for seven principal components, showing contributions of PCs in variability

The first principal component (PC1) had an eigenvalue of 2.494, explaining 35.6% of the total variability. This component was primarily influenced by BP (-0.597), SP (-0.614), and JP (-0.483) (Table 8) all of which exhibited significant negative loadings exceeding ±0.3. These results suggest that PC1 represents a general performance factor, distinguishing observations based on these key variables. The second principal component (PC2) had an eigenvalue of 1.831, accounting for 26.2% of the total variance. The most significant factor loadings were observed for SL (-0.569), SG (-0.529), and SCW (-0.583) (Table 8) indicating that PC2 is associated with structural or compositional traits. The negative loadings suggest an inverse relationship among these variables, consistent with findings from Wold et al. (1987), who demonstrated that PCA effectively differentiates structural components in complex datasets.Wang et al. (2008) applied PCA in sugarcane breeding programs and found that PC2 often captures variations in stalk morphology and fiber content, further supporting these results. Reyes et al. (2020) applied PCA in sugarcane breeding programs and found that PC2 often captures variations in stalk morphology and fiber content, further supporting these results.

The third principal component (PC3) had an eigenvalue of 1.046, capturing 14.9% of the total variability. This component was strongly influenced by NMC (0.872) and SL (0.321), highlighting their dominant role in this dimension. Given the high positive loading of NMC, PC3 may represent a measure of growth or reproductive potential. Similar studies in sugarcane by Ramirez-Madero et al. (2023) and Tolera et al. (2024) showed that secondary components often relate to tillering ability and early-stage growth patterns, making PC3 critical in identifying high-yielding clones. According to Tesfa et al. (2024), factor loadings exceeding ±0.3 are considered significant, validating the importance of the identified variables in each principal component. Similar findings were reported by Barreto et al. (2021), where key performance indicators were grouped under the first few principal components, emphasizing their role in dimensionality reduction and data interpretation.

The PCA biplot serves as a comprehensive tool for visualizing the relationships among traits and sugarcane clones, effectively illustrating both the magnitude of trait contributions to the principal components and their intercorrelations. This graphical representation facilitates the differentiation of genotypes based on trait performance, thereby supporting selection decisions. Figure 4 presents a PCA biplot constructed using seven quantitative and qualitative morphological traits, effectively demonstrating their interrelationships. The plot distinctly segregates yield traits (characterized by a high PC1 score) from quality traits (associated with a high PC2 score), suggesting that these trait groups contribute differently to genetic variation. In PCA biplots, the cosine of the angle between trait vectors indicates correlation. Acute angles (<90°) imply a positive

Table 8: Loadings (Eigenvectors) of correlation Matrix among seven cane yield and juice quality traits

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
No. of millable canes	-0.043	0.183	0.872	0.4	-0.185	0.101	-0.002
Stalk length (cm)	-0.038	-0.569	0.321	-0.42	-0.263	-0.571	0.003
stalk girth (cm)	-0.089	-0.529	-0.286	0.565	-0.522	0.197	0
single cane weight	-0.148	-0.583	0.201	0.037	0.683	0.361	-0.001
Brix (%)	-0.597	0.102	-0.079	0.206	0.141	-0.326	-0.677
Sucrose (%)	-0.614	0.103	-0.063	0.127	0.087	-0.227	0.73
Juice purity (%)	-0.483	0.048	0.066	-0.534	-0.361	0.58	-0.091

