



Genetic Variability and Heritability among Sugarcane Genotypes in Plant Crop for Some Agronomic Traits under Tropical Dry Climate of Ferké, Ivory Coast

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Authors' contributions

This work was carried out by both authors in collaboration. Author MYB designed the study, wrote the protocol and performed the statistical analysis. Author CBP wrote the first draft of manuscript, managed analyses of study and literature searches. Both authors read and approved the final manuscript.

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ABSTRACT

Aims: The study aimed to determine the best performing cane genotypes among 29 clones tested under sprinkler irrigation, in comparison with a check variety (R579).

Study Design: The experimental design used was a randomized complete block (RCB) with 30 cane genotypes in three replications. Every plot consisted of two dual rows of five meters with 0.5 and 1.90 m of inter-row spacing, i.e. 19 m² per plot and about 600 m² for the whole experiment.

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Place and Duration of Study: It was carried out on a commercial sugarcane plantation of Ferké 2 located in the northern part of the country, over 10 months as a late season crop from late May 2018 to late March 2019.

Methodology: Over each micro-plot, data were collected at harvest from both dual rows consisted of millable stalk number/ha, cane yield, juice quality traits (sucrose, purity, and recoverable sucrose), fiber content, and damaged internodes by stem borer *Eldana saccharina*.

Results: Based on sugar yields, seven cane genotypes were equivalent to the check variety R579 which gave 17.6 t/ha. Their yield performances ranged from 12.2 to 15.4 t of sugar/ha and from 134.2 to 160.8 t of cane/ha compared to 176.0 t/ha for the check. Higher heritability values ranging from 52 to 85% were observed in traits like sugar yield, juice purity, juice sucrose, recoverable sucrose, sucrose percent, fiber content and stem borer infestations. Differences between PCV and GCV for most traits were small, indicating high prospects for genetic progress through selection under conditions of this study.

Conclusions: Findings obtained need to be confirmed over the 2019-20 cropping season in first ratoon crop to determine promising cane genotypes for the advanced selection stage.

Keywords: Phenotypic correlation; genotypic correlation; coefficient of variation; genetic advance; yield trait; juice quality.

1. INTRODUCTION

Sugarcane is a C4 plant grown in tropical and subtropical regions of the world as an important cash crop which contributes to approximately 80% of the world sugar production, greatly exceeding sugar beet as another source of sugar [1]. In addition to being a source of sugar, sugarcane is an important bioenergy crop, with an energy ratio of ethanol production five times higher than that of maize [2-3]. It is considered by the US Environmental Protection Agency as a feedstock for production of advanced biofuel due to its superior contribution to reduce the life cycle greenhouse gas production in the fight against global warming and climate change [4]. In 2003, the FAO estimated that sugarcane had a worldwide gross production value of \$81.5 billion [5]. It was grown on about 27.1 million ha with a world harvest of 1.9 billion metric tons, higher than maize (1.0 billion t), rice (741.0 million t) and wheat (729 million t) [6]. Sugarcane is ranked third in quantity of plant calories in the human diet [7]. As a result of its very high biomass production, well-established farming, harvesting and processing technologies, sugarcane is a leading candidate for bioenergy production and a feedstock for bio-refineries. However, productivity improvements in sugarcane have been negligible in the past three decades, and production statistics are reflecting decreased yields globally [6]. In all cases, increased sugarcane production is linked to expansion of land surface rather than to increases in yield [8].

Breeding superior commercial cultivars is crucial for maintaining sugarcane production, which will benefit from research in sugarcane genome

sequencing and genetic mapping. These research areas focused on understanding sugarcane's genome structure, organization and inheritance patterns. They also help in understanding genetic variations within sugarcane populations or germplasms that control important agronomic traits [9].

Usually, the ultimate objective of sugarcane breeding programs is to release varieties which improve the profitability of the sugar industry being targeted. That is why breeders need to determine the optimal weightings that should be applied to each trait being selected for. A first step towards this involves identifying all traits influencing industry stakeholders and determining the relative economic value of variation in each trait, preferably in quantitative terms [10]. As industries change, the economic value of traits may change. In recent decades, weightings of some traits have changed in response to developments such as the introduction of mechanical harvesting, increased use of sugarcane for energy production and change in agronomic practices. In all sugarcane breeding programs worldwide, the key targeted traits are resistance to important local diseases and pests, commercially extractable sucrose content, cane yield, acceptable fiber content and ratooning performance. In some programs, other traits affecting costs of harvesting or crop management are of importance.

