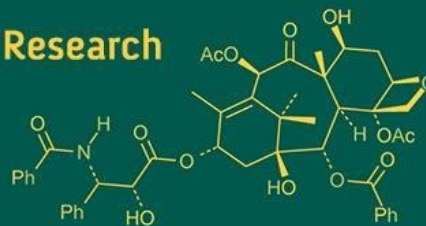
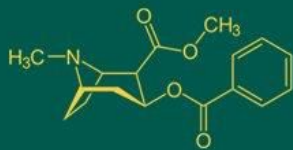


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Genetic variability, heritability, and genetic advance in interspecific and intergeneric clones of sugarcane

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Abstract

This study evaluated twenty sugarcane genotypes, including interspecific and intergeneric clones alongside standard check varieties, under controlled irrigation at Norman E. Borlaug Crop Research Centre, Pantnagar, India. The experiment was conducted using a randomized block design with three replications, and twelve morphological and quality traits were assessed, such as germination percentage, tiller number, cane length and diameter, number of millable canes, juice quality parameters, single cane weight, commercial cane sugar (CCS), and cane yield. Analysis of variance revealed significant genetic variability among the genotypes for all traits, confirming the presence of considerable diversity. The phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV), indicating a moderate influence of environmental factors on trait expression. Traits related to yield and biomass exhibited substantial genetic variability, while juice quality traits showed comparatively lower variation. High broad-sense heritability coupled with significant genetic advance was observed for most yield-related traits, suggesting that these are primarily governed by additive gene effects and can respond well to selection. In contrast, quality traits such as juice purity and sucrose content showed lower heritability and genetic advance, reflecting the greater impact of environmental factors or complex genetic control. Overall, the findings highlight substantial genetic variability and the potential for effective selection in sugarcane breeding programs, particularly for improving yield and sugar recovery. This study provides valuable insights and a strong genetic foundation for future crop improvement efforts aimed at enhancing both productivity and quality in sugarcane.

Keywords: Genetic variability, heritability, sugarcane breeding, yield traits, juice quality, selection

Introduction

Sugarcane (*Saccharum* spp.), a vital member of the Gramineae family, is globally recognized for its remarkable capacity to accumulate sucrose and for possessing one of the highest biomass production potentials among cultivated plants. Its unparalleled efficiency in converting solar energy into carbohydrates has positioned it as one of the most economically valuable crops for both sugar and renewable bioethanol production (Gianotto *et al.*, 2011; Hoang *et al.*, 2015; Mirajkar *et al.*, 2019) ^[1, 2, 3]. Historically, sugarcane has been cultivated on all inhabited continents, contributing substantially to local economies and food industries. In Ethiopia, the historical relevance of sugarcane dates back to the 16th century, when it began appearing in household gardens and farmers' fields, long before formal commercialization (Tena *et al.*, 2018) ^[4]. Since the establishment of commercial sugarcane production in the country in 1951, the crop has significantly supported both domestic sugar demand and employment generation. It also facilitates the production of by-products such as molasses and bagasse, which are utilized in various industrial applications (Teklemariam, 1991; T. Esayas *et al.*, 2016) ^[5, 6]. As sugarcane continues to gain importance for both food and energy security, breeding efforts have intensified to meet rising demands, particularly under changing environmental conditions. Breeding improved varieties requires a fundamental understanding of genetic variability within the germplasm pool, as well as the ability to evaluate heritable traits and predict genetic gains from selection. Knowledge of the magnitude and nature of genetic variation for yield and its contributing traits forms the foundation for any crop improvement program. In this regard, dissecting the genetic architecture of complex traits enables breeders to better understand the inheritance patterns,

