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Genetic variability, correlation studies and path analysis in sugarcane early clones

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Abstract
An experiment was conducted at CCS Haryana Agricultural University, Regional Research Station, Kaul, Kaithal during February 2022- March 2023 using a set of twelve early sugarcane clones along with three checks to explore variation and the association among them. The analysis of variance revealed significant differences among the genotypes for all the characters under study indicating the existence of genetic variability. Phenotypic coefficient of variation (PCV) was found higher than genotypic coefficient of variation (GCV) for all the traits. Results showed that cane yield exhibited highly significant positive correlation with CCS yield, number of millable canes, stalk length, stalk diameter, single cane weight and germination% at both genotypic and phenotypic levels. Path analysis revealed that single cane weight exerted maximum positive direct effect on cane yield. Overall the data generated from this particular trial gives an estimation and prediction of cane yield and provides reliable guidance for selecting the best clones for planting in future years.

Keywords: Correlation, path, sugarcane, variation

Introduction

Sugarcane (*Saccharum spp.*) is a major food and bioenergy crop grown in tropical and subtropical regions, accounting for a significant sugar and ethanol production worldwide. It belongs to the perennial, monocotyledonous members of the genus *Saccharum*. Modern cultivated sugarcanes are complex between *Saccharum officinarum* (noble cane) and *Saccharum spontaneum*, with genetic contributions from *S. robustum, S. sinense, S. barberi* and other related grass species like Miscanthus, Narenga, and Erianthus (Babu *et al.*, 2022) [7]. It is a polyploid and highly heterozygous with variable levels of ploidy and wide range of chromosome number (2n = 40-128). Thus, it is considered to be a difficult crop from breeding point of view and requires 15 years of experimenting to generate more productive cultivars (Barreto *et al.*, 2021) [4].

In India, sugarcane crop occupied an area of 5.83 million hectares with a production of 494.22 million tons and 84.8 tons per hectare average productivity during 2022–23. In Haryana, during 2022–23 sugarcane was cultivated in 1.08 lakh hectare area with a production of 8.86 million tons and an average cane yield of 82.23 tons per hectare (Anonymous, 2023) [3]. The Indian sugar industry is one of the largest agro-based industries in the world providing a livelihood for 50 million farmers and 0.5 million workers involved in processing and related activities of sugarcane (Agrawal and Kumar, 2023) [1]. Sugarcane mills primarily yield sugar (sucrose) and ethanol following the juice extraction process from the cane (Gadkari *et al.*, 2023) [8]. Sugarcane straw, sugarcane bagasse and sugarcane bagasse pith are three major and widely produced by-products and wastes of the sugarcane industry and farming worldwide (Najafi *et al.*, 2023) [12]. India emerges as the world's second-largest sugar producer and the third-biggest nation in the world in ethanol production after the United States and Brazil, achieved 12% ethanol blending with petrol in 2022-23 and holds its commitment towards green energy and meet India's COP 26 targets (Ministry of Consumer Affairs, Food & Public Distribution, 2023).

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Crop improvement for better yield and quality is the prime objective of plant breeder. The selection of ideal early and mid-late varieties has the potential to improve sugar recovery. Efforts to maximize yield, quality and resilience in this crop are imperative for the sugar industry to remain competitive and sustainable. The efficiency of selection depends on the identification of genetic variability from the phenotypic expression of the character. It is an authentic fact that greater variability among the genotypes leads to better chance for improvement in the crop. It is the basic tool of breeding strategies which could be achieved through hybridization of diversified genetic material (Momotaz et al., 2024) [11].