Sugarcane varieties tend to run out or decline after some years of cultivation in a specific area [11]. To obtain high yield on a sustainable basis, it has been essential to substitute varieties regularly grown with new clones. Sugarcane

varieties are clonally propagated and therefore are not expected to undergo genetic changes as it may occur in a seed propagated crop except for the variety decline over several ratoons due to disease incidence and other environmental constraints with therefore a need for replacement [12].

The objective of study was to evaluate, in pre-advanced selection stage, the variability of thirty sugarcane genotypes through heritability, genetic gain and genetic variations of some yield and juice quality traits.

2. MATERIALS AND METHODS

2.1 Site Characteristics

The study was carried out on Ferké 2 sugarcane field R3-002 sprinkler irrigated with center pivot, in northern Ivory Coast (9°20' – 9°60' N, 5°22' – 5°40' O, 325 m). The prevailing climate is tropical dry with two seasons: One, starting from November to April, is dry and the other, from May to October, is wet. The dry season is marked by the boreal trade wind which blows over mid-November to late January. The rainfall pattern is unimodal and centered on August and September which total amount of rainfall reaches almost half of the average annual rainfall (1200 mm) with an average daily temperature of 27°C. Average maximum and minimum daily air temperatures are 32.5 and 21°C, respectively. To meet sugarcane crop water requirements, the total amount of irrigation water required reaches 700 mm/year [13-15]. Both Ferké sugar mill plantations cover around 15 500 ha with 10 000 ha under irrigation and 3 500 ha of rainfed village plantations, lie mainly on shallow or moderately deep soils built up on granites. Main soil units encountered are ferralsols and temporally waterlogged soils in valley bottoms of Bandama and Lokpoho river basins with a sandy-clay texture.

2.2 Cane Genotypes Used

All 29 cane genotypes tested, of Reunion and Ivory Coast origin (RCI), derived from about 8,000 true seeds of 60 different families (or crosses) provided by Sugarcane Development Centre of Reunion Island (eRcane) in November 2014 and sowed late December 2014. They were pre-selected within families over a period of three years involving three consecutive steps starting from one seedling to one stool of tillers and one line of 3 m length per genotype without

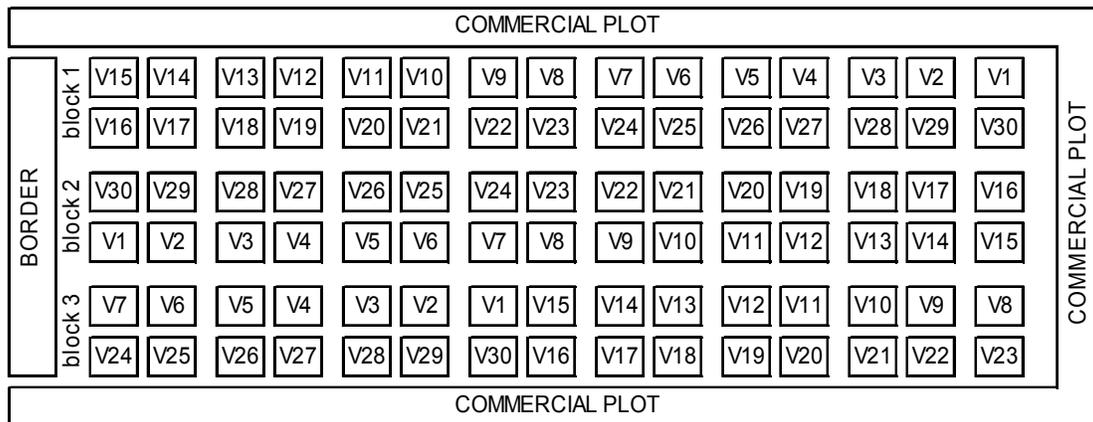
replication. During this process, the genotypes used were pre-selected following ratings based on hybrid vigor, tillering ability, ratooning performance and tolerance to endemic diseases like smut, leaf scald, pokkah boeng and sugarcane streak mosaic (SCSM). Parents of genotypes investigated, as complex polyploids, were commercial varieties of different origins. The heterozygous and polyploidy nature of sugarcane has resulted in generations of greater genetic variability. Knowledge on the nature and the magnitude of variability present in the genetic material is therefore of prime importance for breeders to conduct an effective selection program. Coefficients of variation along with heritability as well as genetic advance are very essential to improve any trait of sugarcane because this would help in knowing whether or not the desired objective can be achieved from the material to be investigated [16].