enhance selection efficiency, and achieve targeted genetic improvements. Understanding the components of phenotypic variance, particularly the heritable and non-heritable portions, is critical in determining the extent to which a trait can be improved through selection. This process provides insights into the degree of genetic control over a trait and the predictability of its expression under varying environmental conditions (Ullah *et al.*, 2012) ^[7]. However, high heritability alone is not a guarantee for significant genetic gain. It must be evaluated in conjunction with genetic advance estimates to accurately assess the scope for effective selection and long-term improvement (Amin *et al.*, 2004; Johanson *et al.*, 1955; Udeh & Ogbu, 2011) ^[8, 9, 10]. Genetic variability serves as the raw material for plant breeding. Its presence is essential to develop improved cultivars capable of coping with both biotic and abiotic stresses. The diversity within and between genotypes offers the flexibility to select desirable traits for enhancement. By broadening the genetic base of sugarcane through interspecific and intergeneric crosses, breeders can tap into novel alleles that contribute to superior yield, stress tolerance, and adaptability. This expansion of variability becomes even more critical when addressing the challenges of climate change, disease pressure, and resource limitations. Moreover, variance component analysis provides a powerful tool to quantify heritable variation and estimate the potential genetic progress achievable through selection. It helps in identifying promising genotypes for use as parents in hybridization programs, based on their performance and trait inheritance patterns. In sugarcane, where vegetative propagation and complex polyploidy present unique challenges, such assessments become even more vital for strategic planning in breeding (Kumar *et al.*, 2018) ^[11]. Selection efficiency is also influenced by trait interrelationships. For instance, in multi-trait selection approaches, traits that demonstrate moderate to high heritability along with significant genetic advance, and that are strongly and positively correlated with the primary yield component sugar yield are prioritized (Borém *et al.*, 2016) ^[12]. Therefore, for effective crop improvement, not only should traits be heritable, but they should also translate into substantial genetic gain under selection pressure.

However, the extent of observed variability and heritability is influenced by several factors, including the nature of the genetic material, the target traits, and the environmental conditions under which the plants are evaluated (Dabholkar, 1992; Falconer & Mackay, 1996) ^[13, 14]. These interactions highlight the importance of conducting location- and material-specific studies to draw accurate inferences for breeding applications. Given the importance of exploiting genetic variation for sugarcane improvement, the current study was undertaken to assess the genetic variability, heritability, and genetic advance in a diverse set of interspecific and intergeneric sugarcane clones. This investigation aims to provide essential insights into the potential of these clones for use in future breeding programs, ultimately contributing to the development of high-yielding and resilient sugarcane cultivars.

Materials and Methods

Experimental Material

The present study was conducted using a total of twenty sugarcane genotypes, comprising 17 interspecific and intergeneric clones along with three standard check

varieties. The experimental clones included:

ISH 501, ISH 502, ISH 512, ISH 519, ISH 534, ISH 536, ISH 548, ISH 567, ISH 584, ISH 585, ISH 587, ISH 590, ISH 594, IGH 823, IGH 829, IGH 833, and IGH 834.

The check varieties used for comparative evaluation were CoPant 90223, CoPant 97222, and CoPant 5224.

Experimental Design

The field experiment was carried out during the cropping season under controlled irrigation and recommended fertilization conditions at the Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The trial was laid out in a Randomized Block Design (RBD) with three replications to ensure uniform environmental influence across plots and enhance statistical precision. Standard agronomic practices were followed to ensure healthy crop growth throughout the season.

Data Collection

Observations were recorded on 14 morphological and quality-related traits during the course of the experiment. Germination percentage was calculated 30 days after planting by counting the number of germinated buds and expressing it as a percentage of the total buds planted, providing an estimate of initial plant establishment. Tillers at 90 days were manually counted in each plot to assess early shoot proliferation and plant vigor. Cane length (cm) was measured from the base of the stalk to the top visible dewlap in five randomly selected millable canes per plot, while cane diameter (cm) was recorded at the midpoint of these canes using a Vernier caliper to evaluate stalk thickness. The number of millable canes was determined at harvest by counting the stalks that had matured to a harvestable stage. Juice quality parameters were assessed through brix percentage at 300 and 360 days to evaluate the soluble solids content in the cane juice. Sucrose percentage at 300 and 360 days was estimated by the standard polarimetric method, following established protocols for juice analysis. Purity percentage at both stages was calculated by expressing sucrose content as a proportion of brix and multiplying by 100, serving as an indicator of juice purity. The single cane weight (SCW) was determined by recording the average weight of five randomly selected millable canes using a digital scale. Commercial cane sugar (CCS%), indicating the amount of recoverable sugar, was computed using standard formulae based on brix and sucrose values. Finally, cane yield (t/ha) was calculated by converting the total weight of cane harvested per plot into tons per hectare, based on the plot dimensions.

