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Original Research Article||

Assessment of Genetic Variability, Heritability, and Genetic Advance in Sugarcane (Saccharum spp.L) Genotypes, at Kessem and Metahara Sugar Estates, Ethiopia

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Abstract

The presences of genetic variation in the germplasm provide a better opportunity for trait enhancement through selection. The study aimed to assess the extent of genetic variability, heritability, and genetic advance for sixteen agro-morphological traits and to identify promising genotypes for future sugarcane breeding programs. A total of 187 sugarcane genotypes were evaluated at Kessem and Metahara Sugar Estates in Ethiopia, using an alpha-lattice design with two replications. The analysis of variance (ANOVA) revealed highly significant variation ($p<0.001$) among the genotypes for all measured traits, indicating that the genotypes are genetically diverse.The estimates of genetic variability, heritability, and genetic advance indicated the presence of notable genetic diversity in sugarcane genotypes and the extent of selection response for these traits in the population to develop superior genotypes for sugarcane improvement. Several traits had high to moderately high broad-sense heritability (h^2_β) and moderate genetic advance as a percent of mean (GAM): number of sprouted buds ($h^2_\beta = 63.55$; GAM = 19.00), number of tillers ($h^2_\beta = 75.80$; GAM = 14.55), cane yield ($h^2_\beta = 52.66$; GAM = 13.04), millable cane count ($h^2_\beta = 70.15$; GAM = 12.09), internode length ($h^2_\beta = 72.73$; GAM = 10.86), single cane weight ($h^2_\beta = 66.67$; GAM = 11.73), and estimable recoverable sugar % ($h^2_\beta = 84.51$; GAM = 10.11). These results indicate that these traits are influenced by additive gene, and selection based on these traits could effectively achieve the desired genetic improvements. The sugarcane genotypes with the highest sugar yields are B630-5, B58230, B57150, FG06787, FG08533, FG05414, 26-Wonji, C132/81, and B516-60. Thus, these genotypes require additional multi-location and multi-season testing to verify their stability, and suitability for breeding and commercial release at the Metahara and Kessem sugar estates in Ethiopia.

Key words: Agronomy; Heritability; Genotypes; Selection; Sugarcane; Variability

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INTRODUCTION

Modern sugarcane (*Saccharum spp.*) cultivars have been emerged from the interspecific hybridization of the wild species *Saccharum spontaneum* and the cultivated species *Saccharum officinarum*. This process, which began in the early 1900s (D'Hont et al. 1996; Cuadrado et al. 2004, and Lu et al. 2024), initially involved backcrossing the first interspecific hybrids with *S. officinarum* using the "nobilization" technique. This technique was aimed to enhance the desirable high sugar-producing characteristics of *S. officinarum* while mitigating the negative traits associated with *S. spontaneum* (Sreenivasan and Ahloowalia, 1987). This process improved cane yields, ratooning capacity, and resistance to biotic and abiotic stressors (Anna et al. 2015, and Govindaraj et al. 2014).

Sugarcane is geographically distributed and cultivated in tropical and subtropical climate regions (Flack-Prain et al. 2021; Cordeiro et al. 2007), and it plays a pivotal role in the global economy (Ali et al. 2024). It ranks third among the plant-based calorie sources for human consumption, following wheat and rice (Rathna et al. 2019). Moreover, sustainable sugarcane cultivation can promote ecosystem health (Filoso et al. 2015). Its high yield per area makes it an efficient crop for land use, eco-friendly farming practices can enhance soil fertility and reduce erosion (Tabriz et al. 2021; Adeel and Jadhav, 2025). In Ethiopia, sugarcane was utilized as a food source for humans and as fodder for livestock before the establishment of commercial sugar production (Tena et al. 2016; Coote, 1987).

Commercial sugar production in Ethiopia commenced in 1951 after a concession agreement between the Ethiopian Empire and the Dutch company Handels Vereeniging Amsterdam, which led to the establishment of a sugar estate at Wonji (Kassie, 2022). This initiative began with the development of a 5,000-hectare sugarcane plantation, laying the foundation for the country's modern sugar industry. In 1962, a second sugar factory was commissioned at Wonji Shoa, supported by an additional 2,000 ha sugarcane plantation (Mohammed, 1969; Kebede et al. 2011). Subsequent expansions included >10,000 ha at Metahara (1969) and >8,000 ha at Finchaa (1998) (Tafesse & Haile-Michael, 1970). In 2009, the Arjo Diddessa Sugar Factory manages over 16,000 ha. Omo-Kuraz II and III exceed 40,000 ha, at present, Kesem Sugar Factory (20,000 ha) is suspended because of the earthquake (Lewi et al. 2025). Tana Beles Sugar Factory covers 20,000 ha, and Welkait Sugar Factory planned~20,000 ha close due to war (Zikargie et al. 2022). Generally, Ethiopia cultivates 105,000 ha of sugarcane and produces 400,000 tons of sugar annually (Tena et al., 2023).

In Ethiopia, the average annual sugar consumption has increased from 3.6 kg to 10 kg per person. However, only 7 kilograms are produced locally per person; therefore, the remaining amount of sugar must be imported from abroad to satisfy national demand (Hamza et al. 2017). The sugar industry in Ethiopia is currently facing several challenges, among which declining cane yield represents a major challenge. A major factor contributing to this issue is the lack of improved sugarcane varieties that are better suited to the various agro-ecologies and growing conditions of the country's sugar plantations (Kebede et al. 2011). Evidence from major sugar estates indicates a substantial reduction in cane yield per hectare over time. Between the 1998 and 2019 harvesting seasons, productivity at Finchaa Sugar Estate declined from 166 to 84 t ha^{-1}, at Wonji from 140 to 101 t ha^{-1}, and at Metahara from 165 to 157 t ha^{-1} (Tolera et al. 2023). Therefore, improving sugarcane productivity through the development of high-yielding varieties is essential for mitigating sugar shortages by maximizing sugarcane yield per unit area.

Sugarcane yield is a complex quantitative trait governed by multiple genes and strongly influenced by both genetic and environmental factors (Hoarau et al. 2022). Because yield represents the cumulative expression of several yield-related traits and generally exhibits low heritability, direct selection for high yield alone may be inefficient for genetic improvement (Singh, 2000). In contrast, yield-contributing traits in sugarcane typically display simpler inheritance and less affected by environmental variation; therefore, selection based on these component traits can be more effective (Gatti et al. 2005). Thus, improvement in sugarcane yield can be achieved through indirect selection for traits with high heritability and strong associations with cane and sugar yield (Jackson, 2005).

Assessment of genetic variability, broad-sense heritability (h^{2}_{β}), and genetic advance as a percent of mean (GAM) provides a reliable basis to determine the extent of exploitable genetic diversity in populations, which is crucial for effective breeding, crop enhancement, and selecting superior genotypes (Sandhu et al. 2022, Xu et al. 2023). An estimate of phenotypic and genotypic coefficients of variation (PCV and GCV) also helps to identify genetically diverse parents for hybridization, thereby maximizing variability in successive generations (Ram et al. 1990; Singh and Singh, 1999). Breeding success depends on the magnitude of genetic variability, as greater variation increases the possibility of selecting superior genotypes (Cobb et al. 2013). Selection efficiency is primarily determined by heritability and expected genetic advance, while sustained genetic variability supports long-term genetic improvement (Fasoula and Fasoula, 2002).

Previous studies have reported promising outcomes where broad-sense heritability is high, accompanied by considerable genotypic coefficients of variation and high estimates of genetic advance expressed as a percentage of the mean (Tolera et al. 2023). Such conditions indicate that selection for traits such as millable cane number and single-cane weight can lead to significant improvements in cane yield (Jamoza et al. 2014; Gilles et al., 2022). For effective single-trait selection, genotypes should be prioritized based on traits exhibiting moderate to high heritability coupled with considerable genetic advance (Gallais, 1984; Yin et al. 1996; Merrick et al. 2022).

