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Genetic parameters, trait associations for yield traits and red rot resistance in seedling and clonal stages of sugarcane

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Abstract
The present study was taken up to evaluate genetic variability for physiological traits, drought tolerance and disease resistance in seedling and clonal stages in sugarcane to identify promising genotypes for yield enhancement and stress resilience. Moderate estimates of GCV and PCV coupled with high heritability and genetic advance over mean (GAM), were recorded for NMC, single cane weight, cane volume, and cane yield, indicating the predominance of additive gene action in inheritance of these traits. Traits like green leaf number, leaf area index (LAI), brix, sucrose, purity, and cane diameter showed low to moderate variability and heritability, indicating non-additive inheritance. Meanwhile, traits such as CCS percent, shoot population (120–240 DAP), NMC at 300 DAP, single cane weight, and cane yield were influenced by both additive and non-additive gene effects, suggesting the need for combined breeding strategies. Drought tolerance assessed based on LAI and SPAD chlorophyll meter readings (SCMR), in first and second clonal stages, led to the identification of 20 drought-tolerant clones. Subsequent red rot screening under artificial inoculation revealed eight elite clones. These stress-resilient and disease-resistant genotypes represent valuable genetic resources for future varietal improvement in sugarcane breeding programs.

Keywords: Sugarcane, genetic parameters, gene action, drought tolerance, red rot resistance

INTRODUCTION

Sugarcane (*Saccharum spp.*) is one of the most economically important crops worldwide, primarily cultivated for its high sucrose content, making it the leading source of commercial sugar and an increasingly vital raw material for renewable bioenergy, including ethanol and electricity generation (Nunavath *et al.,* 2025a, b; Aswini *et al.,* 2025; Amaresh *et al.,* 2025). Understanding the heritable and non-heritable components of observed variability is fundamental for assessing the genetic control of trait expression and the phenotypic reliability required to predict breeding value (Vinu *et al.,* 2025; Pathy *et al.,* 2022). While high heritability is desirable in breeding programs, it does not always guarantee high genetic advance. Therefore, it is critical to consider both heritability and genetic advance simultaneously, as their combination provides a more reliable prediction of selection efficiency and expected genetic gains. High heritability coupled with high genetic advance is generally indicative of additive gene action, which enhances the response to selection for trait improvement (Burton and DeVane, 1953; Falconer and Mackay, 1996).

The magnitude of genetic variability within breeding materials, along with heritability estimates, offers insights into the feasibility of genetic improvement through selection. The success of genetic advance under selection depends on three key parameters: genetic variability, heritability, and selection intensity (Stevenson,1965). When traits exhibit both high heritability and high genetic advance, simple selection procedures become more effective, often reflecting the dominance of additive genetic effects. Conversely, high heritability with low genetic advance may indicate non-additive gene effects or strong environmental influences (Pathy and Mohanraj, 2021; Tabassum *et al.,* 2023). Hence, understanding the mode of inheritance and the underlying gene action of agronomic and physiological traits is crucial for developing efficient breeding strategies. Despite the economic importance and genetic complexity of sugarcane, a highly polyploid and heterozygous crop, research on the inheritance of key traits such as cane yield, sucrose content, and stress tolerance remains limited, necessitating deeper genetic studies (Selvakumar *et al.,* 2025). Rewati Chaudhary (2001) reported high heterosis along with high genetic advance for traits such as cane yield, sugar yield, internodal length, brix, sucrose, and CCS percentage, indicating the predominance of additive gene action. Similarly, Sabitha *et al.* (2009) and Anbanandan and Saravanan (2010) found that traits like shoot population, single cane weight, number of millable canes, cane yield, and sugar yield are governed by additive gene action, while cane length, cane diameter, and sucrose content are predominantly influenced by non-additive gene action. These findings highlight the stability and consistency of certain sugarcane traits across different environments, underscoring the importance of studying variability that can be effectively utilized in breeding programs (El-Hinnawy and Mersi, 2009). Evaluating genetic variation aids in the identification of compatible genotypes suited for diverse agro-climatic regions and supports effective germplasm exchange. The ultimate goal of such research is to evaluate and disseminate high-performing genotypes, which is fundamentally dependent on the presence of significant genetic variability (Dillewijn, 1952). Partitioning total phenotypic variance into its genotypic and environmental components helps in evaluating the influence of environmental factors on trait performance (Ullah *et al.,* 2012). Falconer and Mackay (1996) emphasized that heritability is more accurately estimated in closely related individuals. This parameter assists in resource optimization and improves the efficiency of selection (Smalley *et al.,* 2004). High heritability, when accompanied by high genetic advance as a percentage of the mean, reflects the reliability of phenotypic selection under field conditions (Kumar *et al.,* 2014). Correlation studies further enhance selection efficiency by identifying associations among traits (Zeeshan *et al.,* 2013), and the degree of variability and trait association can be quantified through correlation coefficients (Bocanski *et al.,* 2009). Voss-Fels *et al.* (2021) reported the involvement of both additive and non-additive gene actions in the inheritance of quantitative traits in sugarcane. Relisha Ranjan and Balwant Kumar (2017) observed high heritability coupled with high genetic advance as percent of the mean for cane yield, CCS yield, single cane weight, cane width, germination percentage, and number of shoots at 120 DAP, suggesting the effectiveness of selection. Pooja Kumari *et al.* (2020) also confirmed the predominance of additive gene action for traits like sugar yield, cane yield, germination at 45 days, cane height, single cane weight, and fibre content at harvest, indicating the potential of clonal selection in varietal improvement programs. Recent findings by Tolera *et al.* (2023) revealed a wide range of genetic variability and high heritability coupled with high genetic advance for tiller number, number of millable canes, and cane yield. Likewise, Sudheer Sharma *et al.* (2024) showed that CCS yield, number of millable canes, stalk length, stalk diameter, and single cane weight had significant positive correlations and exerted strong direct effects on cane yield at the genotypic level, as confirmed through correlation and path coefficient analysis.

