



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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www.agronomyjournals.com
2024; SP-7(11): 559-565
Received: 03-09-2024
Accepted: 04-10-2024

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Studies on genetic variability, heritability, genetic advances and association of yield contributing traits and their relation with yield in sugarcane

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DOI: <https://doi.org/10.33545/2618060X.2024.v7.i11Sh.2057>

Abstract

The research work conducted at the Vasantdada Sugar Institute, Pune, total 21 sugarcane clones assessed in two plant crops during the year 2022-2023 and 2023-2024 in randomized block design. The study focused on genetic variability, correlation and path analysis for nine morphological and qualitative traits. ANOVA results indicated highly significant differences among genotypes, confirming genetic diversity. The analysis revealed that the phenotypic coefficients of variation (PCV) was consistently higher than the genotypic coefficients of variation (GCV), suggesting a minimal environmental impact on trait expression. High heritability combined with substantial genetic advance as a percentage of mean was observed for traits such as millable height, sucrose percentage, single cane weight, CCS percentage, cane diameter, cane yield, and CCS (t/ha). This indicates a strong additive genetic influence on these traits. Positive associations with cane yield were found for characters, including the number of millable canes, single cane weight, tillering at 120 days, millable height, and cane diameter. Path analysis identified the number of millable canes, millable height, cane diameter, tillering at 120 days, and commercial cane sugar (t/ha) as having the largest positive direct effects on cane yield. These traits are recommended for use in future selection processes aimed at enhancing sugarcane production.

Keywords: GCV, PCV, sugarcane, heritability, genetic advance, correlation, path, cane yield

Introduction

The sugar industry is the second-largest agro-based industry after textiles and modern sugarcane cultivars primarily result from interspecific crossings between *Saccharum officinarum* L. (n=80) and wild species *S. spontaneum* L. (n=40-128). Evaluating existing genetic stock is crucial for any breeding program. The success of these programs largely hinges on selecting promising parents from this genetic pool. Understanding genetic variability and the associations among morphological and physiological traits is essential, particularly regarding their impact on final yield. Heritability and genetic advance are key parameters for selection; heritability indicates how well traits are passed from parents to offspring (Falconer, 1981) ^[12], while genetic advance measures the expected improvement in the mean genotypic value of selected populations compared to their parents. Heritability estimates combined with genetic advance provide valuable insights for predicting potential improvements in crops through the selection of elite genotypes. Understanding the relationships between yield and its components as well as among other traits, is vital for effective selection aimed at enhancing yield. To pinpoint which trait contribute most significantly to yield, it is important to partition correlation coefficients into direct and indirect effects (Allard, 1960) ^[6]. Quantitative traits, which are typically under polygenic control are also influenced by environmental factors (Wright, 1921) ^[36]. The objectives of the present investigation are to estimate genetic variability, heritability, and genetic advance for yield and yield-contributing traits in sugarcane and to study the association and direct and indirect effects of various yield and yield-contributing traits.

Materials and Methods

This research work was conducted at the Vasantdada Sugar Institute's research farm during the 2022-23 and 2023-24 seasons and conducted two plant crops.

Total of 21 sugarcane clones, including 16 advanced generation clones and 5 check varieties were evaluated using a Randomized Block Design (RBD) with two replications. Each genotype was planted in 5 rows and 6 meters long, with a spacing of 1.37 meters between rows. The quantitative and qualitative characters recorded are commercial cane sugar (t/ha), cane yield (t/ha), CCS at the 12th month stage, sucrose% at the 12th month stage, single cane weight (kg), number of millable canes, cane diameter (cm), millable height, and tillering at 120 days. Data for morphological traits were recorded from five randomly selected plants in each replication of each clones. Yield and its associated characters were initially recorded on a per plot basis, and then conversion formulas were applied to express them on a per hectare basis. Analysis of variance was performed using Fisher (1925) method to assess variations among genotypes through the F-test. Heritability, genetic advance, and correlation coefficients were calculated following the methods of Panse and Sukhatme (1967) [28]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were determined using the formulas provided by Burton and Devane (1952) [10].

The mean data of these parameters obtained in the field were subjected to statistical analysis of variance and co-variance. Analysis of variance (ANOVA) is given below.