The heritability of various agro-morphological traits in sugarcane has been extensively quantified in previous studies. For example, Tena et al. (2023); Tolera et al. (2023) estimated heritability coupled with genetic advance expressed as a percent of mean using 400, and 196 sugarcane genotypes, respectively, originating from diverse geographic regions. Morphological markers, as simple and direct indicators of phenotypic expression, facilitate rapid and cost-effective assessment of genetic diversity and thereby support large-scale screening and selection in breeding programs (Kumar et al. 2024).

The present study examined 187 sugarcane genotypes introduced from various countries, including 102 newly imported hybrid seeds (Fuzz) from Barbados, 39 genotypes from CIRAD, 12 local landraces, and 34 older collections of uncharacterized genotypes. The main objective of this study was to estimate the phenotypic variability, heritability, and genetic advance as a percentage of the mean for various agro-morphological quantitative traits for effectively selecting sugarcane varieties for commercial purposes and identifying potential sugarcane genotypes for future breeding programs.

MATERIALS AND METHODS

Experimental Sites

The experiments were conducted during 2021-2022 cropping season at the Kessem and Metahara Sugar Estates of Ethiopian. Kessem Sugar Estate is located in Awash Fentale and Dullecha districts, zone three of the Afar Regional Government State, 250 km from Addis Ababa and 52 km from Metahara town. Its latitude and longitude are 9o 26 'N and 40o 30 'E, respectively, at an elevation of 700-150 masl. The maximum and minimum temperatures are 38 °C and 15 °C, respectively, and the average annual rainfall is 569 mm. Metahara Sugar Estate is located 8 km south of Metehara Town, in the Eastern Shewa Zone of the Oromia Regional Government State, 200 km from Addis Ababa. Its latitude and longitude are 8° 51'N and 39° 52'E, respectively, and its elevation is 950 masl. The maximum and minimum temperatures are 32.6°C and 17.5°C, respectively, and the average annual rainfall is 554 mm (Ambachew, 2005).

Experimental Materials

The study involved 187 sugarcane genotypes, of which 175 were introduced genotypes from many countries, including F1 hybrid genotypes derived from true botanical seed (fuzz), 12 genotypes were local landraces. The experimental materials were selected through random sampling techniques from the existing germplasm pool, taking into account their year of introduction, countries of origin, and seed types. All the experimental materials were sourced from the germplasm collections at the conservation garden of the Ethiopian Sugar Industry Group Research Centre. The commercial standard varieties NCo-334 and B52-298 were used as controls. Comprehensive details about genotypes, including their origins of country and years of introduction, are presented in the Table 1.

Table 1. List of 187 sugarcane genotypes based on country of origin and year of introduction grown at the Metahara and Kessem Sugar Estate in Ethiopia during 2021/22 cropping season.

Name of the genotypes	Number of genotypes	Country of origin	Year of introduction
FG03104, FG05088, FG05221, FG05404, FG05405, FG06-87,FG06790, FG07320, FG03447, FG05045, FG05-256, FG05-387, FG05414, FG06680, FG07004, FG07252, FG04356, FG05300, FG05360, FG05450, FG04333, FG06787, FG07210, FG03097, FG08109, FG07018, FG08971, FG08755, FG08758, FG07188, FG06544, FG06691, FG07338, FG08096, FG08177, FG08355, FG08533, FG08747, FG08-763	39	France	2014
5-Yhabesha shenkora, 8-Kay Shenkora, 13-Kay Shenkora, 19-BUS, 26-Wonji, 3-Kay Shenkora, 42-kay Ageda Shenkora, 46-Wotete, 92-YE Bako Shenkora, 158-Ancha, 183-Alaa,189 Erero	12	Ethiopia	2011
B153-5, B154-1, B358-1, B358-2, B489-5, B489-6, B491-2, B491-12, B491-13, B498-4, B498-5, B498-14, B516-1, B516-10, B516-11, B516-20, B516-21, B516-31, B516-40, B516-41, B516-50, B516-51, B516-60, B516-61, B517-6, B517-15, B517-16, B517-25, B517-26, B517-35, B517-36, B517-45, B517-46, B519-5, B519-6, B519-16, B527-5, B527-6, B527-15, B527-16, B528-5, B528-15, B528-16, B528-26, B528-5, B528-6, B528-15, B528-16, B546-5, B546-6, B546-15, B546-16, B549-5, B549-6, B549-15, B549-25, B552-16, B552-25, B556-5, B556-6, B556-15, B556-16, B558-15, B558-16, B563-6, B563-15, B563-16, B563-25, B56326, B564-5, B564-6, B566-5, B566-6, B566-15, B566-16, B566-26, B568-5, B568-6, B572-5, B572-15, B572-16, B594-5, B628-5, B630-5, B635-5, B635-6B651-5, B658-15, B658-16, B658-25, B644-5, B644-6, B644-15, B644-16, B688-5, B688-6,B690-6, B691-5, B691-6, B694-5, B694-6, B694-15	102	Barbados	2011
B52-298, B53164, B60-267, B49224, B41227, B59212, B52290, B49388, B52158, B4425, B58230, B50210, B60191, B52313, B51410, B5490, B4906, B39250, B4681, B522107,B5116, B5736, B57371, B51131, B57150	25	Barbados	1962
NCO-334, N 14	2	South Africa	1968
CP961029	1	USA	NA
C132/81	1	Cuba	NA
Co680	1	India	NA
Mex54/245	1	Mexico	NA
MPT96261, MPT97004, MPT981832	3	Philippines	NA

Experimental Design

The experiments were arranged in an alpha lattice design with two replications across 11 blocks, each block comprising 17 plots. Each plot constituted an area of 21.75 m². The planting materials, which come from seven-month-old canes, are cut into two-budded sets and planted in an end-to-end arrangement within three furrows, each plot measuring 5 m in length and 1.45 m in width. The plots were spaced 1.45 m apart, with 2 m between blocks and 3 m between replications. All trial entries were managed according to the standard crop management practices of the respective sugar estates. Urea was applied two months after planting at rates of 400 kg/ha at Metehara Sugar Estate (Tena et al., 2018) and 200 kg/ha at Kessem Sugar Estate (Ayele et al., 2023).

Data Collection

Agro-morphological traits were assessed according to USDA-ARS descriptor protocols (GRIN, 2004). Sixteen quantitative traits were recorded at different growth stages. The number of sprouted buds (NSB) was counted 45 days after primary shoot emergence. Tiller counts were recorded at three (TC3MAP) and five (TC5MAP) months after planting, while hand-refractometer Brix (HR-Brix7MAP) was measured at seven months after planting. At harvest, data were collected on the number of millable cane (MC), single-cane weight (kg), number of internodes per stalk, internode length (cm), stalk diameter (cm), and stalk length (m). Stalk diameter was measured using a vernier caliper and stalk length using a tape measure. Cane yield per hectare (CYPH) was calculated as follows:

$$\text{Cane yield t/ha} = \text{Number of millable cane per hectare} \times \text{single-cane weight (kg)} \qquad (1)$$

Juice quality traits, including Brix%, pol%, purity%, and ERS%, were evaluated from composite juice samples collected 21 months after planting at the Metahara and Kessem Research Stations. Juice was extracted from ten randomly selected stalks per genotype using a Jeffco cane crusher. Brix% was determined as total soluble solids using a precision refractometer calibrated at 20°C following the method of Meade and Chen (1977). Filtered composite juice samples (Whatman No. 91 filter paper with Kieselguhr) were used for Brix determination. Pol% was measured using Horne's dry lead acetate method, in which a 300 mL juice sample treated with lead acetate (1 g per 100 mL) was filtered and polarized at 20°C. Purity% was calculated as the ratio of pol% to Brix%, while ERS% was estimated using the Winter–Carp formula (Sukhchain et al., 1997):

$$\text{ERS\% of cane} = [\text{Pol\%} - (\text{Brix\%} - \text{Pol \%}) \times 0.7] \times 0.75 \qquad (2)$$

Where 0.75 represents the correction factor between theoretical yields of molasses mixed juice as established by milling test at Metahara and Kessem sugar factories, and 0.7 designates the quantity of sucrose lost in the final processing. Finally, sugar yield per hectare was calculated by multiplying cane yield per hectare by the estimated recoverable sucrose percentage, following the method described by Tesfa and Ayele (2018).

