Genetic Variability Studies in Promising Sugarcane Genotypes

DR J. M. REPALE[1], A. B. GAWHANE[2], DR A. D. KADLAG[3]
[1]*Senior Scientist, Plant Breeding*
[2]*Research Associate, Plant Breeding*
[3]*Principal Scientist (Crop Production and Protection), Vasantdada Sugar Institute, Pune*

Abstract- ***Genotypic and phenotypic variances, along with their coefficients of variance, heritability and genetic advance were analyzed for nine quantitative traits in 14 sugarcane cultivars (Saccharum officinarum L.). The highest genotypic coefficient of variance and phenotypic coefficient of variance were noted in cane yield (t/ha), commercial cane sugar (CCS) (t/ha), single cane weight (kg), tillering at 120 days and the number of millable canes at harvest. Most of the traits exhibited significant genetic advance except for cane diameter (cm), single cane weight (kg), sucrose and CCS percentage. This indicates potential for improvement in sugar yield through selection, particularly for traits with high variance and genetic advance.***

Indexed Terms- ***Genotypic, Phenotypic, Variance, Heritability, Genetic Advance, Sugarcane.***

I. INTRODUCTION

Success in sugarcane breeding depends on the proper choice of parent with desirable characters and use of appropriate breeding procedure. Burton (1952) suggested that genetic variation together with heritability estimate would give the best estimate of the amount of advance to be expected from selection. Johnson, et al. (1955) also reported that for selection to be reliable, heritability and genetic variability along with genetic advance should be considered. The information available on the genetic of some the economic characters such as yield and sugar content at an early stage in early maturing sugarcane is not sufficient to improve the existing breeding procedures. Therefore, the present investigation are undertaken to determine genetic variability, heritability and genetic advance of yield and its components in certain sugarcane varieties.

Success in sugarcane breeding relies heavily on selection of parents with desirable traits and implementing effective breeding strategies. As Burton (1952) emphasized, understanding genetic variation and heritability estimates is crucial for predicting the potential improvement from selection. Johnson, et al. (1955), further, noted that reliable selection must consider heritability, genetic variability and genetic advance.The information available on the genetic of some the economic characters such as yield and sugar content at an early stage in early maturing sugarcane is not sufficient to improve the existing breeding procedures. Therefore, the present investigation was undertaken to determine genetic variability, heritability and genetic advance of yield and its components in certain sugarcane varieties.

II. MATERIAL AND METHODS

The present investigation was carried out at nursery farms of Shree T. Kore Warana Sugar Mill Ltd.; Shree Chhatrapati Shahu Sugar Mill Ltd. and Jawahar Shetkari Sugar Mill Ltd. from Kolhapur district of Maharashtra State in RBD design with two replications during 2021-22 and 2022-23. The two plant crops and one ratoon crop of I plant were conducted. The material for the experiment consists of nine promising genotypes viz.CoVSI 18121, CoVSI 19121, CoVSI 15002, VSI 16002, CoVSI 17001, Co 11015, Co 12009, Co 13008 and PDN 15012 along with the five standards viz., Co 86032, CoM 0265, VSI 08005, MS 10001 and VSI 434.The plot size was six rows of six meters length each with spacing of 1.37 meter between two rows.The seed rate of twelve buds / meter was used in all the genotypes. All recommended package of practices were followed to raise the good crop growth.

The characters viz., tillering at 120 days, single cane weight (kg), number of millable canes/ha, cane diameter (cm), millable cane height, CCS % at 12th month, sucrose % at 12th month, commercial cane sugar (t/ha) andcane yield (t/ha) were recorded. Analysis of variance was estimated according to Fisher, (1925) to test the variations among genotypes by using F-test. Heritability genetic advance and correlation co-efficient outlined by Panse and Sukhatame, (1985). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated according to the formulae given by Burton and Devane, (1952).The mean data of these parameters obtained in the field were subjected to statistical analysis ofvariance and co-variance. Analysis of variance (ANOVA) are given below.