Skeleton of Analysis of variance (ANOVA)

Source	DF	SS	MSS	F value (calculated)
Replication	r-1	SSr	SSr-----= MSR (r-1)	MST ----- MSE
Treatment	t-1	SSt	SSt-----= MST (t-1)	
Error	(r-1) (t-1)	SSe	SSe-----= MSR (r-1) (t-1)	
Total	(rt-1)	TSS		

Where,

r = number of replications

t = number of treatments

DF = degree of freedom

SSr = replication sum of squares

SSt = treatment sum of squares

SSe = error sum of squares

TSS = Total sum of squares

MST = treatment mean sum of squares

MSR = replication mean sum of squares

MSE = error mean sum of squares

The genetic variability mean, range, components of variance, such as genotypic, phenotypic, environmental, SMI, CD, CV were calculated. PCV (%), GCV (%), ECV (%) were also calculated using formula given by Burton (1952). The heritability (Broadsense) using the formula of Burton and Devane (1953), genetic advance as per the formula of Johnson *et al.*, (1955) and analysis of co-variance was also analyzed as given below.

Genetic variability

Mean

Mean is the average value of the character in a sample, i.e., it is the average of all the observations on a character in sample.

$$\text{Mean } X = \frac{\sum X}{N}$$

Where,

$\sum x$ = Sum of all observations for each character in each replication

N = Corresponding number of observations

Range

It was taken as the difference between the highest and lowest mean value for each character. It is the simple measure of variability and gives an idea of the dispersion or spread of the observations in a sample.

$$\text{Range} = X_n - X_1$$

Where,

X_n = Highest mean value of character

X_1 = Lowest mean value of character

Components of variance

It is defined as the average of the square deviation from the mean or it is the square of the standard deviation. It is an effective measure of variability which permits partitioning of various components.

Genotypic variance

The genotypic variance V_G or σ^2_g is variance due to the genotype present in the population. This was calculated by the formula suggested by Burton (1952) [10]

$$\sigma^2_g = \frac{MS_t - EMS}{\text{No of replication (r)}}$$

Where,

MS_t = Mean sum of squares due to treatment

EMS = Error mean sum of squares

Phenotypic variance

Phenotypic variance (V_P or σ^2_p) denotes the total variance present in a population for particular character and is calculated by following formula.

Phenotypic variance (σ^2_p) = Genotypic variance + Error variance

Environmental variance

The environmental variance (V_E or σ^2_e) is the variance due to environment deviation.

$V_E = EMS$

Standard error of mean (SEM)

Standard error of mean was calculated by following formula

$$SEM = \sqrt{\frac{2EMS}{r}}$$

Critical differences (CD)

The critical difference was calculated by following formula

$$CD = \sqrt{\frac{2EMS}{r}} \times t\text{-value}$$

Where,

T-Value = table value at error degree of freedom at 5% level of significance

R = Number of replication

EMS = Error mean sum of squares

Significant F-value indicates that there is significant difference among the treatments. But to compare any two particular treatments, it is tested against CD value.

Coefficient of variation (CV)

A measurement of variance which is independent of the unit of measurement is provided by the standard deviation expressed as percentage of mean. This is known as coefficient of variation (CV).

$$CV (\%) = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) were calculated by the formula given by Burton (1952) [10].

Phenotypic coefficient of variation

$$PCV (\%) = \frac{\text{Phenotypic standard deviation}}{\text{Grand Mean}} \times 100$$

Genotypic coefficient of variation

$$GCV (\%) = \frac{\text{Genotypic standard deviation}}{\text{Grand Mean}} \times 100$$

Environmental coefficient of variation

$$ECV (\%) = \frac{\text{Error standard deviation}}{\text{Grand Mean}} \times 100$$

Heritability (Broad sense)

Heritability in broad sense was calculated using the formula suggested by Burton and Devane (1953).

$$h^2 = \frac{VG}{VP} \times 100$$

Where,

h^2 = Heritability

VG (σ^2g) = genotypic variance VP (σ^2p) = phenotypic variance

Heritability (%) = Heritability coefficient x 100

Genetic advance

Improvement in the mean genotype value of selected plants over the parental population is known as genetic advance. The genetic advance i.e., the expected genetic gain was worked out by using the formula suggested by Johnson *et al.*, (1955) [21].