Selection efficiency is related to the magnitude of heritability and genetic advance (Singh and Narayanan, 1993) [18] and heritability estimates along with genetic advance are important selection parameters and normally more helpful in predicting the gain under selection than heritability estimates alone. Genetic advance refers to the improvement in the mean genotypic value of selected individuals over the parental population and is influenced by the genetic variability, heritability and selection intensity (Saleem et al., 2023) [16]. In order to accumulate optimum combination of yield contributing characters in a single genotype, it is essential to know the inter-relationships among the component traits. Further, the cane yield is influenced by its various components directly or indirectly via other traits, which create a complex situation before a breeder for making effective selection. Therefore, path coefficient analysis could provide a more realistic picture of the interrelationship, as it partitions the correlation coefficient in direct and indirect effects of the variables (Parihar, 2020) [14]. Keeping the above fact in mind, the present investigation was planned 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
Field Experimentation
The field experiment was conducted during February 2022-March 2023 at CCS Haryana Agricultural University Research Farm, Regional Research Station, Kaul, Kaithal.

Plant Materials: The research was conducted with 12 early sugarcane clones along with 3 checks (Table 1).

Table 1: List of twelve early sugarcane clones along with three standards

12-416	15-1755	15-1763	15-2314	15-2387	16-266
16-369	16-371	16-405	16-434	16-440	18-140
Std's					
Co0238		Co05009		CoJ64	

Experimental Design and Layout
The experiment was laid out in a Randomized Block Design (RBD) with 4 rows of 6 m length each, in three replications. A row to row distance of 90 cm was maintained. 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 whilst the observations were recorded on five randomly tagged plants for single cane weight, stalk length, stalk diameter, respectively.

Statistical analysis
Analysis of variance was done for partitioning the total variation due to treatments and replications according to the procedure given by Panse and Sukhatme (1954) [13]. PCV and GCV were calculated by the formula given by Burton (1952) [5], heritability in broad sense was calculated according to the formula suggested by (Johnson et al., 1955) [9] and expected genetic gain or advance for each character was estimated by using the following method suggested by Johnson et al. (1955) [9]. Correlation coefficient and path coefficient were worked out as method suggested by Al Jibouri et al. (1958) [2] and Dewey and Lu (1959) [6], respectively.

Results and Discussion
Pooling information about the genetic variability, relationships and mechanisms of inheritance of different traits is the key task in genetic improvement of any crop plant. In the present study, the analysis of variance for all the characters under study revealed significant differences indicating presence of substantial genetic variation among the sugarcane clones. High range was observed for all the traits viz., cane yield (t/ha), CCS (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). PCV for all the traits was higher than GCV (Table 1). It is likely to occur because phenotypic variations contain both genotypic and environmental components and delineates genotypes by environment interaction in the expression of all the traits. This was confirmed by Sharma et al. (2023) [17], Barreto et al. (2021) [4] and Tena et al. (2023) [19].

PCV values were highest for CCS (t/ha) followed by cane yield (t/ha), single cane weight (kg), germination (%) at 45 DAP, number of tillers at 120 DAP. GCV values were highest for CCS (t/ha) followed by cane yield (t/ha), single cane weight (kg), 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 length (cm) exhibited least phenotypic and genotypic coefficients of variation. High GCV and PCV for commercial cane sugar, germination (%) at 45 DAP, single cane weight, stalk length and cane yield were reported earlier by Sharma et al. (2023) [17].

Heritability provides valid information about the traits that are transmitted from parents to offspring and also to the successive generations, this helps plant breeders to predict a successful cross. Among all the traits number of tillers at 120 DAP, CCS (t/ha), number of shoots at 240 DAP single cane weight (kg), stalk length (cm), stalk diameter (cm) had moderate heritability (60-80%) whereas cane yield (t/ha), germination (%) at 45 DAP number of millable canes at harvest showed low heritability (Table 1). None of the trait exhibited high heritability (>80%). In contrast high heritability (>80%) values were also obtained by Kumari et al. (2020) [1] for traits like germination% at 45 days, pol% in juice at 12 month and fiber % at harvest.