Given the complex nature of sugarcane as a polyploid crop and the limited inheritance information available, the present study was undertaken to assess the genetic variability for cane yield and its contributing traits, including sugar yield and physiological attributes. The study also aims to understand the nature of gene action through genetic parameter estimation and to identify red rot-resistant genotypes at early clonal stages. Early identification and elimination of undesirable genotypes can save considerable time and resources in sugarcane breeding programs.

MATERIALS AND METHODS

The study was conducted at the Regional Agricultural Research Station (RARS), Anakapalle, during 2019–20 to 2021–22, covering seedling nursery, first clonal, and second clonal generations. The experimental material included 38 bi-parental crosses and 18 General collections (GCs). In the seedling nursery stage, 17,311 seedlings were planted in 18 blocks using an augmented randomized complete block design (ARCBD) with four standard checks—Co 6907, 87A 298 (early maturity), Co 7219, and Co 86249 (mid-late maturity). The seedlings were planted in 10 m rows at 80 × 40 cm spacing during April 2018–19. From these, 520 promising genotypes were advanced to the first clonal generation in 2019–20, planted in two rows of 2.5 m length spaced 80 cm apart alongside the same standards. Subsequently, 114 genotypes were selected based on vigour of the clump, HR brix per cent, number of canes / clump, bud size, bud shape, splits on the cane, inter nodal length, spines on the leaf sheath, leaves, stalk diameter, stalk length, hollowness of the cane, colour of the cane / stalk, for evaluation in the second clonal generation in 2020–21, which was planted in four rows of 5 m length at 80 cm spacing with the standard checks. Recommended package of practices was followed throughout the crop cycles to maintain healthy growth.

Observations were recorded on multiple agronomic and physiological traits across stages. In the seedling nursery, traits such as number of millable canes per clump, single cane weight, cane yield, cane length, cane diameter, cane volume, and Brix percentage assessed by hand refractometer (HR) were recorded. In clonal stages, observations included number of green leaves at 60 and 120 days after planting (DAP), leaf area index (LAI) at 60 and 120 DAP, shoot population at 90, 120, 180, and

240 DAP, number of millable canes at 300 DAP and at harvest, cane yield, single cane weight, cane length, cane diameter, cane volume, and juice quality parameters including Brix and sucrose percentages. Cane yield and Commercial Cane Sugar (CCS) yield was also calculated using standard protocols. In RARS Anakapalle, study of setlting & selection nurseries are under drought conditions (whenever needed – irrigation was provided. SPAD & LAI were recorded at formative (stress conditions) and grand growth stage (240 DAP) under stress conditions, enabling simultaneous selection for drought tolerance.

The number of green leaves were counted manually in five tagged canes on 60 and 120 DAP and expressed as mean per plot. LAI was estimated using the linear measurement method standardized for sugarcane, by multiplying maximum leaf length, leaf breadth, a constant factor, and the number of green leaves. SPAD chlorophyll meter readings (SCMR) were taken on the third leaf from the apex on 20 randomly selected plants per genotype during first and second clonal stages, and the mean values were used for analysis. The CCS percentage was calculated using the formula

$$CCS\% = 1.03 \times S - 0.3 \times B,$$

where S and B represent sucrose and Brix percentages, respectively (Meade and Chen, 1977; Ramiah and Varahulu, 2023). CCS yield per plot was computed by multiplying CCS percentage with cane yield per plot and dividing by 100.

Screening for red rot resistance was done in the selected 114 clones in second clonal generation adopting the plug inoculation method (Prakasam *et al.,* 1971). At seven months of crop age, ten canes per clone were inoculated at the third internode with a spore suspension containing 6×10^5 spores/mL prepared from three predominant red rot pathotypes (*Cf*419, *Cf* 671, and *Cf* 997) as per Satyanarayana *et al.* (1984). The inoculation site was sealed with plasticine, and disease assessment was done 60 days post-inoculation by recording lesion width, nodal transgression, presence of white spots, and nature of tops. Disease severity was rated on a 0–9 scale following Srinivasan and Bhat (1961).