$$\text{SY (t/ha)} = \text{Cane yield (t/ha)} \times \text{ERS\% of cane} \qquad (3)$$

STATISTICAL ANALYSIS

Analysis of Variance (ANOVA)

Data were screened to verify compliance with ANOVA assumptions for each quantitative trait across locations. Homogeneity of error variances among locations was tested using Bartlett's test, and normality was evaluated using the Shapiro -Wilk test. For combined analysis, variance homogeneity was further evaluated using Hartley's F-max test by comparing the largest and smallest mean square errors (MSE) from individual-location analyses. Error variances were considered homogeneous when the MSE ratio was ≤ 3. Upon satisfying these assumptions, combined ANOVA across locations was performed using PROC GLM in SAS version 9.4 under a linear model, treating locations as random. Mean squares for blocks, replications, genotype × location interaction, and residuals were appropriately pooled. Genotype effects were tested against the genotype × location interaction mean square, and interaction effects against the residual mean square. The statistical model used for the analysis of variance (ANOVA) in an alpha lattice design is as follows:

$$Yijkm = \mu + \tau i + \lambda j + (\tau\lambda)ij + \rho k(j) + \beta m(jk) + eijkm \qquad (4)$$

Where; Yijkm: The phenotypic observation of the i-th genotype, in the m-th incomplete block, of the k-th replication, at the j-th location. μ: The overall population mean. τi (or gi): The random effect of the i-th genotype (i=1,2,…,187). λj: The random effect of the j-th location (j=1,2 [Kessem and Metahara]). (τλ)ij: The random interaction effect of the i-th genotype and the j-th location (G×L). ρk(j): The random effect of the k-th replication nested within the j-th location (k=1,2). The (j) in the subscript mathematically denotes this nesting. βm(jk): The random effect of the m-th incomplete block nested within the k-th replication at the j-th location. The (jk) demonstrates it is nested inside both layers. eijkm: The residual of intra-block experimental error.

Estimation of variance components

Variability among 187 sugarcane genotypes was estimated using rang, and an average values, as well as phenotypic ($\delta 2p$), genotypic ($\delta 2g$), genotype × location ($\delta 2gl$), and error ($\delta 2e$) variances. The results of the variance component were used to compute the phenotypic and genotypic coefficient of variation as well as heritability in a broad-sense (h^2b), and genetic advance as a percent of mean. The phenotypic, genotypic, genotype × location interaction and error variances were estimated following the method described by Falconer and Mackay (1996) using the following formulas:

$$\sigma^2 p = \sigma^2 g + (\sigma^2 gl)/l + (\sigma^2 e)/rl \qquad (5)$$

$$\sigma^2 g = (MSg - MSgl)/r \qquad (6)$$

$$\sigma^2 gl = (MSgl - MSe)/r \qquad (7)$$

$$\sigma^2 e = MSe \;\; s \qquad (8)$$

Where; $\sigma 2p$ is phenotypic variance; $\sigma 2g$ refers to genotypic variance; $\sigma 2gl$ is genotype by location interaction variance; $\sigma 2e$ is environmental variance; MSg is the mean square for genotype; MSgl is the mean square for genotype by location interaction; MSe is the mean square for error; l is the number of locations; g denotes the number of genotypes; and r indicates the number of replications.

Estimation of Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), were calculated using the formula described by Singh and Chaudhury (1985). The estimations of variations were classified as low when values were less than 10%, medium when values were between 10 and 20%, and high when values were greater than 20% (Allard, 1960).

$$\text{Phenotypic coefficient of Variation: PCV (\%)} = \sqrt{\sigma^2 p}/\bar{X} * 100 \qquad (9)$$

$$\text{Genotypic Coefficient of Variation: GCV (\%)} = \sqrt{\sigma^2 g}/\bar{X} * 100 \qquad (10)$$

Where $\bar{x}$ represents the trait mean, $\sigma 2p$ is the phenotypic variance, $\sigma 2g$ is the genotypic variance, and $\sigma 2e$ is the environmental variance. PCV and GCV are the phenotypic and genotypic coefficients of variation, respectively.

Estimation of Heritability

Broad-sense heritability (h^2b) is estimated as the ratio of genotypic variance to phenotypic variance and expressed as a percentage, following the procedure described by Falconer (1989). Heritability estimates were classified according to the criteria proposed by Allard (1960) as low (0–30%), moderate (30–60%), and high (>60%). The broad-sense heritability was calculated using the following formula:

$$h^2b=(\sigma^2 g)/(\sigma^2 g+(\sigma^2 gl)/l+(\sigma^2 e)/rl)\times 100 \quad (11)$$

Where; h^2b is heritability in a broad sense; $\sigma^2 g$ is genotypic variance; $\sigma^2 gl$ is the genotype by location interaction variance; l is the number of locations; r is the number of replications; and $\sigma^2 e$ is environmental variance.

Estimation of Genetic Advance

The expected genetic advance (GA) for each trait at 5% selection intensity (k = 2.06) was estimated following the method of Allard (1960). Genetic advance as a percentage of the mean (GAM) was calculated to compare predicted selection responses among traits using the formula of Comstock and Robinson (1952). According to Johnson et al. (1955), GAM values are classified as low (0–10%), moderate (10–20%), and high (≥20%). GA was also expressed as a proportion of the overall mean to facilitate comparison of traits for potential improvement through selection, following Johnson et al. (1955). The genetic advance (GA) is calculated as:

$$GA = k\times(\sqrt{(\sigma^2 p)}\times(\sigma^2 g/\sigma^2 p) = k\times(\sqrt{(\sigma^2 p)}\times h^2b = k\times\sigma\times h^2b \quad (12)$$

The genetic advance as a percent of mean (GAM) is calculated using the following formula:

$$GAM= GA/\bar{X} * 100 \quad (13)$$

Where GA = is the genetic advance; K = is the standardized selection differential at 5% selection intensity (k = 2.06); $\sqrt{\sigma^2 p}$ is the square root of phenotypic variance; h^2b is heritability in a broad sense; GAM is the genetic advance as a percent of mean; and $\bar{x}$ is the mean of the population in which selection is employed.

RESULTS AND DISCUSSIONS

Analysis of Variance (ANOVA)

The combined analysis of variance (ANOVA) is presented in Table 2. The studied genotypes showed very highly significant ($P \leq 0.001$) variation for all measured traits. This indicated that the existence of genetic variation among the tested sugarcane genotypes. This marked variability suggests excellent opportunities for further genetic enhancement through selective breeding. These findings align with previous reports of significant variation among sugarcane genotypes by Tesfa et al. (2024), Todd et al. (2016), and Tolera et al. (2024).

Similarly, most traits, including NSB TC3MAP, TC5MAP, HR-Brix10MAP, IN. IL, SL, NMC, SCW, SD, CYPH, Brix%, pol%, purity%, ERS%, and SYPH, showed highly significant ($P \leq 0.001$) location effects. Of the 16 traits evaluated, 15 were significantly influenced by location, indicating substantial environmental differences between the two locations, likely due to variations in soil and climatic conditions. These results highlight the importance of multi-location testing for identifying stable and high-performing genotypes (Khan et al., 2004; Chang, 1996). Similar findings were reported by Ftwi et al. (2017) and Tena et al. (2016).

The genotype × location (G×L) interaction was highly significant ($P < 0.001$) for all measured traits except stalk length (SL). Significant G×L effects were observed for NSB, TC3MAP, TC5MAP, HR-Brix7MAP, IN, IL, NMC, SCW, SD, CYPH, Brix%, pol%, purity%, ERS, and SYPH. These results indicate that genotype performance varied across locations, reflecting differences in environmental responses. Such interactions hinder the identification of consistently superior genotypes, highlighting the importance of multi-location testing to identify stable and widely adapted genotypes. Similar findings have been reported by Ftwi et al. (2016) and Seife and Tena (2020).

Table 2. Combined analyses of variances (ANOVA) for 16 Agro-morphological traits of 187 sugarcane genotypes grown at the Kessem and Metahara Sugar Estates of Ethiopia.