$$G. A. = \frac{\sigma^2g}{\sigma^2p} \cdot k \cdot \sigma p = h^2 \cdot K \cdot \sigma p$$

Where,

h^2 = Heritability coefficient

K = Selection differential standard units which is 2.06 for 5% selection intensity

σp = Phenotypic standard deviation G.A. = Genetic advance

Genetic advance as percent of mean (GA % M)

It was calculated by the following formula:

Genetic Advance as Percentage of Mean = $[GA/\bar{X}] \times 100$

GA = Genetic advance

$\bar{x}$ = Mean of character

Analysis of covariance

Analysis of covariance was worked out for different character combinations. It is helpful in determining the correlation coefficient between different characters. The table for analysis of covariance was formed by arranging the sum of products in the following manners.

Skeleton of Analysis of covariance (ANCOVA)

Source of variation	D.F	S.P.	M.S.P.	Expected mean sum of squares
Replication	(r-1)	RSP	Cov.r	$\sigma^2e(xy) + g\sigma^2r(xy)$
Treatment	(n-1)	TrSP	Cov.t	$\sigma^2e(xy) + r\sigma^2g(xy)$
Error	(r-1)(n-1)	ErSP	Cov.e	$\sigma^2e(xy)$
Total	(nt-1)	TSP		

Covariance

Genetic covariance

Genotypic covariance was calculated by following formula:

$$\text{Cov. P} = \frac{\text{Cov. t} - \text{Cov. e}}{\text{Number of replication (r)}}$$

Phenotypic covariance

$\text{Cov. p} = \text{Cov. g} + \text{Cov. e}$

Results and Discussion

The analysis of the genetic variation observed among the different traits in the sugarcane genotypes, highlighting the potential for selection. The presentation of broad-sense heritability estimates for each trait, indicating the extent to which genetic factors influence phenotypic variations. The assessment of genetic advance as a percentage of the mean, providing insights into the expected improvement through selection for each trait. The correlation analysis examination of the relationships between traits, including both phenotypic and genotypic correlations, to understand the associations affecting yield. The path analysis of direct and indirect effects of yield-contributing traits on cane yield, facilitating the identification of key traits for selection in breeding programs. The each section elaborates on the findings, supported by statistical data, and discusses their implications for sugarcane breeding and improvement efforts.

Analysis of Variance

The analysis of variance (ANOVA) results for the different characters are summarized in Table 1. The significant differences observed among the varieties for all traits indicate substantial variability, which provides an opportunity for further selection and the breeding of superior genotypes. These variations stem from the inherent genetic differences among the sugarcane clones, suggesting that considerable improvement can be achieved through targeted selection based on these traits. This finding is consistent with earlier research conducted by Patil *et al.* (2014) [30]; Sanghera *et al.* (2014) [32]; Gowda *et al.* (2016) [15, 16]; and Hiremath and Nagaraja (2016) [18], reinforcing the idea that genetic diversity is crucial for advancing sugarcane breeding programs.

Variability, heritability and genetic advance

The per se performance (mean) of the genotypes for all quantitative traits is detailed in Table 2. In Table 3, estimates of

range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense), and genetic advance are presented.

A significant range of variation was observed across all quantitative traits, highlighting ample opportunities for improvement in the desired direction. This variability indicates the potential for selection to enhance traits that contribute to overall yield and quality in sugarcane. Such findings emphasize the importance of utilizing diverse genotypes in breeding programs to achieve optimal results.

Variance (Phenotypic and Genotypic)

The parameters assessed phenotypic and genotypic coefficients of variation, heritability in broad sense (h^2), and genetic advance as a percentage of mean, provide insight into the variation among the genotypes under study. The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all nine characters, indicating that environmental factors have influenced the expression of these traits.

The moderate values of variation suggest significant potential for improvement through direct selection. However, the lower estimates of GCV imply that direct selection may yield only limited gains for certain traits. These findings align with earlier studies by Bhatnagar *et al.* (2003) [9], Agrawal and Kumar (2017) [1], Kumar *et al.* (2018) [23], Ahmed *et al.* (2019a) [2, 3], and Kumari *et al.* (2020) [25], reinforcing the importance of considering both genetic and environmental influences in breeding programs.

