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## Studies on estimates of genetic variability, character association and path analysis of yield components in sugarcane

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### Abstract

A set of twenty sugarcane genotypes were evaluated in randomized block design (RBD) at CCS Haryana Agricultural University, Regional Research Station, Uchani, Karnal from February, 2021- March, 2022 to study the genetic variability, correlation and path analysis of nine characters. The analysis of variance revealed significant differences among the genotypes for all the characters under study indicating the existence of genetic variability. Coefficients of variation at genotypic and phenotypic levels, heritability (broad sense) and expected genetic advance (as percent of mean) were high for commercial cane sugar, germination (%) at 45 DAP, single cane weight, stalk length and cane yield. The commercial cane sugar, single cane weight, stalk length, number of millable canes at harvest and stalk diameter exhibited significant and positive correlation with cane yield. Commercial cane sugar (t/ha) exhibited positive and significant genotypic and phenotypic association with cane yield, single cane weight, stalk length, stalk diameter, number of millable canes at harvest, number of tillers at 120 DAP and number of shoots at 240 DAP. The analysis of path coefficient indicated that the highest positive direct contribution to cane yield was manifested by number of shoots at 240 DAP, commercial cane sugar and single cane weight. Hence, on the basis of this study it could be concluded that number of shoots at 240 DAP, commercial cane sugar and single cane weight are most important characters while selecting genotypes for higher cane yield.

**Keywords:** Sugarcane, genetic variability, heritability, correlation and path analysis

### Introduction

Sugarcane (*Saccharum* spp. Complex) is an important cash crop in many tropical and subtropical countries and is one of the main source of sugar production in the world. In India this is a major commercial crop that sustains sugar industry in particular and so many allied industries like ethanol, industrial alcohol, liquor, paper, rubber, wax card board etc. in general. Sugarcane, apart from being the chief source of sweetening agent to the millions of agriculturist in the country, is an insurance against economic distress on account of sugarcane being an important cash crop coupled with its capacity to withstand the climatic vagaries better than most of the other crops. It is cultivated in most of the states of India with total area of 4.86 million hectare with average productivity of 77.6 tons per hectare. Sugarcane was cultivated in 0.11million hectare area with average cane yield of 80.65 tons per hectare during 2019-20 in Haryana (Anonymous, 2020) [2].

The ploidy level of sugarcane is very high which makes it more challenging for the breeders to develop new cultivars. Sugarcane possesses interspecific hybrid genome which is the result of unevenly inherited genetic material from both parental species and this uneven distribution of genetic material make its genome more complex than that of its parental species (D'Hont *et al.*, 1996) [8]. In sugarcane, complex traits like cane yield and quality are influenced by number of characters. These characters directly and indirectly contribute to the yield (Chaudhary and Joshi, 2005) [7]. Swaminathan (1991) [21] emphasized that genetic diversity and location specific varieties are essential for achieving sustainable advances in productivity. Variety is the pivot and the cheapest technology for boosting cane production and productivity through sugarcane varietal improvement program and this program proceeds via choosing parents and making crosses. Progress in any crop improvement programme depends on the magnitude of genetic variability and heritability present in the source material. The extent of variability is measured by GCV and PCV which provides the information about relative amount of variation present in different characters. The knowledge on the nature and magnitude of genetic variation in respect of quantitative characters like yield and its components is essential for effective crop

improvement. Selection of high yielding varieties based only on grain yield will not be much effective unless adequate information on genetic parameters are available to formulate hybridization and selection program for further improvement because the estimate of the mean serves as a basis for eliminating the undesirable genotypes. Cane yield character is quantitative in nature and polygenetically controlled. Correlation analysis studies the joint variation of two or more variables for determining the amount of association between those variables. Trait correlation stipulated by correlation coefficient is a vital criterion for selecting superior genotypes for advancement through consideration of attributing traits on yield. Path coefficient is the standardized partial regression coefficient, which measures direct influence of one variable upon another, as such are categorized into causal and effect groups. It partitions the components of correlation coefficient into direct and indirect effect and visualize the relationship in a more meaningful manner. Path coefficient analyses are fundamental in identifying traits that are helpful as selection criteria in order to advance superior crops in a breeding programme. The present study was therefore, undertaken to estimate the genetic variability, correlation and path analysis in diverse sugarcane genotypes with the view to identify the genotypes with best potentiality for enhancing sugarcane yield and its component characters.