The mean data of above observations were subjected to analysis of genotypic and phenotypic coefficients of variation (GCV and PCV) as per the method of Burton and Devane (1953) and the same were classified as suggested by Sivasubramanian and Menon (1973). Broad-sense heritability was calculated as per Hanson *et al.* (1963), while genetic advance and genetic advance as percentage of mean (GAM) were computed based on formulas from Lush (1949) and Johnson *et al.* (1955a). Genotypic and phenotypic correlations were derived following Falconer (1964). Path coefficient analysis was conducted following Wright (1921) and Dewey and Lu (1959) to determine the direct and indirect effects of traits on cane and sugar yield, with effect classifications as per Lenka and Mishra (1973). All statistical computations were performed using appropriate biometric tools in SPAR 2.0 for reliable interpretation.

RESULTS AND DISCUSSION

Genetic parameters and variability: Genetic variability forms the cornerstone of any effective selection program. The present investigation assessed a wide array of agronomic and quality traits across three sequential selection stages, namely, seedling nursery, first clonal stage, and second clonal stage in sugarcane (**Tables 1,2,3**). Analysis of variance revealed significant differences among genotypes for traits such as green leaf number, leaf area index (LAI) at 60 days after planting (DAP), shoot population at multiple growth stages (90–240 DAP), number of millable canes (NMC) at 300 DAP, single cane weight, cane length, cane volume, and sugar yield, indicating sufficient genetic variability for effective selection.

Moderate genotypic and phenotypic coefficients of variation (GCV and PCV), coupled with high heritability and genetic advance as percent of mean (GAM), were observed for NMC, single cane weight, cane volume, and cane yield. These findings suggest a predominance of additive gene action in governing these traits, making them amenable for improvement through simple selection (Sabitha and Prasada Rao, 2008; Sabitha *et al.,* 2009; Mohana Krishna *et al.,*2009; Kumar *et al.,* 2014; Feyissa *et al.,* 2014; Esayas *et al.,* 2016; Barreto *et al.,* 2021; Madhavi and Reddy, 1992). In contrast, traits like cane diameter and hand refractometer (HR) brix recorded low GCV and PCV but high heritability with low GAM, indicative of non-additive gene action (Sabitha *et al.,* 2009; Mali and Patel, 2013; Alam *et al.,* 2017; Kumar *et al.,* 2018; Japheth *et al.,* 2019; Singh *et al.,* 2001).

Moderate variability estimates for shoot population at 90 DAP, NMC, cane volume, and sugar yield reinforce the influence of additive genetic effects (Sabitha *et al.,* 2009; Rao & Rao, 2015). However, traits such as green leaf number, LAI, brix, sucrose content, purity, and cane diameter demonstrated low to moderate genetic variability, suggesting non-additive gene effects (Rahman and Bhuiyan, 2009; Gagandeep *et al.,* 2004; Alam *et al.,* 2017). Several traits, including CCS percent, shoot population (at 90–240 DAP), NMC, single cane weight, cane length, and cane diameter appeared to be governed by both additive and non-additive gene action (Singh *et al.,* 2006; Singh *et al.,* 2002; Jain *et al.,* 2001), which implies that population improvement or recurrent selection strategies could be more effective for such traits.

Correlation and Repeatability Analysis: Phenotypic correlation analysis (**Table 4**) highlighted significant and consistent positive associations of NMC, single cane weight, cane diameter, and CCS yield with cane

Table 1. Mean, range of variation and genetic parameters for cane yield and yield components in seedling nursery

S.No	Character(s)	Mean	Range		GCV (%)	PCV (%)	Heritability (h^2)	GA	GAM
			Min.	Max.					
1.	Number of canes/clump	3.72	2.00	6.13	20.33	20.69	96.47	1.53	41.13
2.	Single Cane Weight (kg)	1.20	0.87	1.69	11.52	12.04	91.55	0.27	22.70
3.	Cane Length (cm)	254	179	306	5.40	6.72	63.77	22.38	8.83
4.	Cane Diameter (cm)	2.45	2.05	3.05	5.04	5.94	72.00	0.22	8.81
5.	Cane Volume (cm^3)	4.39	2.03	7.32	19.71	21.72	83.02	1.63	37.13
6.	Cane Yield (kg)	4.32	2.00	7.80	18.50	19.05	90.76	1.54	35.63
7.	HR Brix (%)	19.60	12.00	22.24	3.17	3.85	67.53	1.05	5.36

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; GA: Genetic advance; GAM: Genetic advance as percent of mean

Table 2.Mean, range of variation and genetic parameters for cane yield and yield, sugar yield and yield components in first clonal stage (Settling Nursery)