Coefficient of variation

The data in Table 3 highlight considerable variation across all studied traits, as evidenced by both phenotypic and genotypic coefficients of variation.

Specifically, traits such as tillering at 120 days (PCV: 11.465), CCS (t/ha) (PCV: 10.709), cane yield (PCV: 10.301), number of millable canes (PCV: 9.061), single cane weight (PCV: 8.939), and millable height (PCV: 8.813) exhibited high phenotypic variation. In contrast, the genotypic coefficients of variation were also substantial for CCS (t/ha) (GCV: 9.299), cane yield (GCV: 9.190), millable height (GCV: 8.519), and single cane weight (GCV: 8.214).

While several traits demonstrated wide genotypic variation, the overall trend indicated that the GCV values were generally lower than their corresponding PCV values. The small differences between PCV and GCV for most traits suggest that environmental factors have a minimal effect on their expression, indicating that these traits could be effectively selected for improvement in breeding programs.

Heritability and genetic advance

The estimates of heritability (broad sense) and genetic advance expressed as a percentage of mean, presented in Table 3, reveal significant insights into the traits evaluated. Heritability values ranged from 16.253% to 93.468% with high estimates for millable height (93.468%), sucrose percentage (88.275%), single cane weight (84.434%), CCS percentage (83.225%), cane diameter (80.476%), cane yield (79.582%), and CCS (t/ha) (75.413%). The other traits exhibited moderate levels of heritability.

The highest genetic advance as a percentage of mean was observed for millable height (16.967%) followed by cane yield (16.888%), CCS (t/ha) (16.636%) and single cane weight (15.548%). The remaining traits showed lower genetic advances.

According to Panse (1942) [27] and Johnson *et al.* (1955) [21], the combination of high heritability and genetic advance suggests that these traits are influenced by additive gene action, making them suitable for selection to enhance cane yield. Similar findings have been reported by Agarwal and Kumar (2017), Kumar *et al.* (2018) [23], and Ahmed *et al.* (2019) [2, 3].

Conversely, traits with high heritability but moderate genetic advance indicate non-additive gene action, suggesting that more careful selection strategies will be required for improvement. These results align with previous studies by Kumari *et al.* (2020) [25], Jain *et al.* (2001) [19], and Khaled *et al.* (2013) [22], reinforcing the understanding of genetic variability in sugarcane.

Genetic variability

The establishment of an effective plant breeding program relies heavily on the presence of genetic variability. In this study traits exhibiting a wide range of variation including CCS (t/ha), cane yield (t/ha), CCS at the 12th-month stage, sucrose percentage at the 12th month, single cane weight (kg), number of millable canes, cane diameter (cm), millable height and tillering at 120 days offer significant potential for selection. This variability underscores the opportunity to improve these traits through targeted breeding strategies, ultimately enhancing sugarcane yield and quality.

Correlation

Selection based on traits that exhibit a strong positive correlation with cane yield and juice quality has been shown to be beneficial. The genotypic correlation coefficients were consistently higher than phenotypic coefficients, suggesting that the observed associations are largely influenced by genetic factors, allowing for effective selection based on phenotype. However, the phenotypic coefficients were higher, indicating environmental factors may be suppressing the expression of those traits. The highest positive genotypic correlation with cane yield was found for the number of millable canes (0.998**) followed by single cane weight (0.813**), tillering at 120 days (0.799**), millable height (0.794**) and cane diameter (0.755**). Equally, cane yield exhibited negative correlations with commercial cane sugar percentage (-0.225) and sucrose percentage (-0.181). At the phenotypic level, strong positive associations with cane yield were evident for CCS (t/ha) (0.941**), number of millable canes (0.739**), cane diameter (0.730**), single cane weight (0.727**), millable height (0.671**) and tillering at 120 days (0.345**). The traits commercial cane sugar percentage (-0.102) and sucrose percentage (-0.100) displayed non-significant negative associations with cane yield. Notably, cane yield demonstrated a significant positive association with CCS (t/ha) and single cane weight at both genotypic and phenotypic levels, indicating that selection based on these traits could yield substantial benefits. Similar findings have been reported by Singh *et al.* (2005) [33], Mali and Patel (2013) [26], Kumar and Kumar (2014) [24], Anbanandan and Eswaran (2018) [7], Ahmed *et al.* (2019b) [2, 3], and Parihar (2020) [29]. Both genotypic and phenotypic coefficients aligned closely, reinforcing the reliability of these results as noted in the work of Parihar (2020) [29].

