www.ThePharmaJournal.com

The Pharma Innovation

PK Mallikarjun
Ph.D. Scholar, Department of
Genetics and Plant Breeding,
University of Agricultural
Sciences, Dharwad, Karnataka,
India

Sanjay B Patil
Professor and Head, Department
of Genetics and Plant Breeding,
College of Agriculture,
Vijayapura, University of
Agricultural Sciences, Dharwad,
Karnataka, India

Study of genetic variability in productivity and juice quality traits among first clonal generation sugarcane clones (*Saccharum* spp.)

PK Mallikarjun and Sanjay B Patil

Abstract
Sugarcane serves as a significant source of sugar, constantly facing the pressure to enhance productivity due to rising cost of cultivation and the volatile nature of global market prices. A panel of 225 sugarcane clones of clonal-I generation were planted in an augmented design during 2022-23 at ARS, Sankeshwar, Karnataka, to study the variability in productivity and juice quality traits. The analysis of variance revealed significant effects due to genotypes and checks for most of the studied traits, while block effects were non-significant for all traits except average cane girth and sucrose per cent, indicating the homogeneity of evaluation blocks. Among the studied traits, the highest coefficient of variation was observed for commercial cane sugar yield (13.58%) and cane yield (12.11%). The PCV is greater than GCV for most of the traits under study. High heritability and genetic advance were observed for number of millable canes per plot, average single cane weight at 240 DAP, average single cane weight at 300 DAP, average single cane weight at 360 DAP, brix per cent at 240 DAP, commercial cane sugar per cent at 240 DAP, Juice extraction per cent, cane yield and commercial cane sugar yield. This observation implies that clonal selection can be highly effective in enhancing productivity traits. Consequently, these current traits can be utilized in subsequent rounds of selection and genetic improvement in sugarcane.

Keywords: Genetic variability, clonal-I generation, augmented design and juice quality

Introduction

Sugarcane (*Saccharum* spp.) is a major commercial crop next to cotton (Dagar *et al.*, 2002) [6] stands as a perennial tropical tall grass within the Poaceae family. This monocot plant boasts a variable chromosome count ranging from 2n = 80-120, depending on the species. The *Saccharum* genus is composed of six species, two of which are wild i.e. S. *spontaneum* L. and S. *robustum* Brandes & Jesw ex Grassl; and four cultivated species i.e. S. *officinarum* L, S. *barberi* Jesw, S. *sinense* Roxb. and S. *edule* Hassk (Daniels and Roach, 1987) [7]. Globally, it contributes significantly to sugar production, accounting for approximately 56% of the world's sugar output (Chauhan *et al.*, 2022) [5]. India, in particular, stands as the second-largest sugar producer after Brazil, cultivating sugarcane across 5.15 million hectares, about 2.50% of the gross cropped area with production of over 431.81 million tonnes, with a productivity of 83.89 tonnes per hectare in 2021-22 (Ministry of Agriculture & Farmers Welfare, GOI, 2021-22). In the region of Karnataka, sugarcane thrives across 0.74 million hectares, yielding a production of 70.26 million tonnes and a productivity of 98.00 tonnes per hectare during the same period. As the global population continues to increase, so does the demand for sugar. To meet the needs of this growing population within limited agricultural space necessitates a focus on enhancing yield efficiency. Sugarcane play a key role in the economies of sugarcane cultivating regions and enhancing its production could substantially boost the economic well-being of farmers and other agents involved in sugarcane cultivation.

Beyond its role as a valuable crop, Sugarcane serves as a raw material for the sugar industry and is utilized for various by-products, including jaggery, molasses, filter cake and wax (Singh and Singh, 2015) [16]. While a segment of the yield is allocated to small-scale enterprises for producing gur and juice of sugarcane itself serves as a raw material for manufacturing white sugar, jaggery and diverse by-products such as bagasse and molasses. Bagasse serves multiple purposes, functioning as a fuel source and being employed in the production of wooden boards, furfural, plastics and paper. The recovery percentage in the form of sucrose ranges between 12-18%, contingent upon factors such as variety, soil conditions, maturity timing, and farming practices.