### Materials and Methods

The experiment material for the present study consists of twenty mid late maturing sugarcane clones evaluated in randomized block design with three replications, each genotype planted in four rows of six meter length with plot size of 21.6 m<sup>2</sup> during February, 2021 at CCS Haryana Agricultural University, Regional Research Station, Uchani, Karnal. The growth characters viz., number of tillers at 120 DAP, number of shoots at 240 DAP, number of millable canes and cane yield at harvest were recorded on plot basis from February, 2021 to March, 2022. The observations were recorded on five randomly tagged plants for single cane weight, stalk length, stalk diameter, respectively. Analysis of variance was done for partitioning the total variation due to treatments and replications according to the procedure given by Panse and Sukhatme (1967) [16]. PCV and GCV were calculated by the formula given by Burton (1952) [5], heritability in broad sense (h<sup>2</sup>) by Burton and De Vane (1953) [6] and genetic advance was calculated by using the procedure given by Johnson *et al.* (1955) [13]. Correlation coefficient and path coefficient were worked out as method suggested by Al Jibouri *et al.* (1958) [1] and Dewey and Lu (1959) [9], respectively. The estimated values were compared with table values of correlation coefficient to test the significance of correlation coefficient prescribed by Fisher and Yates (1967) [10].

### Results and Discussion

The analysis of variance for all the characters under study revealed significant differences thereby indicating presence of substantial genetic variation among the sugarcane clones. The estimates of variability parameters for cane yield and its component traits in twenty sugarcane clones are presented in Table 1. In the present investigation high range was observed for majority of the characters viz., cane yield (t/ha), germination (%) at 45 DAP, number of tillers at 120 DAP, number of shoots at 240 DAP, number of millable canes at

harvest, single cane weight (kg) and stalk length (cm). In general, the phenotypic coefficient of variation (PCV) was higher than its corresponding genotypic coefficient of variation (GCV). This suggested the role of environment in the expression of characters. PCV values were highest for CCS (t/ha) followed by single cane weight (kg), germination (%) at 45 DAP, cane yield (t/ha), number of tillers at 120 DAP and stalk length (cm). GCV values were highest for CCS (t/ha) followed by germination (%) at 45 DAP, single cane weight (kg), cane yield (t/ha), stalk length (cm) and number of tillers at 120 DAP indicating availability of sufficient variation and thus exhibited scope for genetic improvement through selection for all these traits. However, stalk diameter exhibited least phenotypic and genotypic coefficients of variation. High genotypic and phenotypic coefficient of variation for commercial cane sugar (t/ha) were reported earlier by Behou and Pene (2020) [3], Patra *et al.* (2022) [18].

The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability. The genetic coefficients of variation along with heritability estimates give a better indication of the amount of genetic variation for a character than either parameter alone. The estimates of heritability in broad sense was high for germination (%) at 45 DAP (81.20%), stalk length (79.83%), commercial cane sugar (79.18%), cane yield (70.16%), single cane weight (67.38%) and number of millable canes at harvest (62.43%). This suggests that simple selection for these traits would be effective for selection of superior clones. High heritability values were also obtained by Patil *et al.* (2014) [17] and Belwal and Ahmad (2020) [4] in sugarcane for majority of the above mentioned traits. In contrast, Marwa *et al.* (2018) [14] discovered high heritability values for sugar yield, brix percent, and purity percent. Johnson *et al.* (1955) [13] reported that heritability estimates together with expected genetic gain will be more useful in predicting the resultant effect for selecting the best genotypes through selection. The high genetic advance along with high heritability showed most effective condition for selection. High heritability coupled with high genetic advance as percent of mean was recorded for commercial cane sugar, germination (%) at 45 DAP and single cane weight suggesting that these characters are governed by additive gene action and selection for these characters will be effective for further improvement in cane yield. These results are in conformity with Tolera *et al.* (2023) [23] for germination (%) at 45 DAP. High heritability with moderate genetic advance as percent of mean was observed for cane yield, number of millable canes at harvest and stalk length indicating prevalence of non-additive gene action and it requires careful selection for the desired improvements in these characters. These results were akin with the findings of Tolera *et al.* (2023) [23] for number of millable canes at harvest and stalk length.