Traits	Replication (1)	Block(Rep) (10)	Location (1)	Genotype (186)	G x L (186)	Error (363)	CV (%)	R^2
NSB45DAP	43.31*	7.25 ns	187.00***	81.07***	34.64***	8.65	14.03	0.89
TC3MAP	225.83 ns	129.06 ns	1318.24***	506.72***	175.66***	73.80	11.74	0.85
TC5MAP	3.61 ns	54.33 ns	3396.83***	690.77***	308.83***	83.83	12.31	0.87
HR-Brix7MAP	0.048*	0.017 ns	1.187***	0.010***	0.001***	0.004	8.16	0.73
NMC	2.95 ns	51.68*	13.63 ns	341.96***	123.50***	23.49	6.78	0.92
IN (count)	9.20 ns	15.79 ns	4630.10***	48.46***	15.85***	10.14	11.08	0.82
SD (cm)	0.001 ns	0.074*	0.603***	0.113***	0.055***	0.029	6.13	0.76
IL (cm)	0.190 ns	0.943 ns	25.214***	5.494***	1.658***	0.971	9.85	0.80
SL (m)	0.011 ns	0.108*	9.240***	0.123***	0.051 ns	0.046	8.07	0.71
SCW(kg)	0.243 ns	0.017 ns	8.458***	0.266***	0.175***	0.086	16.84	0.75
CY t/ha	2515.27ns	452.2397ns	76823.70***	3397.81***	1756.41***	913.83	18.34	0.76
Brix %	0.043 ns	0.878 ns	16.992***	7.889***	1.394***	0.567	4.00	0.90
Pol %	0.049 ns	0.870 ns	17.07***	7.855***	1.390***	0.557	4.46	0.90
Purity %	0.019 ns	0.392 ns	5.414***	3.266***	0.601***	0.247	0.56	0.89
ERS %	0.028 ns	0.481 ns	9.615***	4.408***	0.782***	0.310	4.81	0.90
SY t/ha	61.98 *	9.304 ns	2048.98***	56.08***	31.53***	14.18	20.18	0.78

NSB = number sprouted buds per plot; TC3MAP and TC5MAP = Tiller count 3 and 5 months after planting per plot; NMC10MAP/P = number of millable cane 10 months after planting per plot; HR-Brix7MAP = Hand refractometer Brix reading 7 months after planting; SCW = Single cane weight (Kg); NI = Number of internode; IL = Internode length (cm); SL= Stalk length (cm); SD = Stalk diameter (cm); = CY t/ha = Cane yield ton per hectare; SY t/ha = Sugar yield ton per hectare; Brix% = Brix percent; Pol % = Pol percent; Purity% = Purity percent; SR% = Sugar percent; G x L = genotype-by-location interaction; Block(Rep) = Block nested under Replication; Rep (Loca) = Replication nested under location; DF = Degree of freedom; *** = p < 0.001 Very highly Significant; ** = p < 0.01: Highly Significant; * = P <0.05 significant; ns = p > 0.05 non-significant.

Range and Mean performance analysis

The minimum and maximum mean values, along with the range of sixteen quantitative traits evaluated across 187 sugarcane genotypes, are presented in Table 3. The mean number of sprouted buds per plot at 45 days after planting was 21.00, ranging from 7.00 in genotype FG08755 to 35.00 in genotype B635-6, indicating substantial phenotypic variability. Higher sprouted bud counts were predominantly observed in genotypes derived from Barbados (fuzz), reflecting considerable genetic diversity for this trait. This suggests that germplasm from France and Barbados (fuzz) possesses broad variability in sprouted bud number. Therefore, by selecting the best genotypes, such as B635-6, from the tested fuzz genotypes, it is feasible to develop sugarcane genotypes with improved potential for sprouted bud counts. In alignment with the current findings, Tolera et al. (2023) evaluated 196 sugarcane genotypes and found that the average number of sprouted buds per plot was 20.86, with a range of values from 4.74 to 48.85. Three months after planting, the average tiller count per plot was 72.87, with recorded values ranging from 42.75 for genotype FG05360 to 103.00 for genotype C0680. Five months after planting, the average tiller count per plot was 77.00, with recorded values ranging from 42.75 for genotype 158-Ancha to a maximum of 103.00 for genotype B546-15. Higher tiller counts were observed in genotypes derived from Barbados and USA, considerable genetic diversity for this trait.

Table 3. Estimates of range and mean performance for 16 Agro-morphological traits of 187 sugarcane genotypes grown at the Kessem and Metahara Sugar Estates of Ethiopia during 2021/22 cropping season.

Trait	Range		Mean
	Minimum	Maximum	
Number of sprouted buds 45 days after planting	7.00	35.00	21.00
Tiller number at four months after planting	42.75	103.00	72.87
Tiller number at five months after planting	40.75	113.25	77.00
Hand Refracto-meter Brix reading 7 months after planting	0.73	1.00	0.87
Number of millable cane per hectare	45.75	97.25	71.50
Internode number per stalk	19.00	43.00	31.00
Stalk diameter (cm)	2.10	3.30	2.70
Internode length (cm)	7.51	13.66	10.58
Stalk length (m)	2.04	3.14	2.59
Single cane weight (kg)	1.14	2.44	1.79
Cane yield (t/ha)	122.02	241.66	181.89
Brix %	14.46	21.61	18.03
Pol %	12.35	19.47	15.91
Purity %	84.21	90.92	87.56
Estimable recoverable sugar percent (%)	8.30	13.65	10.97
Sugar yield (t/ha)	9.94	30.12	20.03

Genotype from USA and Barbados possesses a broad variability in tiller count. Genotypes C0680 and B546-15, which produced the highest tiller counts, are promising candidates for tiller improving ability through selection. These findings are consistent with reports by Tena et al. (2018) and Tolera et al. (2023).

Hand Refractometer Brix (HR-Brix) is a convenient tool for estimating sugar content at the early growth stage of sugarcane. In this study, HR-Brix values ranged from 0.73 in genotype 5-YE Habsha Shenkora to 1.00 in genotype B527-6, with a mean of 0.87, indicating variation among genotypes during the early maturation stage. However, HR-Brix is an indirect measure of sugar content and is influenced by environmental factors such as soil conditions, climate, and crop management practices (Swapna et al., 2012). Therefore, while the observed variation may reflect genetic differences, definitive conclusions regarding genetic variability require additional sugar quality assessments and consideration of environmental effects, as noted by Ram et al. (2022) and Senthilkumar et al. (2022).

The tested sugarcane genotypes exhibited a mean millable cane count of 72.87, with values ranging from 45.75 in genotype B690-6 to 97.25 in genotype B154-1. Both the minimum and maximum millable cane counts were recorded among the fuzz genotypes introduced from Barbados. This wide range of variation indicates substantial genetic diversity in stalk production capacity among the evaluated genotypes. Such variability provides considerable opportunities for the genetic improvement of sugarcane through the selection and breeding of high-performing genotypes with superior stalk populations, such as B154-1. These findings are consistent with Tena et al. (2016), further reinforcing the potential for enhancing sugarcane breeding programs.

Stalk diameter (SD) were varied significantly among genotypes, ranging from 2.10 cm in B154-1 (thinnest) to 3.30 cm in FG05-25 (thickest), with a mean of 2.70 cm. The thinnest and thickest genotypes originated from Barbados (fuzz) and France, respectively. Sugarcane stalk diameters are categorized into five categories, according to Abdul et al. (2017): thin (2.0 cm), medium thin (2-2.5 cm), medium (2.5-3.0 cm), medium thick (3.0-3.5 cm), and thick (>3.5 cm). Based on these criteria, the FG0669 genotype from CRAD, with diameters of 3.30 cm, was categorized as medium-thick. By selecting the best genotypes for this trait, it may be possible to develop thicker-stalked cultivars, as there is significant variability among different sugarcane genotypes. In line with this finding, (Tolera et al., 2023), noted that sugarcane stalk diameters ranged from 1.93 to 3.42 cm with a mean value of 2.65 cm.