Corresponding Author:
PK Mallikarjun
Ph.D. scholar, Department of
Genetics and Plant Breeding,
University of Agricultural
Sciences, Dharwad, Karnataka,
India

A significant challenge in sugarcane cultivation pertains to the limited genetic diversity of parent clones, potentially leading to increased inbreeding among offspring and reduced genetic variability, productivity traits are influenced by numerous factors. Breeders must understand the associations between productivity and quality traits to enhance both cane yield and sugar production effectively.

Sugarcane is a highly heterozygous and complex in terms of its genetic makeup, exhibits a tendency to give rise to significant variability. This variability is typically quantified through measures such as, PCV, GCV (phenotypic and genotypic coefficient of variation) and genetic advance as a percentage of the mean (GAM). Knowledge of the genetic variability and broad sense heritability of traits holds paramount importance to breeders, aiding them in executing effective selection among various clones. The combination of the coefficient of variation with heritability, alongside GAM, facilitates the improvement of traits by providing insights into the attainment of specific objectives using the convenient resources.

Material and Methods
The planting material for the current study consisted of 225 clones from the clonal-I generation. These clones were selected from a seedling nursery of 2360 individuals based on field evaluations, and they were subsequently planted in the year 2021-22. All these clones of two eye budded setts were planted in augmented design (Federer and Raghavarao, 1975) in three blocks with a 3.00 m row spaced 1.20 m apart along with eight commercial standard checks *viz.*, CoC 671, Co 09004, SNK 09211, Co 86032, SNK 09227, SNK 09293, SNK 13374 and SNK 13436 at ARS, Sankeshwar (Peninsular Zone, 16°14′N/74°30′E), University of Agricultural Sciences, Dharwad, India during year 2022-23.

To study the genetic parameters, the crop stand was maintained and crop was raised as per the recommended package and practices for the region. Data were collected by randomly choosing three millable canes from each genotype in every plot to assess productivity and its juice quality parameters., *viz.*, number of millable canes / plot (NMC), average cane girth (cm) (CG), average single cane weight at 240 DAP (kg) (8 M SCW), average single cane weight at 300 DAP (kg) (10 M SCW), average single cane weight at 360 DAP (kg) (12 M SCW), brix per cent at 240 DAP (%) (8 M brix %), brix per cent at 300 DAP (%) (10 M brix %), brix per cent at 360 DAP (%) (12 M brix %), sucrose per cent at 360 DAP (%) (Pol %), commercial cane sugar per cent at 240 DAP (%) (8 M CCS %), commercial cane sugar per cent at 300 DAP (%) (10 M CCS %), commercial cane sugar at 360 DAP (%) (12 M CCS %), juice extraction per cent (%) (JEP %), cane yield (t/ha) (CY), commercial cane sugar yield (t/ha) (CCSY) at harvest. Data analysis was conducted using the R software and MS-Excel.

Statistical analysis
Various parameters of genetic variability were calculated using statistical methods and correlation coefficient among the 225 clones in clonal-I generation for traits studied were performed. ANOVA were done to compare the mean values of different traits among 225 clones/ genotypes with eight checks in clonal-I generations using "R" software and MS-Excel.

Analysis of variance
Analysis of variance (ANOVA) for cane yield and quality traits of 25 clones/ genotypes with checks in early settling generations was carried out using augmented RCBD package in R software, version 0.1.6.

A. Standard error deviation (SE_d)
1. Standard error between any two check means (SE_{d1})

$$SEd1 = \frac{\sqrt{2EMS}}{b}$$

2. Standard error between means of a check and a test genotype (SE_{d2})

$$SEd2 = \sqrt{2EMS}$$

B. Critical difference (CD) at 5 per cent
1. Critical difference between any two check means

$$CD1\ @5\% = SEd1\ \times' t' @\ 5\%\ or\ 1\%\ levels$$

2. Critical difference between means of a check and a test genotype

$$CD2\ @5\% = SEd2\ \times' t' @\ 5\%\ or\ 1\%\ levels$$

Estimation of various genetic parameters
To identify and ascertain the genetic variability among clones for diverse parentage, various genetic parameters were calculated using the following formulae.