S.No	Character(s)	Mean	Range		GCV (%)	PCV (%)	Heritability (h^2)	GA	GAM
			Min.	Max.					
1	Number of green leaves at 60 DAP	7.68	5.26	11.11	7.32	11.59	39.89	0.73	9.52
2	Number of green leaves at 120 DAP	14.31	9.82	17.52	7.05	10.00	49.70	1.46	10.21
3	Leaf Area Index at 60 DAP	1.09	0.76	1.96	9.65	13.45	51.50	0.16	14.27
4	Leaf Area Index at 120 DAP	2.12	1.63	2.99	4.75	6.92	47.26	0.14	6.73
5	Brix percent at harvest	18.98	18.06	24.46	6.95	8.59	65.47	2.20	11.59
6	Sucrose percent at harvest	16.92	10.58	22.30	9.06	10.15	79.56	2.81	16.64
7	CCS percent at harvest	12.08	7.15	16.70	10.25	11.49	79.60	2.26	18.84
8	Purity percent at harvest	89.08	73.17	99.98	3.56	4.76	55.79	4.87	5.47
9	Shoot Population at 90 DAP	117.61	70.90	194.91	10.16	13.82	54.11	18.31	15.39
10	Shoot Population at 120 DAP	167.27	89.45	241.70	9.22	12.43	55.02	23.57	14.09
11	Shoot Population at 180 DAP	138.12	87.26	214.27	9.88	13.32	55.01	21.21	15.09
12	Stalk Population at 240 DAP	123.03	91.98	195.73	9.22	11.81	60.83	18.46	14.80
13	NMC at 300 DAP	111.32	90.12	156.37	9.51	11.39	69.71	18.21	16.36
14	Single Cane Weight(kg)	1.09	0.57	1.54	10.34	11.00	88.36	0.22	20.18
15	Cane Length(cm)	262.70	197.66	338.92	10.06	11.49	76.63	47.64	18.14
16	Cane diameter(cm)	2.26	1.72	2.96	5.39	6.59	66.77	0.20	9.07
17	Cane volume (cm^3)	111.71	54.99	215.03	13.57	15.89	72.89	26.55	23.86
18	NMC/Plot(kg)	105.28	89.24	139.49	12.66	14.73	73.86	23.60	22.41
19	Cane yield(kg/plot)	115.40	48.00	184.53	8.14	9.95	89.10	21.08	18.26
20	CCS yield(kg/plot)	13.98	4.48	25.17	13.35	17.21	60.18	3.00	21.34

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; GA: Genetic advance; GAM: Genetic advance as percent of mean

yield across clonal generations. Particularly, single cane weight and NMC maintained stable and significant associations, suggesting their reliability as indirect selection indices for yield improvement.

Quality parameters like brix, sucrose, and CCS percent demonstrated positive but mostly non-significant correlations with cane yield, especially in the second clonal stage, indicating their limited but supportive roles in influencing productivity. Repeatability analysis further confirmed the stability of traits such as single cane weight and NMC across generations, reinforcing their utility in selection programs.

Table 3. Mean, range of variation and genetic parameters for cane yield, sugar yield and yield components in second cloned stage (Selection nursery)

S.No	Character(s)	Mean	Range		GCV (%)	PCV (%)	Heritability (h^2)	GA	GAM
			Min.	Max.					
1	Number of green leaves at 60 DAP	7.85	5.51	10.13	7.24	10.45	48.23	0.81	10.38
2	Number of green leaves at 120 DAP	14.32	11.63	16.23	4.89	6.90	50.18	0.15	7.13
3	Leaf Area Index at 60 DAP	1.12	0.86	1.48	8.84	12.58	49.43	0.14	12.51
4	Leaf Area Index at 120 DAP	2.15	1.79	2.71	4.72	6.58	51.45	0.15	6.97
5	Brix percent at harvest	19.89	17.89	23.51	5.72	7.52	57.86	1.80	8.96
6	Sucrose percent at harvest	17.91	15.74	21.88	5.02	6.76	55.14	1.39	7.68
7	CCS percent at harvest	12.86	11.09	16.21	8.19	9.25	78.40	1.93	14.93
8	Purity percent at harvest	90.04	80.15	99.45	3.52	4.77	54.46	4.81	5.35
9	Shoot Population at 90 DAP	134.42	71.00	232.00	17.30	18.77	85.00	42.27	32.86
10	Shoot Population at 120 DAP	187.39	126.00	292.00	12.23	14.60	70.18	38.71	21.11
11	Shoot Population at 180 DAP	160.96	105.00	252.00	13.12	15.16	74.92	36.59	23.40
12	Stalk Population at 240 DAP	143.50	103.00	218.00	9.37	11.12	71.01	22.69	16.27
13	NMC at at300 DAP	130.76	92.00	208.00	6.16	7.48	67.87	12.76	10.46
14	Single Cane Weight(kg)	1.16	0.95	1.86	8.20	8.52	92.62	0.20	16.26
15	Cane Length(cm)	246.25	180.00	321.00	8.90	10.30	74.70	40.94	15.85
16	Cane diameter(cm)	2.46	2.00	3.30	4.90	5.35	83.97	0.23	9.25
17	Cane volume (cm^3)	141.72	75.03	277.92	13.49	13.82	95.26	38.03	27.12
18	NMC/Plot(kg)	119.88	88.00	193.00	12.44	14.08	78.06	22.64	20.15
19	Cane yield(kg/plot)	138.33	94.94	223.31	8.29	9.16	81.84	20.96	15.45
20	CCS yield(kg/plot)	17.86	12.58	29.55	10.57	11.78	80.48	3.43	19.53

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; GA: Genetic advance; GAM: Genetic advance as percent of mean

Path Coefficient Analysis: Dissecting Yield Determinants: Path coefficient analysis was performed at all three selection stages to decompose correlation coefficients into direct and indirect effects (**Tables 6 and 7**). In the seedling nursery, cane volume and single cane weight had the highest direct effects (0.7097 and 0.6869, respectively) on cane yield, while cane length and diameter showed negative direct effects despite some positive indirect contributions through other traits.