Statistical Analysis

The statistical analysis for the estimation of genetic parameters, including genotypic and phenotypic coefficients of variation (GCV and PCV), heritability in broad sense, and genetic advance as percent of mean, was performed using the OPSTAT statistical software developed by CCS Haryana Agricultural University, Hisar, India. For data visualization and graphical representation of results, the R software (R Core Team, 2024) ^[15] was used. Trait distribution plots and comparative graphs were created using the 'ggplot2' package (Wickham, 2016) ^[16].

Results and Discussion

The ANOVA results revealed that all observed traits showed significant variation among treatments (genotypes), confirming the existence of substantial genetic variability in the evaluated sugarcane clones (Table 1). Across all 14 characters including germination percentage, tiller number, cane length and diameter, number of millable canes, juice quality traits (Brix, sucrose, purity), single cane weight, commercial cane sugar, and cane yield, the mean sum of squares for treatments was much higher than the corresponding error mean squares. This pattern supports the presence of significant genetic diversity in the test material. In sum, the significant variation observed aligns with studies that emphasize the existence and utility of genetic diversity in sugarcane for targeted selection, particularly when combined with parameters such as heritability and genetic advance (Rani *et al.*, 2024; Tena Alam *et al.*, 2017; Gupta *et al.*, 2024) [17, 18, 19]. This paves the way for further analysis of genetic parameters (GCV, PCV, heritability, genetic advance) on these same clones for advanced breeding work.

Variability

The analysis of variability parameters revealed substantial differences among the sugarcane clones for all observed traits. For each character assessed, the phenotypic coefficient of variation (PCV) was consistently higher than the genotypic coefficient of variation (GCV), suggesting that environmental factors contributed to the overall phenotypic expression, though their influence was generally moderate. High levels of genotypic and phenotypic variability were particularly notable for tiller count (GCV: 41.78, PCV: 42.39), germination percentage (GCV: 26.98, PCV: 28.51), single cane weight (GCV: 26.24, PCV: 28.03), CCS (GCV: 34.54, PCV: 36.35), cane yield (GCV: 28.61, PCV: 31.07), and number

of millable canes at 360 days (GCV: 30.25, PCV: 31.21), signifying a strong genetic basis for variation in these characters (Table 2). In contrast, traits related to juice quality such as Brix and purity exhibited lower GCV and PCV values, pointing to relatively less genetic variation for these attributes (Fig. 1). The environmental coefficient of variation (ECV) values were lower for most traits, indicating acceptable experimental precision for the data. The results indicated a considerable range of variability for critical agronomic and quality traits among the sugarcane genotypes studied. The observation that PCV consistently exceeded GCV aligns with prior reports in sugarcane, underscoring the influence of environment on trait expression, though genetic variation remains the dominant component for most yield-related characters (Khan *et al.*, 2017) [20]. Traits such as tillers, germination percentage, cane yield, single cane weight, CCS, and millable cane number, which exhibited high GCV and PCV, mirror the findings of earlier studies that highlighted the substantial inherent genetic diversity present in sugarcane breeding populations (Rahman *et al.*, 2024; Rani *et al.*, 2024) [21, 17]. This sizable genetic variability is essential for effective selection, as it enhances the prospects for realizing substantial genetic improvement in subsequent breeding cycles. For traits where both GCV and PCV were low, particularly for juice quality traits, the range for potential genetic improvement may be narrower, highlighting the need for targeted strategies to enhance these attributes (Prasad *et al.*, 2021). The close correspondence between GCV and PCV for most yield and biomass traits suggests that selection for these traits is less likely to be confounded by environmental effects, thereby increasing the reliability and effectiveness of selection (Khan *et al.*, 2017; Rani *et al.*, 2014) [20, 17].

Table 1: Analysis of Variance (ANOVA) for Agronomic and Quality Traits in Sugarcane Clones

S. No.	Character	Mean Sum of Squares		
		Replication (df: 2)	Treatment (df: 19)	Error (df: 38)
1.	Germination %	6.026	124.386**	4.644
2.	Tillers	27.655	3773.128**	36.354
3.	Cane length at 360 days	318.733	1081.782**	338.663
4.	Cane diameter at 360 days	0.047	0.285**	0.034
5.	NMC at 360 days	3.558	440.159**	9.212
6.	Brix at 300 days	0.425	3.909**	0.710
7.	Brix at 360 days	9.143	7.839**	2.995
8.	Sucrose at 300 days	0.156	1.613**	0.632
9.	Sucrose at 360 days	3.677	7.377**	1.194
10.	Purity at 300 days	307.361	51.123*	33.995
11.	Purity at 360 days	24.697	51.724*	32.147
12.	Single cane weight at 360 days	0.003	0.267**	0.012
13.	CCS	0.109	6.603**	0.228
14.	Cane yield	4.007	473.394**	26.762