A wide range of genetic diversity was observed in internode length (IL) and stalk length (SL) among the tested genotypes. The mean value recorded for IL was 10.58 cm, while the mean value recorded for SL 2.59 m. For IL, 5-YE Habsha Shenkora had the smallest value at 7.51 cm, whereas 46-Wotete exhibited the largest value at 13.66 cm. Both the shortest and longest internode lengths were found in Ethiopia. Regarding SL, genotype B564-6 had the shortest value at 2.04 m, while genotype FG05-256 had the longest value at 3.14 m. The shortest stalk length was registered from Barbados, while the longest originated from France. Therefore, the study confirmed substantial variation in internode length among genotypes at Barbados and France, while stalk length variation was noted in Ethiopian landrace genotypes. Prior studies by Tolera et al. (2023) emphasized variability in internode and stalk length; however, (Tena et al. 2016) also observed variability in internode length.

Single cane weight (SCW) was varied considerably among the evaluated genotypes, ranging from 1.14 kg in genotype B39250 to 2.44 kg in genotype 183-Alaa, with a mean value of 1.79 kg. The lowest SCW was recorded in a genotype originating from Barbados, whereas the highest SCW was observed in a genotype derived from Ethiopian landraces. This pronounced variation among genotypes highlights the potential for improving single cane weight through the selection of superior genotypes, particularly 183-Alaa, from Ethiopian sugarcane landraces. Comparable ranges and mean values for SCW have been reported by Tolera et al. (2023) and Tena et al. (2016), who documented SCW values ranging from 0.95 to 2.86 kg, with an average of 1.67 kg.

Cane yield (CY, t/ha) exhibited substantial variation among the evaluated genotypes, ranging from 122.02 t/ha in genotype FG05045 to 241.66 t/ha in genotype B630-5, with a mean value of 181.79 t/ha. The lowest-yielding genotypes were introduced from France, whereas the highest-yielding genotype originated from Barbados, indicating marked differences in cane yield among genotypes from different countries of origin. This variability underscores the potential for yield improvement through the selection of superior genotypes, particularly B630-5. Similar variability in cane yield has been reported in previous studies (Tolera et al., 2023; Kumar et al., 2018), corroborating the results of the present study.

Brix% ranged from 14.46% (B52313) to 21.61% (CP961029), with a mean of 18.03%, while pol% varied from 12.35% (B52313) to 19.49% (MPT96261), averaging 16.73%. Juice purity% ranged between 84.21% (FG05360) and 90.92% (C0680), with a mean of 87.56%, and ERS% varied from 8.35% (B52313) to 13.64% (MPT96261), averaging 10.99%. The pronounced variability observed in Brix%, pol%, purity%, and ERS% demonstrates significant potential for genetic improvement through selection. Identifying genotypes with superior mean performance for these traits offers valuable prospects for developing sugarcane varieties with enhanced sugar quality and yield. Genotype MPT96261, exhibited high pol% and recoverable sucrose%, can be considered a promising parental line for future breeding programs. These findings are consistent with earlier reports (Ashagre and Khan, 2020; Abu-Ellail et al., 2020; Tena et al., 2018; Tolera et al. 2023).

Estimated sugar yield (t/ha) showed substantial variation among the evaluated genotypes, ranging from 9.94 t/ha in genotype B549-6 to 30.12 t/ha in genotype B4425, with a mean value of 20.03 t/ha. Both the lowest and highest sugar yield values among Barbados-introduced fuzz genotypes reflect a wide genetic base and pronounced variability for this trait. Such variability is highly desirable in breeding programs, as it provides opportunities for effective selection and genetic gain. The superior performance of genotype B4425 highlights its potential as an elite parent or candidate variety for enhancing sugar yield in future sugarcane improvement. These findings are consistent with earlier reports of variability in sugar yield among fuzz genotypes (Tolera et al., 2023), further emphasizing the value of exploiting this genetic diversity for yield-focused breeding program.

Estimation of variance components

Genetic variance is a critical parameter, as it quantifies the extent of genetic variability present for a specified trait and reinforces the potential for genetic improvement through selection (Houle, 1998). The study revealed that phenotypic variance (σ^2p) was higher than the corresponding genotypic variance (σ^2g), and G × L interaction variance (σ^2gl), for all measured traits (Table 4). The greater magnitude of phenotypic variance indicates a substantial contribution of environmental factors to the total observed variation and reflects the influence of environmental conditions on trait expression. These findings are consistent with Tena et al. (2016), who reported that phenotypic variance exceeded both genotypic and interaction variances for all evaluated traits in sugarcane genotypes. However, genetic variance (σ^2g) was highest for NMC, ERS %, SY t/ha (Table 4), indicating lower environmental influence on these traits. Similarly, Tesfa et al. (2026) reported the highest genetic variance for NMC.

Table 4 Variance Components, Coefficients of Variation, Heritability, and Genetic Advance as a Percent of the mean for 16 Quantitative Traits evaluated in 187 Sugarcane Genotypes

Trait	σ^2p	σ^2g	σ^2gl	σ^2e	GCV	PCV	H^2 (%)	GA	GAM
NSB45MAP	17.28	11.61	13	8.65	16.23	19.79	67.18	7.23	34.43
TC3MAP	126.68	82.77	50.93	73.8	12.48	15.45	65.34	15.18	20.83
TC5MAP	172.69	95.49	112.5	83.83	12.69	17.04	55.29	14.97	19.45
HR-Brix7MAP	0.003	0.002	0.001	0.005	5.43	6.4	72.11	0.085	9.69
NMC	85.5	54.62	50.01	23.49	10.34	12.94	63.88	12.22	17.09
IN	11.4	8.15	2.86	10.14	9.21	10.9	71.48	4.99	16.1
SD (cm)	0.027	0.015	0.010	0.029	4.54	6.08	55.56	0.188	6.98
IL (cm)	1.37	0.96	0.34	0.971	9.26	11.08	69.92	1.68	15.89
SL (m)	0.038	0.018	0.002	0.046	5.22	6.78	59.35	0.215	8.29
SCW(kg)	0.066	0.024	0.042	0.086	8.66	14.42	36.09	0.193	10.76
CY t/ha	849.7	410.35	421.29	913.83	11.14	16.03	48.29	41.59	22.87
Brix %	1.97	1.62	0.412	0.567	7.04	7.79	82.10	2.38	13.2
Pol %	1.97	1.62	0.417	0.557	8.00	8.81	81.94	2.43	15.25
Purity %	0.815	0.665	0.177	0.247	0.93	1.03	81.60	1.51	1.72
ERS %	1.04	0.90	0.23	0.31	8.68	9.3	86.79	1.82	16.63
SY t/ha	11.83	6.14	8.68	14.18	12.37	17.18	51.91	17.18	51.91

σ^2g = Genotypic variance; σ^2p = Phenotypic variance; σ^2e = Environmental variance; σ^2gl = Genotypic by location interaction variance; PCV = Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; h^2b=heritability in broad sense; GA=Genetic advance; GAM=Genetic advance as percent of mean

Estimation of Genotypic, and Phenotypic Coefficients of Variation

Estimates of phenotypic (PCV) and genotypic coefficient of variation (GCV) for 16 quantitative traits are presented in Table 4. PCV values were higher than the corresponding GCV values for all traits, indicating that the observed variation was influenced not only by genetic factors but also by environmental effects. The GCV ranged from 0.93% to 16.23%, and PCV varied from 1.03% to 19.79%. The purity percentage was exhibited the lowest GCV (0.93%), while the number of sprouted buds per plot showed moderate GCV (16.23%). These results indicate differences in the magnitude of genetic variability and environmental influence among traits. Similar findings were reported by Tolera et al. (2023) and Tena et al. (2016) who observed low GCV and PCV values for purity percentage.

Moderate genotypic (GCV) and phenotypic (PCV) coefficients of variation were observed for sprouted buds, tiller counts (3 and 5 months), millable canes, cane yield, and sugar yield. While the higher PCVs reveal environmental influence on these traits, the moderate GCV values indicate sufficient genetic variability to allow for effective improvement through selection. These results revealed considerable genetic variability among the evaluated genotypes, indicating good potential for improvement through selection.