Mean

$$Mean = \frac{Sum\ of\ individual\ values}{Total\ number\ of\ individuals}$$

Range
The minimum (Min.) and maximum (Max.) values were recorded on the basis of individual genotype observations and were used to calculate the range for the traits.
Range (R) = Maximum – Minimum

Coefficients of variability
The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed as per the method suggested by Burton and De Vane (1953).

$$GCV = \frac{Genotypic\ standard\ deviation\ (\sigma g)}{General\ mean\ (X)} \times 100$$

$$PCV = \frac{Phenotypic\ standard\ deviation\ (\sigma g)}{General\ mean\ (X)} \times 100$$

GCV and PCV values were categorized after analysis by using Sivasubramanian and Menon (1973) [17] as follows,
Low: 0-10 %
Medium: 10-20 %
High: 20 % and above

Broad sense heritability (h²_BS)
Broad sense heritability was estimated as the ratio of the total phenotypic variance to genotypic variance as suggested by Hanson *et al.* (1956) [8] and expressed as per cent.

$$\text{Heritability (BS)} = \frac{\text{Genotype variance } (\sigma 2g)}{\text{Phenotype variance } (\sigma 2g)} \times 100$$

Where,
$\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance
The heritability per cent was classified by Robinson *et al.* (1955) [13] as follows,
Low: 0-30 %
Medium: 30-60 %
High: 60 % and above

Genetic advance as per cent of mean (GAM)
Genetic advance as per cent mean was grouped by Johnson *et al.* (1955) [9] as follows

$$\text{GAM} = \frac{\text{Genetic advance (GA)}}{\text{General mean (X)}} \times 100$$

Low: 0-10 %
Medium: 10-20 %
High: 20 % and above

Standard error (SE)
The standard error (SE) is the approximate difference between sample mean and population mean. It was calculated by using the formula.

$$\text{SE} = \frac{\text{Sample standard deviation (SD)}}{\sqrt{\text{samplesize}}}$$

Standard deviation (SD)
The standard deviation (SD) quantifies the extent to which values deviate from their mean value, expressing as a measure of dispersion. It's symbolically depicted as σ or s.

$$s = \frac{\sqrt{\sum_{i=1}^{n}(xi - X)^2}}{n-1}$$

Coefficient of variation (CV)
The Coefficient of Variation (CV) gives the outcome as the ratio of the standard deviation (SD) to the mean value. This is particularly useful when interpreting the SD alone could be misleading, as it doesn't account for the magnitude of the population mean. The CV provides a solution to address this concern.

$$\text{CV} = \frac{\text{SD}}{\text{mean}} \times 100$$

All the analysed statistical data being presented in table 1, 2 and 3. Additionally, Figure 1 and 2 visually illustrate the estimated values of GCV, PCV and broad sense heritability, as well as the GAM of traits in the first clonal stage of sugarcane.

Result and Discussion
Variability stands as a fundamental necessity in present sugarcane breeding programmes. The ANOVA for the 15 characters involved in the study is detailed in Table 1. Notably, the mean sum of squares for all the traits considered in this experiment exhibited highly significant, while block effects were non-significant for all traits except average cane girth and sucrose per cent at harvest. It was seen that standard error of deviation (SEd) along with critical difference (CD) between a check and a genotype was lower for all the traits studied except number of millable canes per plot and cane yield (t/ha), hence selections of genotypes which are significantly superior to check varieties could be made. Similar results were also reported by Bhagyalakhsmi and Somarajan (1999) [4], Sanghera and Jamwal (2019) [15], Somu and Nagaraja (2020) [18] and Khokhar *et al.* (2022) [10]. The observed variations among all the clones and their traits are quite evident, suggesting that a good range of options for selecting those clones with high productivity and sugar yields. This gives us the chance to choose genotype that can bring about better productivity in terms of both cane yield and sugar production.