Path Analysis

Path coefficient analysis helps clarify whether the relationship between cane yield and its component traits stems from direct effects or indirect effects through other traits. At the genotypic level (Table 6), the highest positive direct effect on cane yield was attributed to commercial cane sugar (t/ha) (0.872), followed

by sucrose percentage (0.248), millable height (0.135), cane diameter (0.056), tillering at 120 days (0.030), and number of millable canes (0.006). Notably, both CCS percentage and single cane weight exerted negative direct effects on cane yield. At the phenotypic level (Table 7), the most significant positive direct effect on cane yield came again from commercial cane sugar (t/ha) (1.013), along with millable height (0.025), cane diameter (0.023) and tillering at 120 days (0.011), while other traits exhibited negative direct effects. The findings indicate that CCS (t/ha) has a strong positive direct effect on cane yield, followed

by sucrose percentage, millable height, cane diameter, tillering at 120 days, and the number of millable canes/ha. Therefore, selection for these traits is likely to enhance both cane yield and juice quality.

These results align with previous studies by Thippeswamy *et al.* (2003) [35], Singh *et al.* (2005) [33], Sanghera *et al.* (2017) [31], Anbanandan *et al.* (2020) [8], Parihar (2020) [29], and Somu *et al.* (2020) [34]. To boost cane yield effectively, it is essential to focus on traits with high direct effects and those that influence cane yield indirectly.

Table 1: Analysis of Variance for yield and quality characters in sugarcane clones

Sr. No.	Characters	Mean Sum of Squares		
		Replication (df:1)	Treatment (df:20)	Error (df:20)
1	Tillering at 120 days	4001.210	487.074	344.399
2	Millable height (cm)	1187.743	949.096	32.042
3	Cane diameter (cm)	0.028	0.054	0.006
4	Number of millable canes (000'ha)	47.787	89.855	35.113
5	Single cane weight (kg)	0.019	0.045	0.004
6	Sucrose%	1.554	0.828	0.052
7	CCS%	0.508	0.484	0.044
8	CCS (t/ha)	5.321	8.569	1.201
9	Cane Yield (t/ha)	67.285	411.463	46.783

*Significant at $p \leq 0.05$ level of significance, **Significant at $p \leq 0.01$ level of significance

Table 2: Mean performance of clones traits under study

Character/Clones	TL	MH	CD	NMC	Scw	S%	Ccs%	CCS (t/ha)	CY
CoVSI 7-13	171.88	255.76	3.08	94.87	1.81	20.72	14.74	23.26	157.78
CoVSI 30-71	187.25	285.40	2.89	87.73	1.95	18.92	13.33	21.46	160.99
CoVSI 46-17	171.39	248.95	3.01	92.51	1.74	19.68	14.01	21.28	151.88
VSI 100-71	192.74	274.33	2.77	82.30	1.94	19.28	13.59	20.03	147.35
VSI 124-66	161.67	253.34	2.93	84.31	1.83	20.71	14.70	21.89	149.04
VSI 124-181	194.93	263.03	2.82	95.09	1.67	20.25	14.39	21.30	148.10
VSI 238-46	186.56	262.16	2.97	88.75	1.85	18.72	13.17	19.34	146.97
VSI 270-81	196.60	250.49	3.09	93.38	1.77	19.10	13.59	21.05	154.99
VSI 270-125	201.88	269.75	3.00	92.73	1.85	19.47	13.90	21.83	156.95
VSI 270-141	169.70	258.12	2.97	87.05	1.74	19.50	13.89	20.24	145.78
VSI 270-184	181.65	259.19	3.06	87.17	1.82	20.07	14.16	20.91	147.64
VSI 276-12	182.70	248.71	2.87	96.43	1.66	20.11	14.33	23.14	161.48
VSI 282-9	180.05	232.09	3.11	94.37	1.77	20.17	14.40	22.50	156.33
VSI 290-8	171.36	271.64	2.85	79.08	1.90	19.29	13.77	19.44	143.34
CoVSI 64-4	177.93	265.94	3.21	91.45	1.95	20.02	14.30	23.73	166.07
CoVSI 51-1	139.59	274.28	3.05	85.17	1.90	20.74	14.82	22.67	154.67
Co 86032 (Std.)	177.30	215.51	2.61	83.65	1.46	19.66	14.01	17.74	126.61
CoC 671 (Std.)	151.06	201.40	2.67	72.04	1.41	20.81	14.88	16.06	107.97
CoM 0265 (Std.)	187.29	226.29	2.74	86.71	1.67	18.84	13.40	19.82	147.97
MS 10001 (Std.)	157.56	218.51	2.75	74.71	1.55	19.92	14.19	16.92	118.84
VSI 08005 (Std.)	173.27	243.55	2.71	82.52	1.70	19.59	13.97	18.87	135.05
Total mean	176.87	251.35	2.91	87.24	1.76	19.79	14.07	20.64	146.94