Skeleton of Analysis of variance (ANOVA)

Source	df	SS	MSS	F value(calculated)
Replication	r-1	SSr	SSr / (r-1) = MSR	
Treatment	t-1	SSt	SSt / (t-1) = MST	MST / MSE
Error	(r-1)(t-1)	SSe	SSe / (r-1)(t-1) = MSR	
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 and CV were calculated. PCV (%), GCV (%), ECV (%) were also calculated using formula given by Burton, (1952). The heritability (Broad sense) 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 are given below

Genetic variability

Mean

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

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

Where,
Σx= 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.

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 VG ($\sigma^2 g$)is variance due to the genotype present in the population. This was calculated by the formula suggested by Burton, (1952)

$$\sigma^2 g = \underline{MS_t} - \underline{EMS}$$

No.ofreplication(r)

Where,

MS_t= Mean sum of squares due to treatment

EMS= Error mean sum of squares

Phenotypic variance

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

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

Environmental variance

The environmental variance (VEorσ^2e) is the variance due to environment deviation.

VE = 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).

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).

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

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] x 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 manner.

Skeleton of Analysis of covariance (ANOVA)

Source of variation	d. f	S. P.	M. S. P.	Expected mean sum of squares
Replication	(r-1)	R SP	Cov. r	$\sigma^2e(xy)+g\sigma^2r(xy)$
Treatment	(n-1)	Tr SP	Cov. t	$\sigma^2e(xy) +r\sigma^2g(xy)$
Error	(r-1) (n-1)	Er SP	Cov. e	$\sigma^2e(xy)$
Total	(nt-1)	TS P		

Covariance

Genetic covariance

Genotypic covariance was calculated by following formula:

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

Phenotypic covariance

Cov. p = Cov. g + Cov. e

Result and Discussion

Table 1 presents the analysis of variance for various traits. The findings indicated a highly significant difference in most of the traits examined across the fourteen genotypes. This implies that there are fundamental genetic differences among the genotypes. These variations arise from the genetic diversity among the clones, and substantial enhancements can be achieved in all these traits through careful selection. Similar results was observed by earlier workers namely Patil, et al. (2014), Sanghera, et al. (2014), Gowda, et al. (2016) and Hiremath & Nagaraja, (2016). The individual performance (mean) of the genotypes for all quantitative traits is shown in Table 2. Table 3 provides estimates for range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, and genetic gain. A significant variation was noted for all quantitative traits being studied, suggesting that there is considerable potential for improvement in a favorable direction.

Coefficient of variation

The data in Table 3 revealed significant variation across all traits examined, showcasing a wide range of both phenotypic and genotypic coefficients of variation. Generally, the values for the genotypic coefficient of variation (GCV) were lower than those for the corresponding phenotypic coefficient of variation (PCV). This comparison highlights the relative magnitudes of phenotypic and genotypic variances across the traits, providing insight into the degree of genetic variation present and the potential for selection and improvement in future breeding efforts. The result of phenotypic coefficient of variation revealed that cane yield (15.55), CCS (t/ha) (14.30), single cane weight (10.72), tillering at 120 days (10.64) and number of millable canes/ha (10.14) the analysis revealed that certain traits exhibited a high phenotypic coefficient of variation (PCV), indicating substantial variability and potential for improvement in those characteristics. In contrast, the remaining traits displayed moderate to low PCV, suggesting that they may have less variability and potentially less room for enhancement through breeding efforts. This variation in PCV across traits underscores the importance of targeted selection strategies when focusing on specific characteristics for future development. Genotypic coefficient of variation was also high for cane yield (14.72), CCS (t/ha) (13.61), single cane weight (9.86) and number of millable canes at harvest (8.47). Additionally, the trait of tillering at 120 days demonstrated a wide genotypic coefficient of variation (GCV), indicating a high degree of genetic variability that could be leveraged for selection and improvement. In contrast, the other traits exhibited moderate to low GCV, suggesting that those characteristics may have less underlying genetic diversity. This disparity in GCV among traits highlights the potential for enhancing tillering through selective breeding, while also indicating that the other traits may require different strategies to optimize their variation and improvement.