2.3 Experimental Design

The experiment was carried out, as late-season trial, from late May 2018 to late March 2019 in plant cane following a randomized complete block design (RCBD) with 30 different genotypes, including the check variety R579, in 3 replicates. A plot comprised 2 dual rows of 5 m long with narrow and wide spacings of 0.50 m and 1.90 m (Fig. 1). Field managements in terms of sprinkler irrigation, fertilizer and herbicide applications were done according to usual practices in commercial plantations. Total amount of water recorded over crop cycle from rainfall and irrigation gave 1250 mm with around 450 mm irrigation applied. To prevent heavy infestations of stem borer and delay to maturity in plant cane grown under newly cleared soil conditions from a forest landscape, a moderate rate of 312 kg/ha of NKP fertilizer (16-8.5-23) was applied mechanically instead of 650 kg/ha used routinely. Pre-emergence chemical weeding based on pendimethalin combined with clorimuron-ethyl (3.5 l/ha) was achieved mechanically two day after planting.

2.4 Agronomic Traits Investigated

Data were collected at harvest from both dual rows for millable stalk number/ha, cane yield, juice quality traits (sucrose, purity, and recoverable sucrose), fiber content, and damaged internodes by stem borer *Eldana saccharina*.



List of treatments (Genotypes)

Trt	Genotypes								
V1	R579	V7	RCI14/18	V13	RCI13/117	V19	RCI13/123	V25	RCI14/130
V2	RCI14/11	V8	RCI12/19	V14	RCI13/118	V20	RCI13/124	V26	RCI14/131
V3	RCI13/12	V9	RCI11/113	V15	RCI13/119	V21	RCI13/125	V27	RCI14/132
V4	RCI14/14	V10	RCI11/114	V16	RCI13/120	V22	RCI13/126	V28	RCI10/133
V5	RCI12/15	V11	RCI11/115	V17	RCI13/121	V23	RCI14/127	V29	RCI13/136
V6	RCI13/17	V12	RCI13/116	V18	RCI13/122	V24	RCI14/129	V30	RCI13/137

Fig. 1. Experimental layout and list of cane genotypes used

Table 1. Analysis of variance calculations regarding a RCBD

Source of variation	Degree of freedom	Mean square	Expected mean square
Replication	r-1	MSr	$\sigma_e^2 + g\sigma_r^2$
Genotypes	g-1	MSg	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1)(g-1)	MSe	σ_e^2

R: number of replicates; g= number of genotypes; MSr mean square due to replicates; MSg= mean square due to genotypes; MSe mean square of error; σ_g^2 , σ_r^2 , and σ_e^2 stand for variances due to genotypes, replicates and error respectively

At harvest, burned cane fresh production of both dual rows of each plot was weighed separately to determine crop yield. Moreover, 50 millable stalks were randomly chosen within every plot and split longitudinally with a machete in order to determine the percentage of bored or attacked internode and cane (%BIN, %BC) by stem borer.

Thirty millable cane stalks were sampled per plot for sucrose analyses in the laboratory. Prior to sample grinding operations in the laboratory for sucrose analyses, every stalk was cut into 3 pieces of almost equal length while separating them in basal, median and top parts. This allowed to randomly reconstitute 3 batches of 10 stalks for a better homogenization of the initial field sample by permutation of the pieces so that each reconstituted stalk was composed of parts coming from 3 different cane stalks. Eventually,

only one batch of 10 reconstituted stalks over 30 (1/3 of initial sample) were ground for a series of sucrose analyses to determine the sucrose content (Pol%C), fiber content (Fiber %C), juice purity (Purity %C) and recoverable sucrose (SE%C). Equipment used comprised a Jefco cutter grinder, a hydraulic press (Pinette Emideceau), a digital refractometer BS-RFM742 and a digital polari-meter SH-M100. Methods used in the determination of required technological parameters were reported by Hoarau [17]. The recoverable sucrose was calculated as follows [18-19]:

$$SE \%C = [(0.84 \times Pol\%C) (1.6 -60/Purity) - (0.05 \times Fib \%C)] \text{ with:}$$

$$Purity \%C = (Pol \text{ juice}/Brix) \times 100 \text{ and } Pol \text{ juice} = Pol \text{ factor} \times Pol \text{ read.}$$