Heritability and Genetic Advance

All major yield and quality traits exhibited a wide range of heritability and genetic advance estimates among the sugarcane clones. Very high broad-sense heritability was observed for traits like tillers (97.16%), number of millable canes (93.97%), germination percentage (89.58%), CCS (90.32%), single cane weight (87.61%), and cane yield (84.76%), indicating that the genetic variance accounted for most of the observed phenotypic variance in these characters. Similarly, these traits showed high genetic advance as a percentage of mean (e.g., tillers: 84.84%, CCS:

67.63%, NMC: 60.41%, cane yield: 54.26%), demonstrating the predominance of additive gene action and suggesting that substantial genetic improvement can be achieved through direct selection (Table 2). Conversely, traits like purity at 300 and 360 days (14.38% and 16.87%, respectively) and sucrose at 300 days (34.11%) exhibited low to moderate heritability, and correspondingly lower genetic advance, indicating a larger role of environmental influence or non-additive gene effects for these quality parameters (Fig. 1).

Table 2: Genetic Variability, Heritability, and Genetic Advance Estimates for Key Traits in Sugarcane Clones

No.	Trait	ECV	GCV	PCV	h ² (Broad Sense)	G.A. (5%)	GA (% of Mean)
1.	Germination%	9.204	26.984	28.5107	89.57852	12.3178	52.61129
2.	Tillers	7.138	41.782	42.38691	97.16415	71.66515	84.84086
3.	Cane length at 360 days	9.480	8.108	12.47404	42.24408	21.07263	10.85526
4.	Cane diameter at 360 days	8.693	13.560	16.10682	70.87339	0.501364	23.51583
5.	NMC at 360 days	7.661	30.252	31.20659	93.97337	23.93431	60.41131
6.	Brix at 300 days	4.597	5.635	7.272119	60.04521	1.648541	8.995112
7.	Brix at 360 days	10.394	7.631	12.89425	35.02708	1.549197	9.30395
8.	Sucrose at 300 days	5.031	3.619	6.19747	34.10879	0.688003	4.3546
9.	Sucrose at 360 days	7.638	10.036	12.61221	63.32187	2.35335	16.45175
10.	Purity at 300 days	6.754	2.768	7.299031	14.37959	1.866528	2.162116
11.	Purity at 360 days	6.555	2.954	7.190145	16.87412	2.16168	2.499344
12.	Single cane weight at 360 days	9.867	26.239	28.03267	87.61136	0.561724	50.59321
13.	CCS	11.308	34.544	36.34736	90.32097	2.854052	67.62834
14.	Cane yield	12.129	28.607	31.07211	84.76319	23.14117	54.25568