Studies purely based on heritability are not very authentic because broad sense heritability contains both additive and non-additive components. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone, thus heritability is studied in combination of genetic advance to get clearer picture. GA as 5% means was highest for single cane weight (kg), CCS (t/ha), number of tillers at 120 DAP, stalk diameter (cm), number of shoots at 240 DAP, germination (%) at 45 DAP, number of millable canes at harvest and stalk length (cm). These results were akin with the findings of Tolera et al. (2023) [20] for number of millable canes at harvest and stalk length.

Study of interrelationships between cane yield and its

contributing components can increase the efficiency of breeding programs through determining the appropriate selection criteria. In correlation studies, CCS (t/ha) had highest degree of association with cane yield (t/ha) followed by single cane weight (kg), germination (%) at 45 DAP, stalk diameter (cm) and stalk length at both genotypic and phenotypic level. Number of shoots at 240 DAP exhibited significant and positive correlation 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, germination%, stalk length and stalk diameter (Table 3).

The correlation coefficient indicates only linear relationship between pair of traits. But, cane yield (dependent character) has interaction of product of many component characters and change in any one component will disturb whole network. Only the knowledge of correlations coefficient is often misleading as the correlations observed may not be always true. The path coefficient analysis (Wright, 1921; Dewey and Lu, 1959) [21, 6] provides an effective means of separating direct and indirect causes of association. If the correlation between cane yield and a trait is due to direct effect of the trait, it reflects a true relationship between them and selection can be practiced for such trait in order to improve yield. Low residual effects in path coefficient analysis indicated a high contribution of independent traits to the dependent trait (cane yield) and there were very few other factors influencing the cane yield, which were not being included in the study.

The trait which exhibited maximum direct effect was single cane weight (kg). Other traits showing positive direct effects were CCS (t/ha), number of millable canes at harvest and number of shoots at 240 DAP (Table 4). Similar findings were reported by Tena *et al.* (2023) [19] exhibiting cane yield had significant positive correlation with tiller number 3 and 4 months after planting, number of millable cane, single cane weight, stem diameter, stalk height, number of internodes, internode length, sugar yield, pol percent, purity percent and recoverable sugar. They also indicated that single cane weight and number of millable canes were the major contributors to cane yield. These results were further confirmed by Rakesh *et al.* (2023) [15], Tolera *et al.* (2024) [20] and Sharma *et al.* (2023) [17] by studying path analysis in different sugarcane clones. The combined results of correlation and path coefficient analysis in the present investigation may help to develop suitable selection criteria particularly for this subtropical ecology.

Table 2: Estimates of mean performance, genotypic and phenotypic coefficient of variance, heritability and genetic advance for cane yield and component characters of sugarcane clones

Sr. No.	Characters	Mean	Range	Co-efficient of variation (%)		Heritability (h²) (%)	Genetic advance (as % of mean)
				PCV	GCV		
1	Cane Yield (t/ha.)	89.79	114.05-63.14	20.046	15.46	59.487	24.565
2	CCS (t/ha.)	10.66	14.25-7.23	22.59	17.728	61.587	28.660
3	Germination % (45 days)	44.32	53.03-33.57	16.340	11.797	52.130	17.547
4	No. of Tillers (000/ha) at 120 days	137.10	178.70-93.67	15.60	13.747	77.649	24.955
5	No. of Shoots (000/ha) at 240 days	107.42	134.73-78.23	14.440	11.654	65.134	19.375
6	No. of millable canes at Harvest (000/ha)	93.49	111.27-69.43	11.606	8.967	59.700	14.273
7	Single cane wt.(kg)	1.0	1.21-0.62	18.618	16.283	76.482	29.334
8	Stalk length (cm)	258.20	292.40-235.33	9.040	7.283	64.903	12.087
9	Stalk diameter (cm)	2.53	3.11-1.95	12.962	11.095	73.258	19.562

Table 3: Genotypic (below) and Phenotypic (above) correlation coefficients among various traits in sugarcane