Heritability and genetic advance

The heritability (broad sense) and genetic advance as percent of mean are given in table 3. The heritability ranged from 53.77 percent to 90.62. High heritability estimate was exhibited by CCS (t/ha) (90.62), cane yield (89.68), single cane weight (84.58), sucrose % (76.06), number of millable canes (69.83) and cane

diameter (65.03). The remaining characters exhibited moderate levels of heritability. The cane yield (34.26) followed by tillering at 120 days (20.50), millable height (19.54) and number of milllable canes/ha (10.52) showed highest genetic advance as a percent while the remaining traits showed narrow genetic advance. The plant estimate of genetic advance as percent of mean was the highest for cane yield (28.72) followed by CCS (t/ha) (26.69), single cane weight (18.68), number of millable canes at harvest (14.58) and tillering at 120 days (13.07) while the remaining traits showed narrow genetic advance. Heritability estimates along with genetic advance as percent of mean play an important role in determining the effectiveness of selection of a trait as suggested by Panse, (1942) and Johnson, et al. (1955). The cane yield (t/ha), tillering at 120 days per hector, millable cane height and number of millable canes per hector at harvest showed high heritability and genetic advance as percent of mean suggesting that these characters exhibit additive gene action and selection for these characters is going to be beneficial for further improvement in cane yield. Agarwal and Kumar, (2017), Kumar, et al. (2018) and Ahmed, et al. (2019) reported similar results. High heritability along with moderate genetic advance as percent of mean indicates that these traits are governed by non-additive gene action and it requires careful selection for the desired improvements. These results were in parallel with the findings of Jain, et al. (2001), Khaled, et al. (2013) and Kumari, et al. (2020) obtained similar results.

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

Sr. No.	Characters	Mean Sum of Squares		
		Replication (df:2)	Treatment (df:13)	Error (df:26)
1	Tillering at 120 days/ha (‘000)	2090.52	610.40	112.35
2	Millable height at harvest (cm)	4913.00	531.77	92.18
3	Cane diameter (cm)	0.13	0.09	0.01
4	Number of millable canes (000’ha)	479.56	128.27	16.15
5	Single cane weight (kg)	0.23	0.09	0.01
6	Sucrose %	9.77	1.02	0.10
7	CCS %	6.06	0.60	0.13
8	Cane yield (t/ha)	4082.39	960.78	35.51
9	CCS (t/ha)	132.36	16.248	0.54

Table2: Mean performance of the 14 genotypes of sugarcanefor all traits under study

Character/ Genotypes	TL	MH	CD	NMC	SCW	S (%)	CCS (%)	CY	CCS (t/ha)
CoVSI 18121	170.18	279.60	3.56	76.39	1.93	20.03	14.22	141.18	20.11
CoVSI 19121	151.54	270.66	3.17	69.14	1.53	19.26	13.54	101.35	13.82
CoVSI 15002	155.02	250.56	3.19	68.01	1.60	19.76	14.38	108.22	15.50
VSI 16002	160.20	249.11	3.30	64.16	1.67	19.50	13.79	106.84	14.81
CoVSI 17001	134.66	269.84	3.26	62.95	1.80	19.34	13.66	110.30	15.26
Co 11015	133.68	262.17	3.16	65.33	1.46	20.81	14.77	94.52	13.97
Co 12009	145.70	284.06	3.38	70.46	1.87	19.66	13.91	129.18	17.98
Co 13008	162.58	263.73	3.40	74.75	1.83	19.33	13.61	133.00	18.20
PDN 15012	173.63	262.93	3.40	82.66	1.73	19.75	13.99	138.67	19.56
Co 86032	167.27	239.94	3.02	79.18	1.50	19.61	13.93	116.26	16.14
CoM 0265	175.05	274.33	3.42	80.29	1.81	18.73	13.26	143.62	19.27
VSI 08005	169.68	269.67	3.40	77.73	1.74	20.08	14.21	132.99	19.01
MS 10001	159.02	263.61	3.49	74.03	1.74	20.39	14.44	124.88	18.11
VSI 434	138.20	242.36	2.98	65.34	1.35	20.75	14.70	89.14	13.56
Total mean	156.89	263.04	3.30	72.17	1.68	19.79	14.03	119.30	16.81