In the current investigation, a total of 225 clones with 8 commercial checks, were assessed using an augmented block design to study various cane yield and its related traits. The mean values of number of millable canes per plot, average cane girth (cm) (360 DAP), single cane weight (kg) (240 DAP), single cane weight (kg) (300 DAP), single cane weight (kg) (360 DAP), brix per cent (240 DAP), brix per cent (300 DAP), brix per cent (360 DAP), sucrose per cent (%) (360 DAP), commercial cane sugar (%) (240 DAP), commercial cane sugar (%) (300 DAP), commercial cane sugar (%) (360 DAP), juice extraction (%) (360 DAP), cane yield (t/ha) (360 DAP), commercial cane sugar yield (t/ha) (360 DAP) were 30.00, 2.64 cm, 1.45 kg, 1.67 kg, 1.82 kg, 15.73%, 20.27%, 21.54%, 20.14%, 9.80%, 13.34%, 14.72%, 49.12%, 146.40 t/ha and 21.49 t/ha respectively with their respective range as shown in Table 2. However, range is the crude method of estimation of variability, which indicates only the observed phenotypic variability. Among the traits studied, the highest coefficient of variation was observed for CCS yield (13.58%) and cane yield (12.11%). Meanwhile, a low level of variation was observed for all the traits except for 10 M SCW (6.49%) and 10 M CCS% (6.30%). Similar results for cane length and cane diameter were reported by Anna Durai *et al.* (2015) [3] and Sanghera and Jamwal (2019) [15].

The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2_{BS}) and genetic advance as a percentage of mean (GAM) were used to quantify variation and aid in the selection of desirable traits for improvement. The narrow difference between PCV and GCV were observed for all the traits studied (Table 3). This suggests a reduced impact of environmental factors on the expression of these traits, consequently resulting in high heritability and genetic advance as a per cent of the mean. Therefore, these traits can be improved through direct selection. Comparable results were also reported by Somu and Nagaraj (2020) [18]. The highest PCV and GCV were observed for 8 M SCW (31.23% and 30.04%), followed by NMC (30.54% and 28.34%) and 10 M SCW.

Table 1: Analysis of variance for cane yield and quality traits in clonal-I generation of 225 clones during 2022-23

Source	Mean sum of squares						Standard Errors		CD @ 5%	
	Treatment	Checks	Genotypes	Genotypes vs. Checks	Blocks	Error	Between two check means	Between means of check & var.	Between two check means	Between means of check & var.
d.f.	232	7	224	1	2	14				
NMC	73.75**	104.12**	73.12**	3.48*	0.82^{NS}	1.04	0.83	1.25	1.78	2.68
CG	0.09**	0.33**	0.08**	0.32**	0.05*	0.01	0.09	0.13	0.19	0.28
8 M SCW	0.20**	0.40**	0.19**	0.27**	0.00^{NS}	0.00	0.04	0.06	0.09	0.13
10 M SCW	0.24**	0.56**	0.23**	0.35**	0.01^{NS}	0.01	0.10	0.14	0.21	0.31
12 M SCW	0.21**	0.70**	0.20**	0.09**	0.02^{NS}	0.01	0.07	0.11	0.15	0.23
8 M brix %	4.84**	13.13**	4.50**	24.47**	0.06^{NS}	0.05	0.18	0.27	0.39	0.58
10 M brix %	2.66**	6.75**	2.48**	14.02**	0.13^{NS}	0.40	0.52	0.77	1.11	1.66
12 M brix %	3.27**	5.13**	3.07**	34.25**	0.48^{NS}	0.32	0.47	0.70	1.00	1.50
Pol %	3.98**	4.49**	3.84**	32.13**	0.41**	0.02	0.12	0.18	0.26	0.39
8 M CCS %	4.19**	9.30**	3.84**	47.15**	0.18^{NS}	0.09	0.24	0.37	0.52	0.79
10 M CCS %	1.81*	4.16**	1.64*	24.46**	0.55^{NS}	0.72	0.69	1.04	1.48	2.22
12 M CCS %	2.49**	1.89**	2.38**	31.09**	0.12^{NS}	0.21	0.38	0.57	0.81	1.21
JEP %	53.31**	47.97**	53.57**	32.63**	0.13^{NS}	0.72	0.69	1.04	1.49	2.23
CY	1068.65**	2470.09**	1027.87**	433.64**	19.5^{NS}	9.57	2.53	3.79	5.42	8.12
CCSY	27.27**	21.19**	27.51**	16.17**	0.08^{NS}	0.60	0.63	0.95	1.35	2.03