Correlation coefficient analysis measures the natural relation between various plant traits and determines the component characters on which selection can be used for genetic improvement in yield. The 'r' values obtained at phenotypic and genotypic levels for the inter se combinations between cane yield and its component traits are presented in Table 2. The results revealed that traits namely commercial cane sugar (0.918), single cane weight (0.721), stalk length (0.484), number of millable canes at harvest (0.389) and stalk diameter (0.376) exhibited significant and positive correlation with

cane yield. Positive and significant association with these traits implied that selection on the basis of these traits would be rewarding. Patra *et al.* (2022) [18] detected that number of millable canes per plot and single cane weight exhibited positive and significant correlation with cane yield. Hiremath *et al.* (2015) [12] observed strong positive and significant genotypic as well as phenotypic correlation of CCS (t/ha) with cane yield and moderately positive and significant association with number of millable canes at harvest. Commercial cane sugar (t/ha) exhibited positive and significant genotypic and phenotypic association with cane yield, single cane weight, stalk length, stalk diameter, number of millable canes at harvest, number of tillers at 120 DAP and number of shoots at 240 DAP. These findings are in accordance with the results of Gowda and Saravanan (2016) [11] and Palachai *et al.* (2019) [15]. The indirect association becomes more complex, less manifest, and somewhat mystifying as we start considering more the number of variables in association studies. Correlation analysis fell short in explaining the causal associations among the traits and thus requires further partitioning into direct and indirect effects. Void in correlation analysis in terms of causal relationships among characters compels the use of path coefficient analysis

in selection process to utilize direct as well as indirect effects among characters. In the present study, the path coefficient analysis was performed for cane yield as dependent variable (Table 3). The results of path analysis revealed that number of shoots at 240 DAP (0.965) exerted the highest positive direct effect on cane yield followed commercial cane sugar (0.686) and single cane weight (0.593). Therefore these characters could be considered as main components for selection in a breeding programme for higher cane yield. These results are in accordance with findings of Thippeswamy *et al.* (2003) [22] for commercial cane sugar and Sanghera *et al.* (2017) [20] for single cane weight. Thus, on the basis of above study it may be stated that number of shoots at 240 DAP, commercial cane sugar and single cane weight are most important characters for cane yield. This study manifested that CCS (t/ha) and single cane weight are significantly and positively correlated with cane yield at both genotypic and phenotypic level. Therefore, these parameters are very important to be considered when selecting for sugarcane yields especially in determining the possibility of obtaining the optimum yield from millable sugarcane particularly for this subtropical ecology.

**Table 1:** Genetic variability parameters for yield and its component traits in Sugarcane

Sr. No.	Characters	Mean	Range		Coefficient of Variation		Heritability (%)	Genetic Advance (%)	Genetic Advance as percent of mean
			Max.	Min.	Genotypic (%)	Phenotypic (%)			
1	Cane Yield (t/ha.)	96.62	112.63	75.83	10.67	12.73	70.16	17.78	18.41
2	CCS (t/ha.)	11.46	13.86	8.82	13.39	15.04	79.18	2.81	24.54
3	Germination % (45 days)	37.55	43.35	28.25	12.47	13.84	81.20	8.69	23.15
4	No. of Tillers (000/ha) at 120 days	137.48	158.61	113.50	8.86	11.76	56.79	18.91	13.76
5	No. of Shoots (000/ha) at 240 days	107.60	127.76	91.52	6.51	10.34	39.59	9.08	8.44
6	No. of millable canes at Harvest (000/ha)	96.50	118.61	78.36	8.11	10.26	62.43	12.73	13.19
7	Single cane wt.(kg)	1.00	1.32	0.80	12.13	14.78	67.38	0.20	20.51
8	Stalk length (cm)	247.59	292.50	198.50	10.19	11.41	79.83	46.44	18.76
9	Stalk diameter (cm)	2.36	2.63	2.21	3.41	4.96	47.43	0.11	4.84