In the first clonal stage, CCS percent (6.9538), brix (1.7424), and CCS yield (1.6708) had high direct effects. Though sucrose percent showed a large negative direct effect (-9.6189), its indirect influence via CCS percent and CCS yield was strongly positive, yielding a high genotypic correlation with cane yield. This underscores the complex interdependence among quality traits and their indirect role in yield formation.

In the second clonal stage, single cane weight (1.1564), sucrose percent (0.9496), and NMC (0.2849) emerged as the key direct contributors. Although CCS yield showed a small negative direct effect (-0.2381), it positively influenced cane yield through its strong indirect effects via single cane weight and sucrose percent. Brix and CCS percent exhibited negative direct effects, but their indirect paths through other components rendered positive genotypic correlations.

Overall, traits like single cane weight, CCS yield, CCS percent, and NMC consistently emerged as crucial yield determinants across all stages, making them ideal targets for selection and genetic improvement.

Physiological Traits and Drought Tolerance: Among the physiological parameters, leaf area showed a significant positive correlation with both cane yield and total dry matter accumulation (Gajera *et al.,* 1991). Canopy closure in sugarcane is typically complete by 150 DAP, after which photosynthetically active radiation interception plateaus due to mutual shading (Bull & Glasziou, 1975; Irvine, 1983). Singh and Gururaja Rao (1987) highlighted that LAI and leaf area ratio (LAR) are reliable predictors of yield, particularly during early crop growth stages.

LAI values in sugarcane range from 2 to 8, depending on genotype and environmental conditions, and continue to rise until 240 DAP (Sudama Singh and

Table 4. Estimates of phenotypic correlation coefficients between yield components and cane yield in first and second clonal generations.

Character (s)	Clonal Gene-ration	No. of green leaves 120 DAP	LAI 120 DAP	Shoot Population 120 Days	NMC/ Plot	CCS yield (kg/ plot)	Single cane weight (kg)	Cane length (cm)	Cane diameter (cm)	Brix (%)	Sucrose (%)	CCS (%)	Purity (%)	Cane yield (kg/plot)
No. of green leaves at 120 DAP	I	**1.0000**	-0.0174	0.0145	-0.0354	-0.0083	-0.0301	-0.0339	0.0263	-0.0358	0.0058	0.0203	0.0815*	-0.0400
	II		-0.1506	0.1056	0.0360	-0.0504	-0.0851	0.0582	-0.0394	-0.0883	-0.0066	0.0267	0.1951*	-0.0672
Leaf area index at 120 DAP	I		**1.0000**	0.0546	0.0720	0.1249**	0.0788	-0.0592	0.1042**	0.1095**	0.1150**	0.1112**	0.0485	0.0883*
	II			-0.1871*	0.0269	-0.0094	-0.0230	-0.0455	0.0663	-0.0503	-0.0127	0.0034	0.0892	-0.0103
Shoot population at 120 DAP	I			**1.0000**	0.3821**	0.2523**	0.2386**	-0.0348	0.2267**	0.0648	0.0556	0.0496	0.0001	0.3648**
	II				0.0132	0.1235	0.1479**	0.0760	0.1506**	0.0955	0.0373	0.0123	-0.1232	0.1405
NMC/ Plot	I				**1.0000**	0.6149**	0.3954**	0.0804*	0.2444**	0.1744**	0.1935**	0.1903**	0.0925*	0.8139**
	II					0.4066**	-0.0304	0.0986	0.0190	0.1204	0.1498**	0.1546**	0.0815*	0.4097**
CCS yield (kg/plot)	I					**1.0000**	0.8538**	0.0855*	0.4060**	0.2437**	0.2731**	0.2695**	0.1393**	0.7780**
	II						0.8985**	0.2183*	0.3734**	0.1434	0.1370	0.1276	0.0068	0.8553**
Single cane weight (kg)	I						**1.0000**	0.0502	0.4174**	0.2272**	0.2571**	0.2546**	0.1383**	0.8538**
	II							0.1854*	0.3983**	0.0934	0.0731	0.0611	-0.0307	0.8985**
Cane length (cm)	I							**1.0000**	-0.2319**	0.0939	0.1172**	0.1196**	0.0844*	0.0855*
	II								-0.0571	0.0748	0.0650	0.0575	-0.0156	0.2183**
Cane diameter (cm)	I								**1.0000**	0.1585**	0.1583**	0.1501**	0.0464	0.4060**
	II									0.0756	0.0373	0.0202	-0.0742	0.3734**
Brix (%)	I									**1.0000**	0.8910**	0.8064**	0.1123**	0.2437**
	II										0.9122**	0.8323**	-0.0548	0.1434
Sucrose (%)	I										**1.0000**	0.9870**	0.5480**	0.2731**
	II											0.9863**	0.3579**	0.1370
CCS (%)	I											**1.0000**	0.6753**	0.2695**
	II												0.5064**	0.1276
Purity (%)	I												**1.0000**	0.1393**
	II													0.0068
Cane Yield (kg/Plot)	I													**1.0000**
	II													