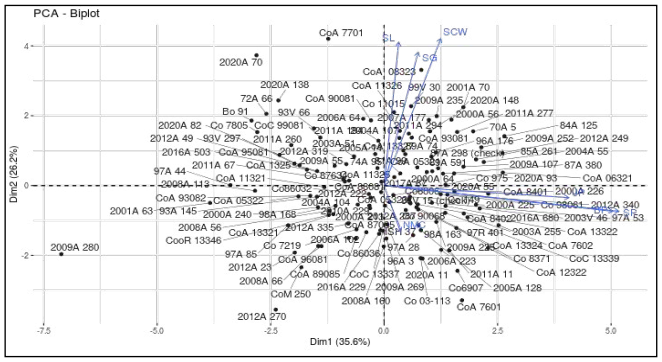

Figure 4: Biplot graph illustrating trait loadings, genotype distribution patterns, and genotype-trait relationships

correlation, meaning these traits tend to increase together. Right angles (90°) suggest no correlation, while obtuse angles (>90°) indicate a negative correlation, meaning one trait increases while the other decreases. From this biplot, SL, SG, and SCW are positively correlated, while JP, BP, and SP are also positively correlated. If NMC forms obtuse angles with JP, BP, or SP, it suggests a negative correlation with them. Similar findings were reported by Mebrahtom et al. (2016), who observed a positive correlation between stalk length, stalk girth, and cane yield. Tesfa et al. (2024) also highlighted similar relationships. The correlations among traits revealed through this PCA approach may be attributed to genetic linkages between loci controlling these traits or the effects of pleiotropy. Understanding these correlations is crucial for enhancing breeding efficiency and effectiveness.

This biplot also highlights specific genotypic performance. The clones CoA 08323, 99V 30 and CoA 11326 exhibits highest mean values for stalk length, stalk girth and single cane weight. making it a promising candidate for high-yielding sugarcane breeding programs. Meanwhile, clones 2000A 226, 2012A 340 and 2012A 249 showed the highest mean values for sucrose, brix percentages and juice purity, (%), indicating its potential for improving sugar quality traits. These genotypes, being divergent from others due to their extreme values for key traits, represent valuable genetic material for sugarcane crop improvement programs. Overall, the PCA biplot provides crucial insights into trait relationships and genotype performance, facilitating targeted breeding strategies for yield and quality improvement in sugarcane.

4. CONCLUSION

The clones 2004A 55 (G58), 2001A 70 (G4), 2000A 226 (G21), 84A 125 (G18), CoA 7602 (G7), CoA 08323 (G1), CoA 90081 (G40), Co6806 (G34), 2007A 177 (G25), CoA 11326 (G8), CoA 06321 (G61), 85A 261 (G29), and 2012A 249 (G19) showed superior cane and sugar yield over standard checks. PCA revealed that brix (%), sucrose (%), and juice purity (%) contributed the highest variation, with strong positive loadings, making them key traits for selecting promising genotypes to enhance sugarcane productivity through breeding.

5. REFERENCES

Abu-Ellail, F.F., Attafy, T.M., Attia, A.E., El-Bakry, A.N., 2023. Variability, heritability, and performance of some sugarcane varieties under three surface irrigation regimes. Journal of Sohag Agriscience 8(2), 220–239. https://jsasj.journals.ekb.eg/article_334537_e2ef307b66e87634ebf4cfcdb4199efc.pdf

Alemu, S., Fetene, T., Tadesse, F., 2022. Morphological diversity and principal component analysis of sugarcane (*Saccharum officinarum* L) genotypes at Finchaa Sugar Estate, Ethiopia. Ratar. Povrt. 59(1), 9–15.

Barreto, F.Z., Balsalobre, T.W.A., Chapola, R.G., Garcia, A.A.F., Souza, A.P., Hoffmann, H.P., Carneiro, M.S., 2021. Genetic variability, correlation among agronomic traits, and genetic progress in a sugarcane diversity panel. Agriculture 11(6), 533.

Chen, S., Zhang, C., Liu, J., Ni, H., Wu, Z., 2024. Current status and prospects of the global sugar beet industry. Sugar Tech 26(1), 1–9.

Ciric, M., Popovic, V., Prodanovic, S., Zivanovic, T., Ikanovic, J., Bajic, I., 2024. Sugar beet: Perspectives for the future. Sugar Tech 26(5), 1208–1219.