**Table 2:** Estimates of genotypic (upper) and phenotypic (lower) correlation coefficients among different characters in sugarcane

Characters	Cane Yield (t/ha.)	CCS (t/ha.)	Germination % (45 days)	No. of Tillers (000/ha) at 120 days	No. of Shoots (000/ha) at 240 days	No. of Millable canes at harvest (000/ha)	Single cane wt.(kg)	Stalk length (cm)	Stalk diameter (cm)
Cane Yield (t/ha.)		0.918**	-0.200	0.271	0.25	0.389*	0.721**	0.484**	0.376*
CCS (t/ha.)	0.923**		0.052 <sup>NS</sup>	0.395*	0.487**	0.597**	0.682**	0.594**	0.310 <sup>NS</sup>
Germination % (45 days)	-0.121 <sup>NS</sup>	0.070 <sup>NS</sup>		0.243 <sup>NS</sup>	0.246 <sup>NS</sup>	0.424**	-0.076 <sup>NS</sup>	0.290 <sup>NS</sup>	0.051 <sup>NS</sup>
No. of Tillers (000/ha) at 120 days	0.404**	0.455**	0.298 <sup>NS</sup>		0.848**	0.821**	-0.020 <sup>NS</sup>	0.369*	0.225 <sup>NS</sup>
No. of Shoots (000/ha) at 240 days	0.436**	0.533**	0.261 <sup>NS</sup>	0.864**		1.010**	-0.246 <sup>NS</sup>	0.202 <sup>NS</sup>	0.041 <sup>NS</sup>
No. of Millable canes at harvest (000/ha)	0.405**	0.574**	0.389*	0.710**	0.771**		-0.109 <sup>NS</sup>	0.293 <sup>NS</sup>	0.220 <sup>NS</sup>
Single cane wt.(kg)	0.658**	0.609**	-0.027 <sup>NS</sup>	0.098 <sup>NS</sup>	0.001 <sup>NS</sup>	-0.004 <sup>NS</sup>		0.612**	0.819**
Stalk length (cm)	0.467**	0.552**	0.263 <sup>NS</sup>	0.311 <sup>NS</sup>	0.213 <sup>NS</sup>	0.267 <sup>NS</sup>	0.570**		0.413**
Stalk diameter (cm)	0.144 <sup>NS</sup>	0.156 <sup>NS</sup>	-0.061 <sup>NS</sup>	-0.052 <sup>NS</sup>	-0.148 <sup>NS</sup>	-0.045 <sup>NS</sup>	0.431**	0.130 <sup>NS</sup>	

\*Significant at 5%, \*\* Significant at 1%, NS – Non Significant

**Table 3:** Direct (diagonal values) and indirect effects of different characters on cane yield at phenotypic level

	CCS (t/ha.)	Germination % (45 days)	No. of tillers (000/ha) at 120 days	No. of shoots (000/ha) at 240 days	No. of millable canes at harvest (000/ha)	Single cane wt. (kg)	Stalk length (cm)	Stalk diameter (cm)	Correlation with yield
CCS (t/ha.)	0.686	-0.001	-0.019	0.470	-0.484	0.405	-0.109	-0.030	0.918
Germination % (45 days)	0.036	-0.014	-0.011	0.237	-0.344	-0.045	-0.053	-0.005	-0.200
No. of tillers (000/ha) at 120 days	0.271	-0.004	-0.047	0.818	-0.666	-0.012	-0.067	-0.022	0.271
No. of Shoots (000/ha) at 240 days	0.334	-0.004	-0.04	0.965	-0.819	-0.146	-0.037	-0.004	0.250
No. of millable canes at harvest (000/ha)	0.409	-0.006	-0.038	0.975	-0.811	-0.065	-0.054	-0.021	0.389
Single cane wt. (kg)	0.467	0.001	0.001	-0.238	0.088	0.593	-0.112	-0.080	0.721
Stalk length (cm)	0.408	-0.004	-0.017	0.195	-0.238	0.363	-0.183	-0.040	0.484
Stalk diameter (cm)	0.212	-0.001	-0.011	0.040	-0.178	0.486	-0.076	-0.098	0.376
Residual effect = 0.15168									

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