* and ** indicate significance at 5% and 1% level, respectively

Table 5.Correlation of yield components with cane yield in three generations (seedling, first and second clonal stages)

S. No	Character		Single cane weight (kg)	Cane length (cm)	Cane diameter (cm)	NMC	Cane yield (kg)
1	Single cane weight (kg)	C_0	1.0000	0.04289**	0.3670**	-0.4825**	0.2426**
		C_1		0.0502	0.4174**	0.3954**	0.8538**
		C_2		0.1854*	0.3983**	-0.0304	0.8985**
2	Cane length (cm)	C_0		1.0000	-0.0359	-0.1694	-0.0039
		C_1			-0.2319**	0.0804*	0.0855**
		C_2			-0.0571	0.0986	0.2183**
3	Cane diameter (cm)	C_0			1.0000	-0.1694	0.0041
		C_1				0.2444**	0.4060**
		C_2				0.0190	0.3734**
4	Number of millable canes	C_0				1.0000	0.8265**
		C_1					0.8139**
		C_2					0.4097**
5	Cane yield (kg)	C_0					1.0000
		C_1					
		C_2					

* and ** indicate significance at 5% and 1% level, respectively

Venkataramana, 1987). Drought stress, especially during the early season from December to April, is a major constraint to yield (Ishaq and Olaoye, 2009; Cha-Um *et al.,* 2012; Khonghintaisong *et al.,* 2018). In this context, SPAD chlorophyll meter readings (SCMR) serve as a proxy for chlorophyll content and photosynthetic efficiency. Higher SCMR values are indicative of superior nitrogen content and drought tolerance (Reddy *et al.,* 2003; Sudhakar *et al.,* 2006; Songsri *et al.,* 2009; Painawadee *et al.,* 2009). Raja Rajeswari *et al.* (2009) and Mukundarao *et al.* (2011) found high SCMR values at 60–150 DAP in rainfed sugarcane to be associated with moisture stress resilience.

Although some reports suggest limited correlation between physiological traits and cane yield during drought

Table 6.Direct and indirect effects of yield components on cane yield at genotypic level infirst clonal stage

Character(s)	No. of green leaves 120 DAP	Leaf area index at 120 DAP	Shoot Population 120 Days	NMC/ Plot	CCS Yield (kg/ plot)	Single cane weight (kg)	Cane length (cm)	Cane diameter (cm)	Brix (%)	Sucrose (%)	CCS (%)	Purity (%)	r' with cane yield
No. of green leaves 120 DAP	**-0.0285**	0.0134	-0.0330	0.0303	0.1329	0.0132	-0.0001	0.0008	-0.0059	0.1731	-0.1536	0.0091	0.1517
Leaf area index at 120 DAP	-0.0085	**0.0449**	-0.0083	0.0129	-0.2118	-0.0326	0.0259	-0.0079	0.2452	-0.3336	-0.0004	0.0527	0.2216
Shoot population at 120 DAP	-0.0134	0.0053	**-0.0703**	0.2099	0.7338	0.0294	0.0121	-0.0254	0.1444	-1.1818	0.9264	-0.0401	0.7302
NMC/ Plot	-0.0030	0.0020	-0.0505	**0.2922**	1.3661	0.0554	-0.0281	-0.0266	0.7387	-3.6562	2.4936	-0.0443	0.8890
CCS yield (kg/plot)	-0.0023	-0.0057	-0.0309	0.2389	**1.6708**	0.0187	-0.0032	-0.0257	1.5556	-8.8177	6.3089	-0.1958	0.7918
Single cane weight (kg)	0.0103	0.0402	0.0567	0.4437	-0.8593	**0.0364**	-0.0846	0.0600	-1.0265	4.2685	-2.7102	-0.0022	0.9273
Cane length (cm)	0.0000	-0.0160	0.0117	0.1137	0.0744	0.0426	**-0.0723**	0.0163	-0.0432	-0.6240	0.6371	-0.0714	0.4163
Cane diameter (cm)	0.0004	0.0053	-0.0268	0.1166	0.6429	0.0328	0.0177	**-0.0667**	0.2553	-1.6194	1.2013	-0.0395	0.5198
Brix (%)	0.0001	0.0063	-0.0058	0.1239	1.4918	0.0215	0.0018	-0.0098	**1.7424**	-9.1922	6.4216	-0.1518	0.4497
Sucrose (%)	0.0005	0.0016	-0.0086	0.1111	1.5317	0.0162	-0.0047	-0.0112	1.6651	**-9.6189**	6.9226	-0.2247	0.3806
CCS (%)	0.0006	0.0000	-0.0094	0.1048	1.5159	0.0142	-0.0066	-0.0115	1.6090	-9.5758	**6.9538**	-0.2438	0.3512
Purity (%)	0.0008	-0.0076	-0.0091	0.0418	1.0559	-0.0003	-0.0167	-0.0085	0.8535	-6.9772	5.4724	**-0.3098**	0.2953

Residual Effect = 0.1217

Bold and diagonal values indicate direct effects

Table 7.Direct and indirect effects of yield components on cane yield at genotypic level in second clonal stage