CCS(t/ha)-Commercial Cane Sugar (t/ha), CY-Cane Yield (t/ha), CCS%-CCS at 12th month stage, S%-Sucrose% at 12th month stage, SCW-Single Cane Weight (kg), NMC-Number of millable canes, CD-Cane diameter (cm), MH-Millable height, TL-Tillering at 120 days

Table 3: Mean, coefficient of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean for cane yield and quality characters in sugarcane clones

Sr. No.	Characters	Mean	Coefficient of Variation		Heritability	Genetic Advance	Genetic advance as percent of mean
			GCV	PCV			
1	Tillering at 120 days	176.872	4.622	11.465	16.253	6.790	3.839
2	Millable height (cm)	251.353	8.519	8.812	93.468	42.646	16.967
3	Cane diameter (cm)	2.910	5.338	5.950	80.476	0.287	9.864
4	Number of millable (000'ha)	87.236	5.997	9.061	43.805	7.133	8.177
5	Single cane weight (kg)	1.757	8.214	8.939	84.434	0.273	15.548
6	Sucrose%	19.788	3.149	3.351	88.275	1.206	6.094
7	CCS%	14.071	3.332	3.652	83.225	0.881	6.261
8	CCS (t/ha)	20.640	9.299	10.709	75.413	3.434	16.636
9	Cane Yield (t/ha)	146.941	9.190	10.301	79.582	24.815	16.888

Table 4: Genotypic correlation matrix effect of the productive traits on cane yield

Trait	TL	MH	CD	Nmc	Scw	S%	CCS%	CCS (t/ha)
TL	1.000							
MH	0.563**	1.000						
CD	0.198	0.558**	1.000					
NMC	0.859**	0.518**	0.694**	1.000				
SCW	0.609**	0.959**	0.694**	0.532**	1.000			
S%	-0.980**	-0.244	0.111	-0.080	-0.254	1.000		
CCS%	-0.991**	-0.300	0.085	-0.103	-0.317*	0.987**	1.000	
CCS(t/ha)	0.413**	0.680**	0.798**	0.998**	0.694**	0.179	0.133	1.000
CY(t/ha)	0.799**	0.794**	0.755**	0.998**	0.813**	-0.181	-0.225	0.935**

*Significant at $p \leq 0.05$ level of significance & **Significant at $p \leq 0.01$ level of significance

CCS(t/ha)-Commercial Cane Sugar (t/ha), CY-Cane Yield (t/ha), CCS%-CCS at 12th month stage, S%-Sucrose% at 12th month stage, SCW-Single Cane Weight (kg), NMC-Number of millable canes, CD-Cane diameter (cm), MH-Millable height, TL-Tillering at 120 days

Table 5: Phenotypic correlation matrix effect of the productive traits on cane yield

Trait	TL	MH	CD	Nmc	Scw	S%	CCS%	CCS (t/ha)
TL	1.000							
MH	0.242	1.000						
CD	0.062	0.454**	1.000					
NMC	0.499**	0.330*	0.592**	1.000				
SCW	0.127	0.858**	0.605**	0.242	1.000			
S%	-0.452**	-0.216	0.168	-0.034	-0.214	1.000		
CCS%	-0.465**	-0.247	0.168	-0.034	-0.230	0.986**	1.000	
CCS(t/ha)	0.182	0.563**	0.765**	0.719**	0.625**	0.227	0.236	1.000
CY(t/ha)	0.345*	0.671**	0.730**	0.739**	0.727**	-0.100	-0.102	0.941**