Pol%C = Factor n x Pol juice

Factor pol depending on brix value (amount of soluble dry matter in juice measured with a refractometer) is provided by Schmidt table relative to a polarimeter for 26 g of glucose. The fiber content and factor n were provided by a table depending on the weight of fiber cake obtained after pressing 500 g of cane pulp resulting from the grinding operation of every sample of cane stalks.

2.5 Phenotypic and Genotypic Coefficients of Variation, Heritability and Genetic Advance

The phenotypic and genotypic variances for each trait were estimated from the RCBD analysis of variance (Table 1). The expected mean squares under the assumption of random effects model was computed from linear combinations of mean squares were determined as follows (Burton and Davane [20], cited by Shitahum et al. [21]:

$$\text{Genotypic variance } (\sigma_g^2) = (MS_g - MS_e)/r$$

$$\text{Environmental variance } (\sigma_e^2) = MS_e$$

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where MS_g and MS_e are mean sum of squares for genotypes and error in the analysis of variance, respectively, and r the number of replicates.

Genotypic and phenotypic coefficients of variation (GCV, PCV) were computed as follows [22]:

$$\text{GCV} = \sigma_g \times 100 / \text{grand mean}$$

$$\text{PCV} = \sigma_p \times 100 / \text{grand mean}$$

$$\text{Broad sense heritability } h^2 = 100 \times \sigma_g^2 / \sigma_p^2$$

Genetic advance (GA) and genetic advance as percent mean (GAM): $GA = k \times h^2 \times \sigma_p$ and $GAM = 100 \times GA/X$

With k: standard selection differential at 5 % selection intensity (k = 2.063) and X: grand mean of trait X.

Phenotypic and genotypic correlation coefficients r_p and r_g between particular pairs of traits A and B are defined as [23]:

$$r_p = \text{Cov}_p(A,B) / (\sigma_{pA} \times \sigma_{pB})$$

$$r_g = \text{Cov}_g(A,B) / (\sigma_{gA} \times \sigma_{gB})$$

where Cov_p and Cov_g are phenotypic and genotypic covariances, respectively.

Phenotypic correlations between traits were determined following the Pearson correlation coefficient calculated from means of observed traits for each cane genotype [24].

Genetic improvement in cane and sugar yields may be achieved by targeting traits closely associated to them. A number of attributes have been proposed as indirect selection criteria for genetic improvement of yields in plant breeding programs [25-26]. Heritability represents the relative importance of genetic and environment factors in the expression of phenotypic and genotypic differences among genotypes within a population [27-29]. Consequently, the knowledge of heritability related to important traits and the correlations among them are key issues to determine the best selection strategy [30-31]. Genotypic coefficient of variation (GCV) is another measure of relative genetic variation of a trait within a population [32]. Chaudhary [33] reported high GCV for single stalk weight and millable cane number per unit area. Genotype x environment interactions (GxE) are a serious concern in breeding programs as they affect selection decisions. When a rank of a genotype changes across environments, it requires evaluation of genotypes across environments to determine their real value [34]. Studies in various sugarcane breeding programs have reported significant GxE interactions for cane and sugar yields [35-36].

2.6 Statistical Analyses

The quantitative data recorded in this study were subjected to the analysis of variance using statistical procedures described by Gomez and Gomez [37] and reported by Shitahum et al [38] with the assistance of R software package version 3.5.1 (Table 1). Differences between means of treatments were determined from Duncan test.