Character(s)	No. of green leaves 120 DAP	Leaf area index at 120 DAP	Shoot Population 120 Days	NMC/ Plot	CCS Yield (kg/ plot)	Single cane weight (kg)	Cane length (cm)	Cane diameter (cm)	Brix (%)	Sucrose (%)	CCS (%)	Purity (%)	r' with cane yield
No. of green leaves 120 DAP	**-0.0324**	0.0165	0.0169	-0.2922	-0.0670	0.4989	0.0011	-0.0014	0.0619	0.1694	-0.2209	0.0033	0.1541
Leaf area index at 120 DAP	-0.0136	**0.0393**	0.0046	-0.0332	0.0991	-0.2441	-0.0024	-0.0015	0.0458	-0.5082	0.3799	-0.0020	-0.2364
Shoot population at 120 DAP	0.0405	-0.0132	**-0.0135**	0.0813	-0.0573	0.2352	0.0021	-0.0014	0.0116	0.0237	-0.0354	0.0005	0.2741
NMC/ plot	0.0333	-0.0046	-0.0039	**0.2849**	-0.1223	0.1122	0.0183	0.0009	-0.1628	0.7764	-0.4655	0.0005	0.4414
CCSyield (kg/plot)	-0.0091	-0.0164	-0.0033	0.1464	**-0.2381**	0.8884	0.0105	-0.0036	0.1488	0.6606	-0.3828	-0.0001	0.9037
Single cane weight (kg)	-0.0140	-0.0083	-0.0028	0.0276	0.1829	**1.1564**	0.0085	-0.0038	0.0316	0.0760	-0.0259	-0.0004	0.9435
Cane length (cm)	-0.0011	-0.0029	-0.0009	0.1617	-0.0774	0.3040	**0.0323**	-0.0010	0.0127	0.0044	0.0129	-0.0003	0.4191
Cane diameter (cm)	-0.0050	0.0066	-0.0021	0.0280	0.0984	0.5076	0.0036	**-0.0088**	0.0216	0.1393	-0.0933	0.0003	0.4562
Brix (%)	0.0156	-0.0139	0.0012	0.3592	-0.2743	0.2826	0.0032	-0.0015	**-0.1291**	1.2886	-0.9478	0.0045	0.5882
Sucrose (%)	-0.0058	-0.0210	-0.0003	0.2329	-0.1656	0.0926	0.0002	-0.0013	-0.1752	**0.9496**	-0.5985	0.0009	0.3084
CCS (%)	-0.0124	-0.0257	-0.0008	0.2286	-0.1571	0.0516	-0.0007	-0.0014	-0.2110	0.9799	**-0.5801**	0.0000	0.2710
Purity (%)	0.0300	0.0228	0.0019	-0.0364	-0.0079	0.1466	0.0030	0.0006	0.1655	-0.2376	-0.0018	**-0.0035**	0.0831

Residual Effect = 0.0655
Bold and diagonal values indicates direct effects

(Songsri *et al.,* 2019), in the present study, evaluation of clones in the first and second clonal stages using LAI and SCMR values led to the identification of promising drought-tolerant clones: 2018A15, 2018A65, 2018A73, 2018A113, 2018A117, 2018A120, 2018A124, 2018A170, 2018A171, 2018A187, 2018A221, 2018A232, 2018A236, 2018A245, 2018A355, 2018A359, 2018A458, 2018A466, 2018A470, and 2018A477 (**Table 8**).

Red Rot Resistance and Pathological Screening: Red rot, caused by *Colletotrichum falcatum*, remains one of the most destructive diseases in Indian sugarcane, with yield losses ranging from 18–31% (Sharma and Tamta, 2019). Although resistant varieties have reduced its incidence, the development of high-yielding, resistant genotypes continues to be constrained by sugarcane's polyploidy and heterozygosity. Efficient screening methods like the plug method have facilitated the identification of resistant clones such as 83R23 (Vijaya, 2000), Co 86249 (Mohan and Sangeetha, 2009), and 2000A225 (Charumathi *et al.,* 2011).

In the present study, screening of second clonal stage clones under artificial inoculation identified elite genotypes—2018A15, 2018A73, 2018A113, 2018A124, 2018A171, 2018A234, 2018A236, and 2018A465—as resistant to three predominant red rot pathotypes: Cf 419, Cf 671, and Cf 997 (**Table 9**). This reinforces their potential as donors in resistance breeding programs. Bharti *et al.* (2024) also demonstrated that only a small fraction of over 4900 genotypes showed moderate resistance, underlining the urgency of integrating red rot resistance into elite genotypes.

Breeding Implications: The characters NMC at harvest, sugar yield, and cane volume, being predominantly governed by additive gene action, can be improved effectively through simple phenotypic selection. Traits such as number of green leaves, LAI, brix, sucrose, purity, and cane diameter—under non-additive gene influence—may require population improvement strategies. Traits such as CCS percent, shoot population at various stages, NMC at 300 DAP, single cane weight, cane length, and cane diameter are best tackled using recurrent selection to exploit both additive and non-additive effects.