*Significant at $p \leq 0.05$ level of significance & **Significant at $p \leq 0.01$ level of significance

CCS(t/ha)-Commercial Cane Sugar (t/ha), CY-Cane Yield (t/ha), CCS%-CCS at 12th month stage, S%-Sucrose% at 12th month stage, SCW-Single Cane Weight (kg), NMC-Number of millable canes, CD-Cane diameter (cm), MH-Millable height, TL-Tillering at 120 days

Table 6: Genotypic path correlation matrix effect of the productive traits on cane yield

Trait	TL	MH	CD	Nmc	Scw	S%	CCS%	CCS(t/ha)
TL	0.030	0.076	0.011	0.005	-0.055	-0.301	0.674	0.360
MH	0.018	0.135	0.031	0.003	-0.087	-0.061	0.163	0.592
CD	0.0068	0.075	0.056	0.004	-0.063	0.028	-0.046	0.696
NMC	0.0268	0.070	0.039	0.006	-0.048	-0.020	0.056	0.869
SCW	0.019	0.129	0.039	0.003	-0.090	-0.063	0.173	0.605
S%	-0.037	-0.033	0.006	-0.0004	0.023	0.248	-0.544	0.156
CCS%	-0.038	-0.040	0.005	-0.0005	0.029	0.248	-0.544	0.116
CCS(t/ha)	0.013	0.091	0.045	0.006	-0.063	0.044	-0.072	0.872

CCS(t/ha)-Commercial Cane Sugar (t/ha), CY-Cane Yield (t/ha), CCS%-CCS at 12th month stage, S%-Sucrose% at 12th month stage, SCW-Single Cane Weight (kg), NMC-Number of millable canes, CD-Cane diameter (cm), MH-Millable height, TL-Tillering at 120 days

Table 7: Phenotypic path correlation matrix effect of the productive traits on cane yield

Trait	TL	MH	CD	Nmc	Scw	S%	CCS%	CCS(t/ha)
TL	0.011	0.006	0.001	-0.013	-0.002	0.023	0.133	0.184
MH	0.003	0.025	0.010	-0.009	-0.011	0.011	0.071	0.571
CD	0.0007	0.011	0.023	-0.015	-0.008	-0.009	-0.048	0.775
NMC	0.006	0.008	0.014	-0.026	-0.003	0.002	0.010	0.729
SCW	0.001	0.021	0.014	-0.006	-0.013	0.011	0.066	0.633
S%	-0.005	-0.005	0.004	0.0008	0.003	-0.051	-0.282	0.230
CCS%	-0.005	-0.006	0.004	0.0008	0.003	-0.050	-0.286	0.239
CCS(t/ha)	0.002	0.014	0.017	-0.019	-0.008	-0.011	-0.067	1.013

CCS(t/ha)-Commercial Cane Sugar (t/ha), CY-Cane Yield (t/ha), CCS%-CCS at 12th month stage, S%-Sucrose% at 12th month stage, SCW-Single Cane Weight (kg), NMC-Number of millable canes, CD-Cane diameter (cm), MH-Millable height, TL-Tillering at 120 days

Conclusion

It could be concluded that the phenotypic coefficients of variation (PCV) was consistently higher than the genotypic coefficients of variation (GCV), suggesting a minimal environmental impact on trait expression. High heritability combined with substantial genetic advance as a percentage of mean was observed for traits such as millable height, sucrose percentage, single cane weight, CCS percentage, cane diameter,

cane yield, and CCS (t/ha). Positive associations with cane yield were found for several characters, including the number of millable canes, single cane weight, tillering at 120 days, millable height, and cane diameter. Path analysis identified the number of millable canes, millable height, cane diameter, tillering at 120 days and commercial cane sugar (t/ha) as having the largest positive direct effects on cane yield. These traits are recommended for use in future selection processes aimed at

enhancing sugarcane production.

Acknowledgement

The authors express their gratitude to the Adviser, Vasantdada Sugar Institute for their encouragement. The authors indebted to Director General of Vasantdada Sugar Institute, Pune, for their unwavering support throughout the research.

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