Sprouted buds (GCV = 16.23%, PCV = 19.79%), tiller count at 3 months (GCV = 12.48%, PCV = 15.45%) and 5 months (GCV = 12.69%, PCV = 17.04%), millable canes (GCV = 10.34%, PCV = 12.94%), cane yield (GCV = 11.14%, PCV = 16.03%), sugar yield (GCV = 12.37%, PCV = 17.18%), and internode length (GCV = 15.38%, PCV = 19.03%) exhibited moderate GCV and PCV values, indicating substantial genetic variability and good potential for selection. Similar moderate variability for millable canes, cane yield, and sugar yield was reported by Tena et al. (2016) while comparable results for stalk length were reported by Tesfa et al. (2026).

Number of internodes (GCV = 9.21%, PCV = 10.90%), single cane weight (GCV = 8.66%, PCV = 14.42%), exhibited low GCV and moderate PCV values. However, internode length (GCV = 5.22%, PCV = 6.78%), HR-Brix (GCV = 5.43%, PCV = 6.40%), and stalk diameter (GCV = 4.54%, PCV = 6.08%), Brix % (GCV = 7.04%, PCV = 7.79%), Pol % (GCV = 8.00%, PCV = 8.89%), purity% (GCV = 0.93%, PCV = 1.03%), exhibited low GCV and PCV values, indicating limited genetic variability. The relatively low GCV and higher PCV indicate that environmental factors had a greater influence on the expression of these traits than genetic factors, limiting their potential for improvement through direct selection. Enhancing these traits may therefore require broadening the genetic base through the introduction of diverse germplasm or other breeding approaches that increase genetic variation. Similar findings for Pol%, purity%, and Brix% were reported by Belwal and Ahmad, (2020) for Brix% and purity% by Tesfa et al. (2023) and for purity% by Shimelis (2018).

Estimation of heritability in broad sense (h^2b)

According to Wright (1921), the integration of the genotypic coefficient of variation (GCV) with heritability provides a more reliable prediction of expected genetic gain under phenotypic selection. Heritability, in this context, represents the proportion of total phenotypic variation that is attributable to genetic factors and is therefore fundamental in predicting the response to selection (Vidadala et al., 2024). Based on the classification proposed by Allard, broad-sense heritability (H^2) is categorized as high (>60%), moderate (30–60%), and low (<30%). In the present study, broad-sense heritability (H^2) ranged from 7.09% to 82.00%, with HR-Brix% exhibiting the lowest estimate and ERS% the highest. The estimates of broad-sense heritability for the evaluated sugarcane traits are presented in Table 4.

High heritability estimates (> 60%) were observed in most juice quality traits, such as brix (82.10%), pol (81.94%),), purity (81.60%),), and estimable recoverable sugar (86.79%). In addition, yield component traits, such as the NSB (67.18%), TC3MAP (65.34%), NMC (63.88%), NI (65.34%), and IL (71.48%), also confirmed high heritability values. This suggests that environmental or non-genetic factors have a limited impact on these trait expressions, making these traits suitable for selection. High heritability values for all juice quality (biochemical) traits such as brix%, pol, purity %, and estimable recoverable sugar % and NSB, TC3MAP, NMC, NI, and IL were reported by Tena et al. (2016), Abu-Ellail et al. (2020).

Moderately high heritability estimates (30–60%) were observed for several traits, including SL (59.35%), SD (55.56%), SCW (36.09), CYPH (48.29%), and SYPH (51.91%). These values suggest that, although genetic factors contribute substantially to the variation observed, environmental or other non-genetic factors also play a considerable role in the expression of these traits compared with traits exhibiting higher heritability. The moderate heritability levels further imply that the phenotypic expression of these traits is influenced by non-additive genetic effect. Thus, genetic improvement through direct selection for these traits may occur at a relatively slower rate than for traits with higher heritability estimates. Moderate heritability estimate for NI, SD, SCW, CYPH, and SYPH was reported by Tolera et al. (2024)

Juice quality traits generally exhibited high heritability, indicating strong genetic control and suitability for improvement through phenotypic selection. As noted by Johnson et al. (1955), knowledge of genetic variability and heritability is essential for effective trait selection. In this study, Brix%, Pol%, purity%, estimable recoverable sugar%, NSB, TC3MAP, NMC, NI, and IL showed high heritability and substantial potential for genetic gain. Likewise, the number of sprouted buds, tillers, stalks, and internode length emerged as reliable selection criteria due to their genetic stability and breeding value for improving sugarcane yield and juice quality.

Estimation of Genetic Advance

Effective crop selection relies heavily on a combination of high heritability and genetic advance as a percent of mean (GAM) (Alam et al. 2017), with the latter predicting the expected genetic gain per selection cycle (Hodge, 1992). Here, estimated GAM values showed considerable diversity, ranging from 1.72% (purity) to 51.91% (SYPH) (Table 4). This wide variation indicates excellent potential for improving specific traits in these sugarcane genotypes. Following the classification by Johnson et al. (1955) where GAM is partitioned into high (>20%), moderate (10–20%), and low (<10%) categories these findings provide a reliable indicator of the genetic progress achievable through future breeding efforts.

High genetic advance as percentage of the mean (>20%) was observed for NSB (34.43%), TC3MAP (20.83%), SYPH (22.87%), and SYPH (51.91%). These High GAM values indicate considerable genetic gain and the predominance of additive gene action, suggesting that phenotypic selection can effectively improve these traits. Similar results have been reported for NSB, TC3MAP CYPH, and SYPH Tolera et al. (2023), Shimelis (2018).

Moderate genetic advance as percentage of the mean (10–20%) values for the traits TC5MAP (19.45%), NMC (17.09%), NI (16.10%), IL (15.89%), SCW (10.76%), Brix % (13.20%) ERS % (16.63), were recorded (Table 4). This suggests that these traits can be improved through selection across successive generations; however, the expected rate of genetic gain is relatively lower than that of traits exhibiting high genetic advance. Similar moderate GAM estimates were reported by Tesfa et al. (2026) for stalk diameter, single cane weight, and internode number and by Tolera et al. (2023) for internode length, Brix% (13.20%), and estimated recoverable sugar% (16.63%). These shared findings indicate moderate expected genetic gains, suggesting these traits can be effectively improved through selection.

Low genetic advance as percentage of the mean (<10%) was observed for HR-Brix7MAP (9.69), SD (6.98), SL (8.29), and Purity % (1.72), indicating limited potential for genetic improvement through selection. The low GAM values suggest a greater influence of non-additive gene action and/or environmental factors on trait expression. Similarly, low GAM estimates for purity% have been reported by Tena et al. (2016), Tolera et al. (2023), and Jamoza et al. (2019). In contrast, the low GAM observed for stalk length (SL) in the present study differs from the moderate values reported by Tena et al. (2016) and Tolera et al. (2023).

Following Johnson et al. (1955), combining high heritability in broad sense (h²b), GCV, and GAM allows for accurate genetic gain predictions. In this study, cane yield, sugar yield, and early bud/tiller traits (NSB, TC3MAP) showed high heritability paired with high GAM and moderate GCV. Meanwhile, later tillers (TC5MAP), millable cane (NMC), and remaining quality/yield traits (NI, SCW, CYPH, Brix%, Pol%, and ERS%) displayed moderate-to-high heritability and GAM alongside moderate GCV. Finally, these joint metrics reveal that additive gene actions largely regulate the expression of all these evaluated traits. Because the phenotypes directly reflect their genetic potential, breeders can reliably develop improved genotypes using simple, straightforward phenotypic selection techniques aligning with previous findings by Tolera et al. (2023) and Abu-Ellail et al. (2017).

CONCLUSION

The research findings showed a wide range of genetic variability in the different genotypes of sugarcane that were evaluated. The values for GCV, h^2_β, and GAM, which measure genetic variability, ranged from 0.93% to 16.23%, 36.09% to 86.79%, and 1.72% to 51.91%, respectively. Several traits, such as the number of sprouted buds, number of tillers at three months after planting, cane yield (t/ha), sugar yield (t/ha), exhibited moderate to high values for GCV, h^2_β, and GAM. The results indicate that additive genetic effects play a substantial role in these traits, and phenotypic selection may improve them. Consequently, the top 5% of sugarcane genotypes with the highest sugar yields (t/ha) are B630-5, B58230, B57150, FG06787, FG08533, FG05414, 26-Wonji, C132/81, and B516-60. These sugarcane genotypes could be selected as potential parent genotypes for crossbreeding and further enhancement of these specific traits. Additionally, the sugarcane genotypes with high sugar yield (t/ha) should undergo testing at multiple seasons and locations to evaluate their stability and suitability for commercial use at the Metahara and Kessem sugar estates and similar agro-ecological zones.