Dumont, T., Barau, L., Thong-Chane, A., Dijoux, J.,

Mellin, M., Daugrois, J., Hoarau, J.Y., 2022. Sugarcane breeding in Reunion: challenges, achievements, and future prospects. Sugar Tech 24(1), 181–192.

Esayas, T., Alemayehu, A., Mekuria, G., 2021. Genetic diversity and clustering of sugarcane genotypes using quantitative traits. Ethiopian Journal of Agricultural Sciences 31(2), 45–60.

Hoarau, J.Y., Dumont, T., Wei, X., Jackson, P., D'hont, A., 2022. Applications of quantitative genetics and statistical analyses in sugarcane breeding. Sugar Tech 24(1), 320–340.

Irnawati, I., Riswanto, F.D.O., Riyanto, S., Martono, S., Rohman, A., 2021. The use of software packages of R factoextra and FactoMineR and their application in principal component analysis for authentication of oils. Indonesian Journal of Chemometrics and Pharmaceutical Analysis, 1–10.

Irnawati, I., Riswanto, F.D.O., Riyanto, S., Martono, S., Rohman, A., 2021. The use of software packages of R factoextra and FactoMineR and their application in principal component analysis for authentication of oils. Indonesian Journal of Chemometrics and Pharmaceutical Analysis, 1–10.

Iwuozor, K.O., Olaniyi, B.O., Anyanwu, V.U., Suleiman, M.A., Omoleye, W.S., Enahoro-Ofagbe, F.E., Opeyemi, A.M., 2023. The effect of ChatGPT on sugar industry research. Sugar Tech 25(6), 1278–1284.

Jamoza, J.E., Owuoche, J., Kiplagat, O., 2019. Estimates of genetic parameters and genotype by environment interactions for sugar yield and its components in sugarcane genotypes in Western Kenya. Journal of Plant Breeding and Crop Science 11(9), 206–212.

Janrao, P., Mishra, D., Bharadi, V., 2019. Performance evaluation of principal component analysis for clustering on sugarcane dataset. In: 2019 International Conference on Advances in Computing, Communication and Control (ICAC3), IEEE, 1–5. https://ieeexplore.ieee.org/abstract/document/9036814.

Karthik, K., Rakshitha, S., Kamat, D.N., 2025. Genetic evaluation of climate resilient sugarcane clones under waterlogged condition. Electronic Journal of Plant Breeding 16(1), 38–45.

Li, Y.R., Zhang, B.Q., Song, X.P., Liang, Q., Verma, K.K., Li, D.M., 2024. Development of sugar industry in China: R&D priorities for sustainable sugarcane production. Sugar Tech 26(4), 972–981.

Maitah, M., Procházka, P., Rojík, S., Cincalová, S., Malec, K., Smutka, L., Tomšík, K., 2024. Future development of sugar market in the European Union in the period 2023–2032. Sugar Tech 26(1), 295–304.

Mall, A.K., Srivastava, S., Mulet, J.M., Popovic, V., Misra, V., 2024. Sugar beet special issue: Biotechnology and breeding techniques for stress-resistant sugar beet. Sugar Tech 26(1), 1–4.

Mebrahtom, F., Firew, M., Eyasu, A., 2016. Multivariate analysis of sugar yield contributing traits in sugarcane (*Saccharum officinarum* L.) in Ethiopia. African Journal of Plant Science 10(8), 145–156.

Mehareb, E.M., Sakina, R.A., Fouz, F.A.E., 2023. Assessment of harvest age of some sugarcane genotypes by using principal component analysis. Direct Research Journal of Agriculture and Food Science 11(8), 244–253.

Nair, N.V., Nagarajan, R., Mathew, M.D., 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.

Niranjan, S., Murali, P., Puthira Prathap, D., Kumaravel, S., Hemaprabha, G., 2024. Impact of wonder cane varieties on sugar production, consumption and prices in India. Sugar Tech 26(3), 809–819.

Pathak, S.K., Kushwaha, R.A., Sah, A.K., 2024. Adoption of trench method cane planting and its role in increasing cane yield and sugar recovery in Uttar Pradesh. Sugar Tech 26(1), 274–281.