^{NS} $p>0.05$; * $p<=0.05$; ** $p<=0.01$, NMC - Number of millable canes / plot, CG - Average cane girth, 8 M SCW - Single cane weight at 240 DAP, 10 M - Single cane weight at 300 DAP, 12 M - Single cane weight at 360 DAP, 8 M brix% – Brix % at 240 DAP, 10 M brix% – Brix % at 300 DAP, 12 M brix% - Brix % at 360 DAP, Pol% – Sucrose per cent, 8 M CCS% - Commercial cane sugar at 240 DAP, 10 M CCS% - Commercial cane sugar at 300 DAP, 12 M CCS% - Commercial cane sugar at 360 DAP, JEP% – Juice extraction per cent, CY - Cane yield, CCSY - Commercial cane sugar yield

(26.76% and 25.96%) (Table 3 and Fig. 1), while the 10 M brix % (7.77% and 7.12%), 12 M brix % (8.10% and 7.66%) and 10 M CCS % (9.55% and 7.16%) exhibited low GCV and PCV, indicating that limited genetic variability was existing for these traits. These findings were noticed previously by Somu and Nagaraja (2020) [18]; Sabitha et al., 2007 [14] and Kumar et al., 2018 [11] for juice quality traits.

Genotypic coefficient of variation should be taken into account together with heritability estimations because it is a reliable indicator of the amount of heritable variation present. High heritability estimates were found in the present experiment for pol % (99.43%), 8 M brix % (98.90%), 8 M SCW (98.74%), JEP % (98.65%), NMC (98.58%) and CCSY (97.83%). This implies that simple selection for these traits would be effective. The present investigation revealed that

most traits had high heritability estimates along with high genetic advance as a percentage of mean (GAM), except for 10 M CCS %, 10 M brix %, average cane girth and 12 M CCS % which had moderate GAM. This finding is in accordance with the results reported by Pandey et al., 2018 [12] and Ahmed and Obeid (2012) [1]. High heritability and high GAM coupled with high GCV and PCV were observed for traits such as NMC, 8 M SCW, 10 M SCW, 12 M SCW, cane yield, CCS yield (Table 3 and Fig. 2). This suggests that the selection for these traits is effective due to the presence of additive gene action. Similar findings were reported by Ahmed and Patil (2019) [2], Somu and Nagaraja (2020) [18] and Sanghera and Jamwal (2021) [15]. Therefore, these traits can serve as direct selection criteria for enhancing the productivity of clones in future improvement efforts.

Table 2: Quantitative statistics for productivity and juice quality traits of 225 clones of sugarcane in first clonal stage during 2022-23

Traits		Number of millable canes / Plot	Cane girth (cm)	Single cane weight (kg)			Brix %			Sucrose %	Commercial cane sugar %			Juice extraction %	Cane yield (t/ha)	Commercial cane sugar yield (t/ha)
				8 M	10 M	12 M	8 M	10 M	12 M		8 M	10 M	12 M			
Mean		30.00	2.64	1.45	1.67	1.82	15.73	20.27	21.54	20.14	9.80	13.34	14.72	49.12	146.40	21.49
Range	Min.	14.00	1.97	0.55	0.73	0.74	9.50	15.46	14.44	13.70	4.83	8.43	9.59	13.01	49.95	7.45
	Max.	55.00	3.53	2.90	3.39	3.44	20.46	24.06	26.38	23.97	13.73	16.84	17.89	63.69	267.61	42.08
CV		3.40	4.71	3.38	6.49	4.74	1.40	3.11	2.63	0.73	3.00	6.30	3.11	1.73	12.11	13.58
Std. Error		0.55	0.02	0.03	0.03	0.03	0.14	0.10	0.12	0.13	0.13	0.09	0.10	0.47	2.12	0.34
Std. Deviation		8.47	0.31	0.44	0.48	0.45	2.12	1.57	1.79	1.97	1.98	1.32	1.55	7.23	32.40	5.17