DISCLOSURE STATEMENT

The authors declare that they have no conflicts of interest.

AUTHORS' CONTRIBUTIONS

Gezahagn Terefe: Writing-review; editing, Writing-original draft, Visualization, Validation, Software, Methodology, Investigation, Formal Analysis, Data curation, Conceptualization. Esayas Tena: Writing-review; and editing, Methodology, Validation, Visualization, Supervision, Conceptualization. Bezuayhu Tesfaye: Writing-review and editing, Methodology, Validation, Visualization, Supervision, Conceptualization. Andargachew Gedebo: Writing-review & editing, Methodology, Validation, Visualization, Supervision, Funding acquisition, Conceptualization.

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REFERENCES

Abdul Qayyum Khan, A.Q.K., Kiya Adare Tadesse, K.A.T. and Berhanu Lemma Robe, B.L.R. 2017. A study on morphological characters of introduced sugarcane varieties (Saccharum spp., hybrid) in Ethiopia, International Journal of Plant Breeding and Genetics, 11(1), 1-12. [Scholar Google]

Abo-Elwafa, A., Bakheit, B.R., El-Taib, A.M. and Noby, N.Y. 2021. Evaluation of some new somaclones of sugarcane for yield and quality. SVU-International Journal of Agricultural Sciences, 3(1):129-139. [Scholar Google]

Abu-Ellail, 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. [Scholar Google]

Abu-Ellail, F., Gadallah, A., and El-Gamal, I. 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. [Scholar Google]

Adeel, A. and Jadhav, A.S. 2025. Identifying the optimal sugarcane residue percentage for soil enhancement, A statistical and GIS approach. Circular Economy and Sustainability, 5(2):1535-1556. [Scholar Google]

Ali, A., Altaf, M.T., Bedir, M., Liaqat, W., Jamil, A., Nadeem, M.A., and Baloch, F.S. 2024. Biotechnological Advancements Toward Sugarcane Crop Improvement. In: Industrial Crop Plants, Springer, 333-352.

Allard, R.J. 1960. Principles of plant breeding. John Willey and Sons, Inc.485.

Alam, M. N., Nath, U. K., Karim, K. M. R., Ahmed M. M. and Mitul, R. Y. "Genetic Variability of Exotic Sugarcane Genotypes," Scientifica 2017 (2017): 5202913. [Scholar Google]

Ambachew, D. 2005. Revision of sugarcane cropping cycle of Metahara Sugar Factory. Project and Productivity Improvement office. Metahara, Ethiopia.

Anna Durai A, Premachandran M, Govindaraj P, Malathi P, and Viswanathan, R. 2015. Variability in breeding pool of sugarcane (Saccharum spp.) for yield, quality and resistance to different biotic and abiotic stress factors, Sugar Tech, 17:107-115. [Scholar Google]

Ashagre, S., and Khan, A. 2020. Determining optimum period of withholding irrigation for inducing maturity of sugarcane (Saccharum spp. hybrid) in Southern Ethiopia. J Appl. Biotechnol, Bioeng, 7(2): 16-25. [Scholar Google]

Belwal, V., and Ahmad S. 2020. Association of quantitative and qualitative characters of sugarcane under water logging conditions, IJCS 8 (2): 1641-1644. [Scholar Google]

Chang, Y. 1996. Estimating heritability of and correlations among Brix, purity, and sugar content in sugarcane using balanced multiple location and year data, Report of the Taiwan Sugar Research Institute, 1-10. [Scholar Google]

Cordeiro, G., Amouyal, O., Eliott, F., and Henry, R. 2007. Sugarcane, In Pulses, sugar and tuber crops (pp. 175-203). Berlin, Heidelberg: Springer Berlin Heidelberg.

Cuadrado, A., Acevedo, R., Moreno Díaz de la Espina, S., Jouve, N. and De La Torre, C., 2004. Genome remodelling three modern S. officinarum × S. spontaneum sugarcane cultivars. Journal of experimental botany, 55(398), 847-854. [Scholar Google]

D'Hont, A., Grivet, L., Feldmann, P., Glaszmann, J.C., Rao, S. and Berding, N. 1996. Characterisation of the double genome structure of modern sugarcane cultivars (Saccharum spp.) by molecular cytogenetics. Molecular and General Genetics, 250(4):405-413. [Scholar Google]

Falconer, D., 1989. Introduction to quantitative genetics.

Filoso, S., do Carmo, J.B., Mardegan, S.F., Lins, S.R.M., Gomes, T.F. and Martinelli, L.A. 2015. Reassessing the environmental impacts of sugarcane ethanol production in Brazil to help meet sustainability goals. Renewable and Sustainable Energy Reviews, 52:1847-1856. [Scholar Google]

Flack-Prain, S., Shi, L., Zhu, P., da Rocha, H.R., Cabral, O., Hu, S., and Williams, M. 2021. The impact of climate change and climate extremes on sugarcane production, Gcb Bioenergy, 13(3):408-424. [Scholar Google]

Ftwi, M., Mekbib F., and Abraha E. 2017. Partitioning of Genotype-Environment Interaction in Sugarcane (Saccharum spp.): Variance Component Analysis, Asian Journal of Plant Science and Research, 8(1): 1-8. [Scholar Google]

Govindaraj P., Amalraj V., Mohanraj, K. & Nair N. 2014. Collection, characterization and phenotypic diversity of Saccharum spontaneum L. from arid and semi-arid zones of northwestern India, Sugar Tech, 1636-43. [Scholar Google]

Gowda, S. S., Saravanan, K. & Ravishankar, C. R. 2017. Genetic variability, heritability and genetic advance in selected clones of sugarcane, 2016; 700-704. [Scholar Google]

Hamza, T.A. and Alebjo, A.L. 2017. Sugarcane Saccharum Officinarum L tissue culture in Ethiopia opportunities for ethiopias sugar industries. International Journal of Scientific & Technology Research, 6(8): 398-406. [Scholar Google]

Hartley, H.O. 1950. The maximum F-ratio as a short-cut test for heterogeneity of variance, Biometrika, 37(3/4): 308-312. [Scholar Google]

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. [Scholar Google]

Hodge, G.R. and White, T.L., 1992. Concepts of selection and gain prediction. In Handbook of quantitative forest genetics (pp. 140-194). Dordrecht: Springer Netherlands.

Jamoza. J.E., Owuoche, J. and 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. [Scholar Google]

Kassie, A., 2022. African Labour and foreign capital: the case of wonji-shewa sugar estate in Ethiopia, Social Sciences, 11(5): 245-253. [Scholar Google]

Kebede, S,, Damtie A., and Yirefu F. 2011. Challenges and Prospects of Sugar Development in Ethiopia, The State of Agricultural Science and Technology in Ethiopia.

Khan, I.A., Khatri A., Siddiqui M.A., Nizamani G.S, and Raza S.J. 2004. Performance of promising sugarcane clone for yield and quality traits in different ecological zones of Sindh, Pakistan Journal of Botany, 36(1): 83-92. [Scholar Google]

Kumar, P., Pandey, S., Kumar, B., Kamat, D., and Kumar M. 2018. Genetic variability, heritability and genetic advance of quantitative traits in sugarcane, International Journal of Chemical Studies. 6(3) 3569-3572. [Scholar Google]

Kumar, N., Sanghera, G.S., Singh, V. and Kashyap, L., 2021. Study of commercial cane sugar contributing traits-their variability, association and implications for selection in advanced clonal stages of sugarcane (Saccharum spp.). Agricultural Research Journal, 58(1), 23-28. [Scholar Google].