Rakesh, G., Reddy, G.E., Dinesh, A., Swapna, N., Saicharan, M., Naik, B.B., Kumar, M.V., 2023. Genetic studies in advanced sugarcane mid-late clones through yield and quality traits. International Journal of Environment and Climate Change 13(10), 4535–4542.

Ramirez-Madero, G., Gomez-Merino, F.C., Bello-Bello, J.J., Trejo-Tellez, L.I., Hidalgo-Contreras, J.V., 2023. Assessment of the genetic diversity of new sugarcane hybrids using principal component and cluster analyses. Agrociencia, 57(8).

Rao, D.P., Chaturvedi, H.P., 2022. Genetic diversity analysis in foxtail millet (*Setaria italica* (L.) P. Beauv.) genotypes. The Journal of Plant Science Research 38(2), 907–918.

Reyes, J.A.O., Carpentero, A.S., Santos, P.J.A., Delfin, E.F., 2020. Effects of water regime, genotype, and formative stages on the agro-physiological response of sugarcane (*Saccharum officinarum* L.) to drought. Plants 9(5), 661.

Singh, R.K., Singh, S.P., Tiwari, D.K., Srivastava, S., Singh, S.B., Sharma, M.L., Singh, N.K., 2013. Genetic mapping and QTL analysis for sugar yield-related traits in sugarcane. Euphytica 191, 333–353.

Solomon, S., Vanichsriratana, W., Duong, C.A., Manimekalai, R., Singh, P., Misra, V., Rao, G.P., 2024. Sustainability issues and opportunities for sugar and integrated industries in ASEAN region. Sugar Tech 26(4), 932–950.

Supriya, Srivastava, A.B., Kumari, B., Yadav, S., Shrivastava, A., Neerugatti, M.P., 2024. Comparative analysis of sugarcane production for South East Asia region. Sugar Tech 26(1), 264–273.

Tabassum, Jeena, A.S., 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., Tadesse, F., Million, F., 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.

Tesfa, M., Tena, E., Kebede, M., 2024. Characterization and morphological diversity of sugarcane (*Saccharum officinarum*) genotypes based on descriptor traits. Journal of Crop Improvement 38(1), 40–71.

Tiwari, D.K., Singh, R.K., Singh, S.P., 2020. Genetic classification of F1 sugarcane hybrids using multivariate cluster analysis. Euphytica 216(4), 89.

Tolera, B., Gedebo, A., Tena, E., 2023b. Genetic diversity of sugarcane (*Saccharum* spp.) genotypes based on agro-morphological and biochemical traits. Cogent Food & Agriculture 9(1), 2254141.

Tolera, B., Gedebo, A., Tena, E., 2024. Phenotypic characterization and diversity estimate in sugarcane (*Saccharum spp*. hybrid) germplasm. Archives of Agronomy and Soil Science 70(1), 1–17.

Venkatarayappa, S., Channappa, M., Amaresh, Kumar, R., Raja, A.K., Meena, M.R., Perumal, G., 2025. Evaluation of saccharum and erianthus introgressed early generation novel sugarcane hybrids as potential sources of biomass for cogeneration. Sugar Tech 27(1), 158–172.

Wang, L.P., Jackson, P.A., Lu, X., Fan, Y.H., Foreman, J.W., Chen, X.K., Aitken, K.S., 2008. Evaluation of sugarcane×Saccharumspontaneum progeny for biomass composition and yield components. Crop Science 48(3), 951–961.

Wold, S., Esbensen, K., Geladi, P., 1987. Principal component analysis. Chemometrics and Intelligent Laboratory Systems 2(1–3), 37–52.

Xie, Y., Chen, R.K., Chen, N., Que, Y., 2024. Operational efficiency and influencing factors in sugar industry: From the perspective of Chinese sugar companies listed on the stock market. Sugar Tech 26(2), 489–501.