CCS(t/ha)- Commercial Cane Sugar (t/ha), CY- Cane Yield at harvest (t/ha), CCS (%)- CCS at 12th month stage, S (%)- Sucrose % at 12th month stage, SCW- Single Cane Weight (kg), NMC- Number of millable canes at harvest, 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/ha (‘000)	156.89	8.21	10.64	59.64	20.50	13.07
2	Millable height (cm)	263.04	4.60	5.87	61.39	19.54	7.43
3	Cane diameter (cm)	3.30	4.80	5.95	65.03	0.26	7.97
4	Number of millable canes (‘000ha)	72.17	8.47	10.14	69.83	10.52	14.58
5	Single cane weight (kg)	1.68	9.86	10.72	84.58	0.31	18.68
6	Sucrose %	19.79	2.80	3.21	76.06	0.10	5.03
7	CCS %	14.03	2.80	3.82	53.77	0.59	4.23
8	Cane yield (t/ha)	119.30	14.72	15.55	89.68	34.26	28.72
9	CCS (t/ha)	16.81	13.61	14.30	90.62	4.49	26.69

ACKNOWLEDGEMENT

The authors are grateful to Hon’ble Director General of VSI, Pune for providing necessary facilities and continuous supports.Authors are thankful to Managing Director and Cane Development Officer from Shree T. Kore Warana Sugar Mill Ltd.; Shree Chhatrapati Shahu Sugar Mill Ltd. and Jawahar Shetkari Sugar Mill Ltd. from Kolhapur district of Maharashtra State for providing the support during the investigation.

REFERENCES

[1] R. K. Agrawal, B. Kumar, Variability, heritability and genetic advance for cane yield and its contributing traits in sugarcane clones under waterlogged condition. IJCMAS 2017; 6(6):1669-1679.

[2] K. I. Ahmed, S. B. Patil, N. G. Hanamaratti, B. T. Nadgouda, N. B. Moger, Genetic variability studies for yield and its component traits in selected clones of sugarcane. J.of Pharmac. and Phytochem. 2019; 8(2):894- 898.

[3] R. W. Allard, Principles of Plant Breeding 1960. John Willeyand Sons. Inc.,USA.

[4] N. Balasundaram and K.V. Bhagyalakshmi, Variability heritability and association among yield and yield component in sugarcane. Indian J. agric. Sci. 1978; 48 (5): 291-295.

[5] P. K. Bhatnagar, A. Q. Khan, A. Singh, K. A. Khan, Studies on genetic variability, heritability and genetic advance in plant and ratoon crops of sugarcane. Indian Sugar 2003; 53(3):183-185.

[6] G. W. Burton, Quantitative inheritance in grasses. Proc. 6th Int. Greassland Conf. 1952; 1: 28-83

[7] G. W. Burton, and E. W. Devane, Estimating heritability in tall Fescue (Festuca arundinacea) from replicated clonal material. Agron. J. 1952; 45:478-481.

[8] R. A. Fisher, Statistical methods for research workers. Oliver and Boyd 1925, London.

[9] R. A. Fisher and F. Yates, Statistical tables for biological, agricultural and medical research. Oliver and Boyd 1963, London.