	Cane Yield (t/ha.)	CCS (t/ha.)	No. of Mill able canes at harvest (000/ha)	Stalk length (cm)	Stalk diameter (cm)	Single cane wt.(kg)	No. of Shoots (000/ha) at 240 days	No. of Tillers (000/ha) at 120 days	Germination % (45 days)
Cane Yield (t/ha.)		0.986**	0.140 NS	0.357*	0.347*	0.849*	0.057 NS	0.097 NS	0.363*
CCS (t/ha.)	0.994**		0.123 NS	0.377*	0.349*	0.841**	0.041 NS	0.091 NS	0.370*
No. of Millable canes at harvest (000/ha)	-0.142NS	-0.135NS		0.329*	-0.556**	-0.392**	0.920**	0.874**	0.243 NS
Stalk length (cm)	0.322*	0.343*	0.324*		0.066 NS	0.196 NS	0.358*	0.426*	0.501**
Stalk diameter (cm)	0.435**	0.443**	-0.810**	0.107NS		0.621**	-0.607**	-0.630**	-0.161 NS
Single cane wt.(kg)	0.904**	0.892**	-0.548**	0.154NS	0.747**		-0.432**	-0.363*	0.244 NS
No. of Shoots (000/ha) at 240 days	-0.229NS	-0.218NS	0.969**	0.397**	-0.838**	-0.610**		0.947**	0.341*
No. of Tillers (000/ha) at 120 days	-0.128NS	-0.105NS	0.920**	0.429**	-0.808**	-0.519**	1.004**		0.425**
Germination % (45 days)	0.492**	0.477**	0.461**	0.919**	-0.179NS	0.238NS	0.561**	0.643**	

Table 4: Path analysis showing direct (diagonal) and indirect (off diagonal) effects of different traits on cane yield in sugarcane

	CCS (t/ha.)	No. of Millable canes at harvest (000/ha)	Stalk length (cm)	Stalk diameter (cm)	Single cane wt.(kg)	No. of Shoots (000/ha) at 240 days	No. of Tillers (000/ha) at 120 days	Germin ation % (45 days)	Correlation
CCS (t/ha.)	0.37683	0.03901	-0.01316	-0.00336	0.59812	0.00493	-0.00437	-0.01162	0.986**
No. of Millable canes at harvest (000/ha)	0.04645	0.31642	-0.01149	0.00535	-0.27855	0.11108	-0.0419	-0.00763	0.140NS
Stalk length (cm)	0.14224	0.10424	-0.03486	-0.00063	0.13934	0.04324	-0.0204	-0.01571	0.357*
Stalk diameter (cm)	0.13134	-0.17585	-0.0023	-0.00963	0.44134	-0.07332	0.0302	0.00505	0.347*
Single cane wt.(kg)	0.31696	-0.12395	-0.00683	-0.00598	0.71109	-0.0522	0.01741	-0.00765	0.849
No. of Shoots (000/ha) at 240 days	0.0154	0.29111	-0.01249	0.00585	-0.30746	0.12073	-0.04539	-0.01072	0.057
No. of Tillers (000/ha) at 120 days	0.03432	0.27668	-0.01484	0.00607	-0.25834	0.11435	-0.04792	-0.01335	0.097
Germination % (45 days)	0.13948	0.07692	-0.01745	0.00155	0.17344	0.04122	-0.02039	-0.03138	0.363

Residual effect: 0.005

Conclusion
The study underscores the significant genetic variability among sugarcane clones, with traits like cane yield, commercial cane sugar (CCS), and single cane weight exhibiting substantial variation. Moderate heritability was observed for several traits, indicating their potential for successful transmission across generations. Genetic advance estimates highlighted traits with significant gains under selection, such as single cane weight and CCS. Correlation and path coefficient analyses revealed important relationships between traits, particularly the strong association of CCS with cane yield. These findings provide valuable insights for breeding programs aimed at improving sugarcane productivity, emphasizing the importance of considering multiple traits and their interactions. Overall, the study contributes to the ongoing efforts in genetic improvement of sugarcane, particularly in subtropical environments.

Acknowledgments

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