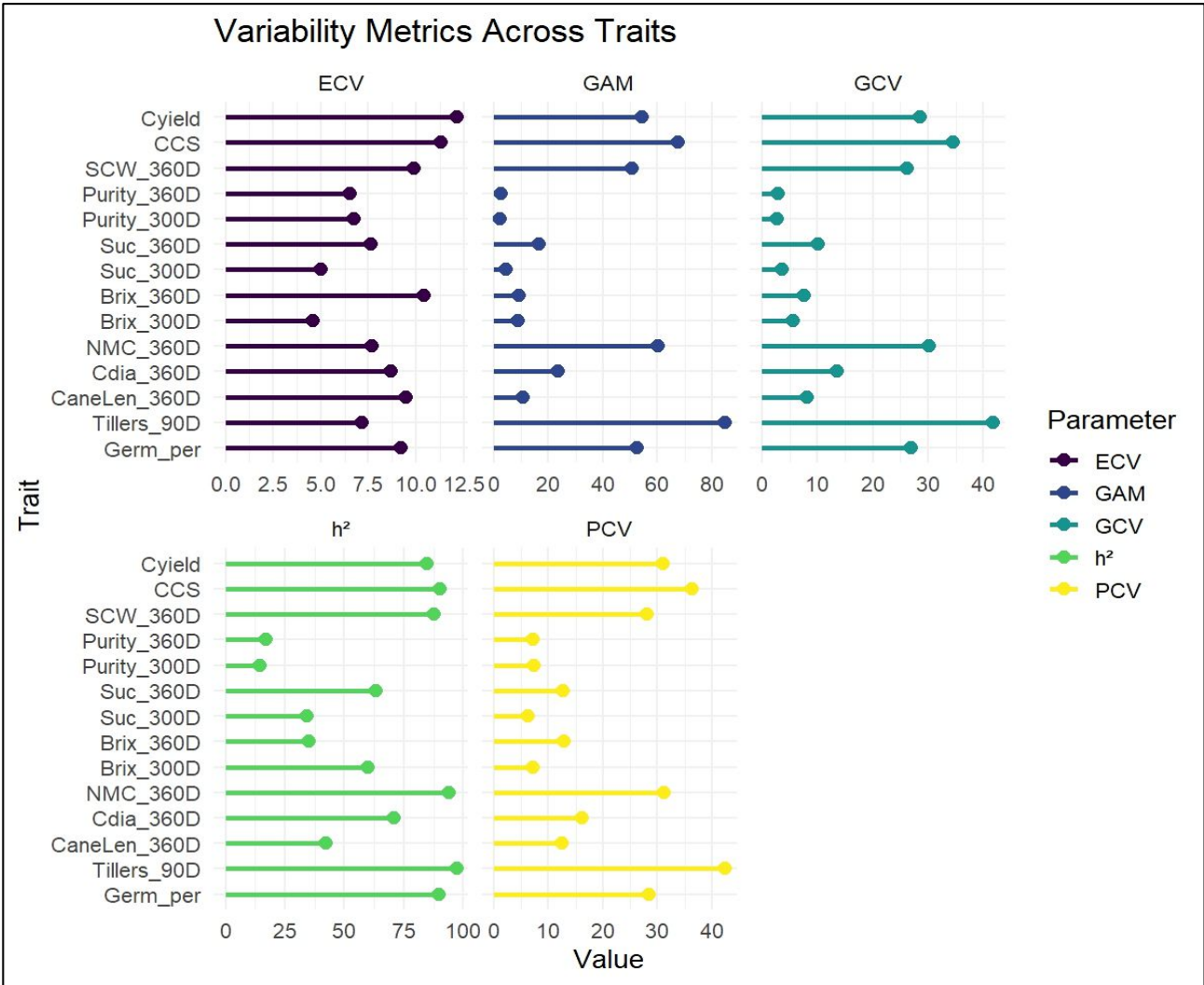


Fig 1: Distribution of Genetic Variability, Heritability, and Genetic Advance for Agronomic and Quality Traits in Sugarcane

The presence of high heritability coupled with high genetic advance for key agronomic traits such as tillers, millable cane number, cane yield, single cane weight, and CCS identifies these as ideal targets for selection in sugarcane improvement programs (Rani *et al.*, 2024; Rahman *et al.*, 2024) [17, 21]. This trend is consistent with previous studies, which demonstrate that selection pressure on such traits can result in effective genetic gain due to the predominance of additive genetic variance (Khan *et al.*, 2017; Singh *et al.*, 2020; Rahman *et al.*, 2024) [20, 23, 21]. High heritability alone, while important, may not always predict selection success;

the combination with high genetic advance is a more robust indicator that improvements in these traits can be reliably inherited by future generations (Gowda *et al.*, 2016) [24]. On the other hand, for traits such as juice purity and initial sucrose content with lower heritability and genetic advance estimates, direct phenotypic selection is expected to be less effective due to substantial environmental influence or complex genetic control. These findings reinforce long-held breeding principles that heritability estimates should always be interpreted in conjunction with genetic advance to determine the realistic prospects for crop improvement.

Conclusion

The present study revealed substantial genetic variability among the interspecific and intergeneric sugarcane clones for key agronomic and quality traits. Traits such as tiller number, CCS, cane yield, and single cane weight exhibited high heritability coupled with high genetic advance, indicating the predominance of additive gene action and their suitability for improvement through direct selection. In contrast, traits like purity and early sucrose content showed low heritability and genetic advance, reflecting greater environmental influence. These findings provide valuable insights for selecting superior genotypes and designing effective breeding strategies aimed at enhancing yield and quality in sugarcane improvement programs.

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