Table 3: Genetic variability parameters for productivity traits in first clonal stage of sugarcane

| Traits	Number of millable canes / plot	Cane girth (cm)	Single cane weight (kg)			Brix %			Sucrose %	Commercial cane sugar %			Juice extraction %	Cane yield (t/ha)	Commercial cane sugar yield (t/ha)
			8 M	10 M	12 M	8 M	10 M	12 M		8 M	10 M	12 M			
GCV (%)	28.34	9.88	30.04	25.96	23.79	13.37	7.12	7.66	9.66	19.64	7.16	9.95	15.79	21.84	24.08
PCV (%)	30.54	10.94	31.23	26.76	24.26	14.45	7.77	8.10	9.96	19.97	9.55	10.43	14.89	22.95	25.34
h^2_{BS}	98.58	81.47	98.74	94.09	96.17	98.90	83.88	89.44	99.43	97.67	86.23	91.03	98.65	95.07	97.83
GAM	58.04	18.40	61.59	51.95	48.13	27.44	13.44	14.94	19.87	40.04	11.08	19.58	30.31	55.53	49.13
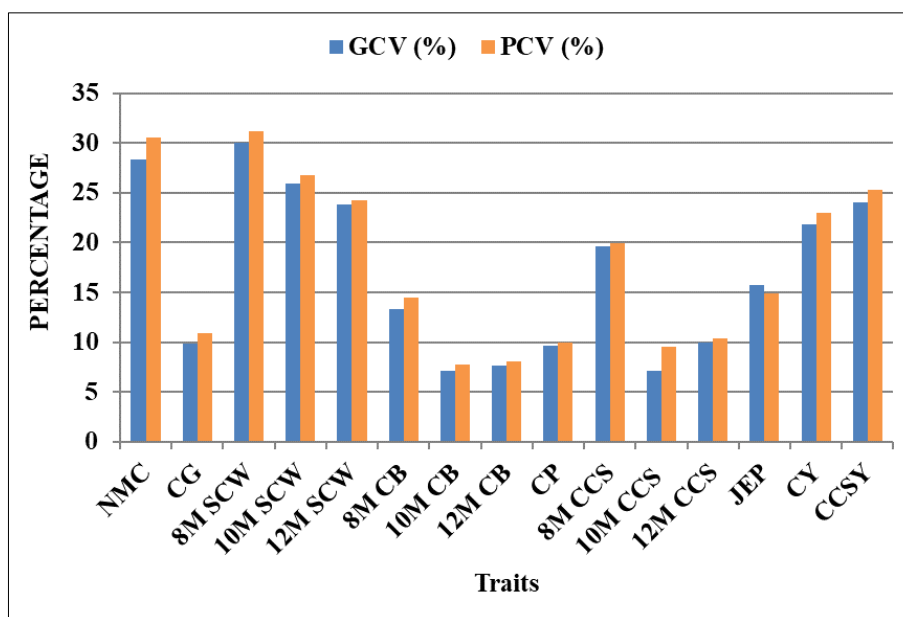
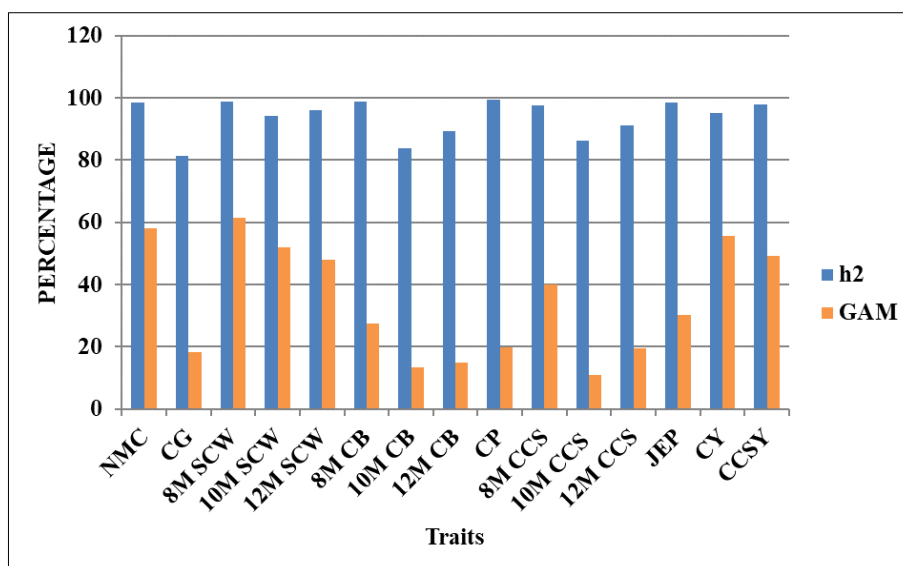**Fig 1:** PCV and GCV for productivity and juice quality traits of clonal-I generation