Kumar, R., Das, S.P., Choudhury, B.U., Kumar, A., Prakash, N.R., Verma, R., Chakraborti, M., Devi, A.G., Bhattacharjee, B., Das, R. & Das, B. 2024. Advances in genomic tools for plant breeding: harnessing DNA molecular markers, genomic selection, and genome editing. Biological Research, 57(1):80. [Scholar Google]

Kumari, P., Kumar, B., Kamat, D., Singh, R., Singh, D,, and Chhaya R. 2020. To study genetic variability, heritability and genetic advance for cane and sugar yield attributing traits in mid-late maturing sugarcane clones. Journal of Pharmacognosy and Phytochemistry, 9(1):1890-1894. [Scholar Google]

Lewi, E., Biggs, J., Ayele, A., Wright, T., Pagli, C., Keir, D., and Zheng, W. 2025. Scientific response to the 2024–2025 dyke intrusions in the Fentale-Dofen Region, Ethiopia: geophysical monitoring, surface manifestations, and hazard mapping. Bulletin of Volcanology, 87(8), 64. [Scholar Google]

Lu, G., Liu, P., Wu, Q., Zhang, S., Zhao, P., Zhang, Y. and Que, Y. 2024. Sugarcane breeding: a fantastic past and promising future driven by technology and methods. Frontiers in Plant Science, 15:1375934. [Scholar Google].

Meade, G.P., and Chen, J.C. 1977. Cane sugar handbook.

Mohammed, D. 1969. Private foreign investment in Ethiopia (1950-1968), Journal of Ethiopian Studies, 7(2):53-78. [Scholar Google]

Ogunniyan, D.J., and Olakojo, S.A. 2014. Genetic variation, heritability, genetic advance and agronomic character association of yellow elite inbred lines of maize (Zea mays L.). Nigerian journal of Genetics, 28(2):24-28. [Scholar Google]

Poehlman, J.M. and Sleeper, D.A., 1995. Breeding Hybrid Cultivars. Breeding Field Crops. USA, Fourth Edition. Relation to Diallel Crossing Systems. Australia, J. Bio. Sci. 9:463-493.

Ram, B., Hemaprabha, G., Singh, B., Appunu, C. 2022. History and current status of sugarcane breeding, germplasm development and molecular biology in India. Sugar Tech, 24(1): 4-29. [Scholar Google]

Rathna Priya, T.S., Eliazer Nelson, A.R.L., Ravichandran, K. and Antony, U. 2019. Nutritional and functional properties of coloured rice varieties of South India: a review. Journal of Ethnic Foods, 6(1):11. [Scholar Google]

Sandhu, K.S., Shiv, A., Kaur, G., Meena, M.R., Raja, A.K., Vengavasi, K., Mall, A.K., Kumar, S., Singh, P.K. & Singh, J. 2022. Integrated Approach in Genomic Selection to Accelerate Genetic Gain in Sugarcane. Plants 2022, 11, 2139. [Scholar Google]

Seife, A. and Tena, E. 2020. Genotype x environment interaction and yield stability analysis of sugarcane (Saccharum officinarum L.) genotypes. Int. J. Adv. Res. Biol. Sci, 7(1):14-26. [Scholar Google]

Senthilkumar, S., Vinod, K.K., Parthiban, S., Thirugnanasambandam, P., Lakshmi Pathy, T., Banerjee, N., Sarath Padmanabhan, T.S. and Govindaraj, P. 2022. Identification of potential MTAs and candidate genes for juice quality-and yield-related traits in Saccharum clones: a genome-wide association and comparative genomic study. Molecular Genetics and Genomics, 297(3):635-654. [Scholar Google]

Shimelis, D. 2018. Estimation of genetic parameters of sugarcane (Sacharrum officinarum L.) varieties grown at Arjo-Dedessa sugar Projest, Western Ethiopia. International Journal of Advanced Research in Biological Sciences, 5(8):30-35. [Scholar Google]

Singh, R.K. and Singh, G.P. 1999. Effect of early evaluation of genotypes on genetic variability repeatability and predictability in plant and ratoon crops of sugarcane. Sugar Tech, 1(4):128131. [Scholar Google]

Singh R., and Chaudhury B.J. 1985. Ludhiana: Biometrical methods in quantitative genetic analysis (Revised Ed.). Biometrical methods in quantitative genetic analysis. 102-118.

Sorrells, M.E. & Wilson, W.A. 1997. Direct classification and selection of superior alleles for crop improvement. Crop Science, 37(3):691-697. [Scholar Google]

Sreenivasan, T., and Ahloowalia, B. 1987. Cytogenetics. In Sugarcane improvement through breeding, Heinz, ed. In.: Elsevier, Amsterdam;

Sukhchain, Sandhu, D. and Saini, G.S.1997. Inter-relationships among cane yield and commercial cane sugar and their component traits in autumn plant crop of sugarcane. Euphytica, 95(1):109-113. [Scholar Google]

Swapna, M. and Srivastava, S. 2012. Molecular marker applications for improving sugar content in sugarcane. In Molecular Marker Applications for Improving Sugar Content in Sugarcane (1-49). Boston, MA: Springer US.

Tabriz, S.S., Kader, M.A., Rokonuzzaman, M., Hossen, M.S. and Awal, M.A. 2021. Prospects and challenges of conservation agriculture in Bangladesh for sustainable sugarcane cultivation. Environment, Development and Sustainability, 23(11):15667-15694. [Scholar Google]

Tadesse F., Negi T., Getaneh A., Dilnesaw Z., Ayele N. and Teferi Y. 2014. Genetic variability and heritability of ten exotic sugar cane genotypes at Wonji Sugar Estate of Ethiopia. 3(4):1-4. [Scholar Google]

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. [Scholar Google]

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. [Scholar Google]

Tena, E., Mekbib, F. and Ayana, A. 2018. Sugarcane landraces of Ethiopia: Germplasm collection and analysis of regional diversity and distribution. Advances in Agriculture, 2018 (1):7920724. [Scholar Google]

Tesfa, M., Tena, E. & Kebede, M. 2024. Multivariate analysis of genetic diversity among sugarcane clones (Saccharum spp.). Scientifica, 2024 (1) 4002024. [Scholar Google]

Tesfa, M., Tena, E. and Kebede, M., 2026. Analysis of Variance Components, Heritability, and Genetic Advance for Agronomic and Biochemical Traits in Sugarcane Genotypes. Advances in Agriculture, 2026(1), p.8331924. [Scholar Google]

Tolera, B., Gedebo, A. & Tena, E. 2023. Variability, heritability and genetic advance in sugarcane (Saccharum spp. hybrid) genotypes. Cogent Food & Agriculture, 9(1):2194482. [Scholar Google]

Tolera, B., Gedebo, A. & Tena, E. 2024. Genetic variability, character association and path analysis in sugarcane genotypes. Archives of agronomy and soil science, 70(1):1-15. [Scholar Google]

Vidadala, R., Kumar, V., Rout, S., Sil, P., Teja, V. and Rahimi, M. 2025. Genetic analysis of quality protein maize (QPM): a review. Cereal Research Communications, 53(1):81-99. [Scholar Google]

Wright, S. 1921. Systems of mating. I. The biometric relations between parent and offspring. Genetics, 6(2): 111. [Scholar Google]

Xu YunBi, X.Y., Li Ping, L.P., Zou Cheng, Z.C., Lu YanLi, L.Y., Xie ChuanXiao, X.C., Zhang XueCai, Z.X., Prasanna, B.M. and Olsen, M.S. 2017. Enhancing genetic gain in the era of molecular breeding. Journal of Experimental Botany, 68, (11), 2641–2666. [Scholar Google]

Yang, X., Li, J., Zhao, T., Mo, L., Zhang, J., Ren, H., Zhao, N. and Gao, Y. 2019. Variation and heritability of morphological and physiological traits among Leymus chinensis genotypes under different environmental conditions. Journal of Arid Land, 11(1):66-74. [Scholar Google] https://doi.org/10.1007/s40333-018-0018-x.

Zikargie, Y.A., Wisborg, P. and Cochrane, L. 2022. State-led modernization of the Ethiopian sugar industry: questions of power and agency in lowland transformation. Journal of Eastern African Studies, 16(3):434-454. [Scholar Google]