[10] S. N. S. Gowda, K. Saravanan, C. R. Ravishankar, Genetic variability, heritability and genetic advance in selected clones of sugarcane. Plant Archives 2016;16(2):700-704.

[11] J. E. Grafius, 1959. Heterosis in barley.

[12] R. S. Hapase and D. G. Hapase, Genetic variability studies in late maturing sugarcane varieties. Bhartiya Sugar 1990; 13-16

[13] G. Hiremath, T. E. Nagaraja, Genetic variability and heritability analysis in selected clones of sugarcane. Inter. J. of Sci. Tech. & Engg. 2016; 2(8):2349-784X.

[14] P. Jain, R. Pal, M. L. Saini, L. Rai, Variability, heritability and genetic advance for yield and contributing traits. Indian Sugar 2001; 47(7):499-502.

[15] H. W. Johnson, H. F. Robinson. R. E. Comstock. Estimates of genetic and environmental variability of Soybeans. Agron. J. 1955; 47:314-318.

[16] K. A. M. Khaled, M. S. Saleh, E. A. M. Amer, Estimation of Genetic Variance and Broad Sense Heritability for Sugarcane. Alexandria Science Exchange J. 2013; 34:121-126.

[17] P. Kumar, S. S. Pandey, B. Kumar, D. N. Kamat, M. Kumar. Genetic variability, heritability and genetic advance of quantitative traits in sugarcane. Inter. J. of Chem. Stud. 2018; 6(3):3569-3572.

[18] P. Kumari, B. Kumar, D. N. Kamat, R. Singh, D. Singh, R. Chhaya, To study genetic variability, heritability and genetic advance for cane and sugar yield attributing traits in mid-late maturing sugarcane clones. J. of Pharmac. and Phytochem. 2020; 9(1):1890- 1894.

[19] A. J. Mangelsadorf, Sugarcane breeding methods. Proc. Int. Soc. Sug. Cane. Technol. 1959; 10: 694-701.

[20] N. V. Nair and T. V. Sreenivasan, Analysis of stalk yield componants in Saccharum officinarum L. Sugarcane.1989; 2: 4-5.

[21] V. G. Panse, Methods in plant breeding. Indian Journal of Genetics and Plant Breeding 1942; 2:151-158.

[22] V. G. Panse and P. G. Sukhatme, Statistical methods for agricultural workers 2nd Edn. 1985 pp. 381, ICAR, New Delhi.

[23] P. P. Patil, D. U. Patel, S. C. Mali, V. A. Lodam, Genetic Variability in Sugarcane (Saccharum spp. Complex). Trends in Bioscience 2014; 7(13):1388-1391.

[24] S. Ramanujam and D. K. Tirumalachar. Genetic variability of certain characters in red pepper (Capsicum annum L.). Mysore J. Agric. Sci. 1967; 1: 30-36.

[25] B. K. Sahi, S. S. Shah and K. A. Patel, Genetics of yield and quality characters in early maturing sugarcane varieties. Indian J. agric. Sci.1987; 57(11): 779-782.

[26] G. S. Sanghera, V. Tyagi, R. Kumar, K. S. Thind, Genetic variability for cane yield, earliness and quality traits in sugarcane under subtropical region of India. Int. J. of Current Res. 2014; 6(8):7763-7765.

[27] R. K. Singh and B. D. Chaudhary, Boimetrical methods in quantitative genetic analysis. Kalyani Publ. 1977 New Delhi, pp.209.

[28] R. R. Singh, B. K. Tripathi and S. Lal, Variability and correlation studies in sugarcane. Indian Sugar 1981;10: 457-459.

[29] S. G. Sreekumar, V. G. Nair and S. S. Nair, Genetic variability in yield and quality componants in sugarcane. Bhartiya Sugar 1988; 13(2): 65, 67, 68.

[30] S. Wright, Systems of mating. II. The effects of inbreeding on the genetic composition of a population 1921; 6(2):124-143.