Despite significant advancements, cane yield at both state and national levels has reached a plateau, partially due to the exploitation of a narrow genetic base in current breeding programs. The present study highlights the limited variability for several traits, emphasizing the urgent need to broaden the genetic base. Reintroducing wild and species clones—as in the earlier phases of sugarcane improvement—offers a promising strategy to enhance variability. Physiological and pathological screening further enabled the identification of resilient clones with both drought tolerance and red rot resistance. These elite clones, including 2018A15, 2018A73, 2018A113, 2018A124, 2018A171, 2018A234, 2018A236, and 2018A465, hold promise for developing climate-resilient, disease-resistant, and high-yielding sugarcane varieties**.**

Table 8. Promising clones with tolerance to drought at 120 DAP identified in the study.

S.No.	Genotype	LAI	SCMR	Genotype	LAI	SCMR
1	2018A15	2.22	52.60	2018A15	2.20	54.60
2	2018A62	2.23	55.20	2018A65	2.08	51.00
3	2018A74	2.06	52.00	2018A73	2.10	50.4
4	2018A75	2.24	54.70	2018A113	2.12	52.00
5	2018A101	2.18	52.90	2018A117	2.08	50.60
6	2018A113	2.13	50.10	2018A120	2.13	51.00
7	2018A120	2.01	52.00	2018A124	2.18	50.60
8	2018A142	2.33	58.60	2018A170	2.08	50.50
9	2018A164	2.12	54.90	2018A171	2.15	51.50
10	2018A171	2.11	51.70	2018A187	2.02	51.30
11	2018A187	2.01	51.00	2018A221	2.63	52.50
12	2018A190	2.22	55.90	2018A232	2.10	50.04
13	2018A208	2.03	54.00	2018A236	2.28	50.60
14	2018A221	2.13	50.02	2018A245	2.14	50.10
15	2018A232	2.08	50.02	2018A355	2.26	51.00
19	2018A234	2.18	50.60	2018A359	2.08	50.80
17	2018A287	1.96	56.90	2018A458	2.14	50.02
18	2018A387	2.10	52.30	2018A465	2.26	50.10
19	2018A465	2.27	50.18	2018A470	2.03	53.80
20	2018A470	2.07	53.00	2018A477	2.22	53.00

Table 9. Promising clones with Resistance to red rot identified in the study.

Red rot reaction	Genotypes
Resistant (0-2.0) (27)	2018A7, 2018A15, 2018A73, 2018A98, 2018A105, 2018A110, 2018A113, 2018A121, 2018A124, 2018A154, 2018A159, 2018A170, 2018A171, 2018A191, 2018A221, 2018A234, 2018A236, 2018A241, 2018A245, 2018A319, 2018A355, 2018A356, 2018A377, 2018A404, 2018A445, 2018A465 and 87A298
Moderately resistant (2.1 – 4.0) (22)	2018A9, 2018A104, 2018A112, 2018A160, 2018A187, 2018A195, 2018A223, 2018A225, 2018A226, 2018A231, 2018A263, 2018A272, 2018A312, 2018A357, 2018A366, 2018A368, 2018A380, 2018A440, 2018A447, 2018A453, 2018A471 and Co 86249
Moderately susceptible (4.1 – 6.0) (19)	2018A20, 2018A50, 2018A94, 2018A183, 2018A257, 2018A280, 2018A304, 2018A325, 2018A337, 2018A383, 2018A387, 2018A418, 2018A419, 2018A427, 2018A444, 2018A452, 2018A458, 2018A460 and 2018A470
Susceptible (6.1 – 8.0) (27)	2018A28, 2018A32, 2018A33, 2018A42, 2018A65, 2018A66, 2018A77, 2018A87, 2018A111, 2018A120, 2018A148, 2018A232, 2018A274, 2018A314, 2018A317, 2018A349, 2018A359, 2018A365, 2018A395, 2018A431, 2018A450, 2018A466, 2018A473, 2018A477, 2018A510, Co 6907 and Co 7219
Highly susceptible (>8.0) (23)	2018A02, 2018A12, 2018A23, 2018A40, 2018A41, 2018A52, 2018A74, 2018A84, 2018A103, 2018A117, 2018A125, 2018A177, 2018A179, 2018A182, 2018A188, 2018A213, 2018A246, 2018A269, 2018A342, 2018A353, 2018A376, 2018A420 and 2018A446

The present study revealed significant genetic variability for yield, physiological, and disease resistance traits in sugarcane across seedling and clonal selection stages. Traits such as number of millable canes, single cane weight, cane volume, and cane yield exhibited moderate GCV and PCV along with high heritability and genetic advance, suggesting the predominance of additive gene action, thereby enabling effective selection. Conversely, traits like cane diameter, cane length, and brix showed lower genetic variability and genetic advance, indicating the role of non-additive gene action. The identification of promising drought-tolerant clones based on LAI and SCMR values, and red rot-resistant genotypes against predominant pathotypes under artificial inoculation, highlights the potential of integrating physiological and pathological screening with selection strategies. The elite clones identified (e.g., 2018A15, 2018A73, 2018A113, 2018A124, 2018A171, and 2018A236) can serve as valuable genetic resources for developing climate-resilient and disease-resistant sugarcane varieties through targeted breeding efforts.

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