Fig 2: Heritability and genetic advance as per cent of mean for productivity and quality traits

Conclusion

The outcome of ANOVA revealed significant effects from both genotypes and checks on the majority of studied traits, emphasizing the high variability present among all clones. Traits such as the NMC, SCW at 240, 300 and 360 DAP, brix% at 240 DAP, CCS% at 240 DAP, juice extraction per cent, cane yield and CCS yield exhibited notably high broad sense heritability and genetic advance as a percent of the mean. This signifies a prevalence of additive gene action and underscores the efficiency of clonal selection in driving improvements in productivity traits. Selection is effective for these traits as they hold potential for further utilization in the realm of sugarcane genetic enhancement and selection.

Acknowledgement

References

1. Ahmed AO, Obeid A. Investigation on variability, broad sense heritability and genetic advance in sugarcane (*Saccharum* spp). International Journal of Agricultural Science. 2012;2(9):839-844.
2. Ahmed KI, Patil SB. Studies on genetic variability parameters for yield and its component traits in advance hybrid clones of sugarcane. Journal of Pharmacognosy and Phytochemistry. 2019;8(2):777-780.
3. Anna Durai A, Premachandran MN, Govindaraj P, Malathi P, Viswanathan R. Variability in breeding pool of sugarcane (*Saccharum* spp.) for yield, quality and resistance to different biotic and abiotic stress factors. Sugar Technology. 2015;17:107-115.
4. Bhagyalakhsmi KV, Somarajan KG. A modified augmented design for early selection stages in sugarcane and its limitation. Sugar Technology. 1999;1:63-66.
5. Chauhan JS, Govindaraj P, Ram B, Singh J, Kumar S, Singh KH, *et al*. Growth, Varietal Scenario and Seed Production of Sugarcane in India: Status, Impact and

Future Outlook. Sugar Technology. 2022;24(6):1649-1669.

6. Dagar P, Pahuja SK, Kadian SP, Singh S. Evaluation of phenotypic variability in sugarcane using principle factor analysis. Indian Journal of Sugarcane Technology. 2002;17:95-100.

7. Daniels J, Roach BT. Taxonomy and evolution. In Developments in crop science. Elsevier. 1987;11:7-84.

8. Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza 1. Agronomy Journal. 1956;48(6):268-272.

9. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agronomy Journal. 1955;47(7):314-318.

10. Khokhar JS, Jamwal NS, Sanghera GS, Singh P. Evaluation of sugarcane (*Saccharum officinarum*) germplasm for quality, yield traits and effects of flowering on cane traits. Indian Journal of Agricultural Sciences. 2022;92(7):842-846.

11. Kumar P, Pandey SS, Kumar B, Kamat DN, Kumar M. Genetic variability, heritability and genetic advance of quantitative traits in sugarcane. International Journal of Chemical Studies. 2018;6(3):3569-3572.

12. Pandey D, Singh SP, Jeena AS, Khan KA, Tabassum Negi A, Koujalagi D. Study of genetic variability, heritability and genetic advance for various yield and quality traits in sugarcane genotypes (Saccharum officinarum). Int. J Curr. Microbiol. App. Sci. 2018;7(4):1464-1472.

13. Robinson HF, Comstock RE, Harvey PH. Genetic variances in open pollinated varieties of corn. Genetics. 1955;40(1):45.

14. Sabitha N, Rao KP, Rao CP, Rao MS. Genetic variation, heritability and genetic advance for yield components in sugarcane. Sugar Technology. 2007;9(4):290-292.

15. Sanghera GS, Jamwal NS. Identification of potential crosses based on vigour, cane characteristics and HR Brix for first clonal selection in sugarcane. Indian Journal of Sugarcane Technology. 2019;34(1):12-16.

16. Singh J, Singh R. Sugarcane seed production: Indian scenario. Journal of Biotechnology and Crop Science. 2015;4(5):43-55.

17. Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras Agriculture Journal. 1973;60(7):1139-1140.

18. Somu G, Nagaraja TE. Genetic variability, heritability and genetic advance in first clonal stage of sugarcane. International Journal of Communication Systems. 2020;8(2):959-963.