3. RESULTS AND DISCUSSION

3.1 Phenotypic Correlations between Pairs of Agronomic Traits

All yield and juice quality traits were negatively correlated with stem borer infestations except for fiber content (Table 2) in line of findings reported by different authors [39-41]. This shows that in stem borer infestations tended to increase fiber content of cane stalks. Fiber content was negatively correlated with cane and sugar yields

as well as juice quality traits like juice sucrose, purity, sucrose percent and recoverable sucrose with coefficients ranging from -0.08 to -0.52. Therefore, a selection based on fiber content could be detrimental to sugarcane yields and juice quality. In contrast, all juice quality traits were positively and quite highly correlated, with coefficients ranging from 0.91 to 0.99. All traits were positively correlated, although loosely regarding juice quality traits, with millable stalk number and coefficients ranged from 0.00 to 0.21. As expected, lower correlations were obtained between juice quality traits and cane yield as well as fiber content, with coefficients ranging from 0.08 to 0.22 in absolute values. Much higher correlation coefficients were expected between stalk number and yields traits, instead of 0.21 and 0.15 values, probably due to late-season plant cane cultivated late May in line of land clearing and preparation delay. High and positive correlation coefficients were recorded between sugar yield and cane yield as well as juice quality traits like juice sucrose, purity, sucrose percent and recoverable, with coefficients ranging from 0.73 to 0.82.

3.2 Genotypic Correlations within Agronomic Traits

Similarly to phenotypic correlations, all yield and juice quality traits were genotypically correlated negatively with stem borer infestations except for fiber content (Table 2), with coefficients ranging from -0.12 to -0.39. Except for millable stalk number and stem borer infestations, fiber content was negatively correlated with all traits investigated, namely yield and juice quality traits, with values ranging from -0.07 to -0.26. Except for cane yield ($r_g = -0.53$), all traits were positively correlated to millable stalk number with coefficient equals to 0.01 for sugar yield and ranging from 0.39 to 0.75 regarding traits like sucrose juice, sucrose percent, recoverable sucrose and fiber content. Much stronger genotypic correlations between millable stalk number and juice quality traits (sucrose content, purity, juice sucrose and recoverable sucrose) were recorded with values ranging from 0.60 to 0.75. This suggests that phenotypic expression of clones investigated in terms of millable stalk number and juice quality traits might be more influenced by the genotype rather than the environment. As reported by several authors [29, 42], such strong and positive genotypic correlations indicate that selection based on millable stalk number could lead to improvement in juice quality traits. In contrast, loose

correlations were observed between yield traits (0.12) on the one hand, and between each yield trait and juice quality traits with coefficients varying from 0.01 to 0.22, much lower values being recorded with cane yield in this regard ($r_g = 0.01$ to 0.04).

3.3 Performance of Cane Genotypes Tested

Except for stalk number/ha, highly significant differences ($P < 0.01$) within genotypes were observed for all agronomic traits investigated (Tables 3a,b,c and 4). Based on sugar yields, seven genotypes were equivalent to the check variety R579 which gave 17.6 t/ha. These genotypes which performances ranged from 12.2 to 15.4 t/ha were the following: RC114/11, RC113/136, RC114/132, RC112/19, RC110/133, RC113/122 and RC113/126. Their cane yield performances ranged from 134.2 to 160.8 t/ha compared to 176 t/ha for the check. Although a relatively high level of stem borer infestation recorded with 14% on average (almost three times the tolerable threshold value of 5%), reasonable data of sucrose percent obtained with some of the promising genotypes ranged from 13.8 to 14.7%, compared with 14.1% for the check. This suggests that higher juice quality traits might be recorded in the context of limited stem borer damage levels ($\leq 5\%$). High stem borer infestation observed might be due to excess of soil nitrogen in plant cane resulting from application of 50 kgN/ha under newly land cleared conditions with higher organic matter content ($> 2\%$), as reported by different authors [18,43-46].

3.4 Phenotypic, Genotypic and Environmental Variance

Regardless the trait considered, phenotypic variance data obtained were higher than those of genotypic variance. This shows a greater influence of environment on genetic variations in line of observations made by different authors [16,29,47]. Moreover, except for cane yield and stalk number/ha, genotypic variances calculated were higher than environmental ones suggesting significant variations among genotypes. Greater environmental variance in millable stalk number/ha compared to the genotypic variance could be explained by no significant difference observed ($P > 5\%$) due to very lower values of genotypic coefficient of variation and heritability obtained, with 1.7 and 1% respectively. Although

Table 2. Phenotypic and genotypic correlation coefficients between agronomic traits investigated (respectively below and above diagonal)

	Juice sucrose	Juice purity	Sucrose	Fiber	Cane yield	Recov. sucrose	Sugar yield	Stalks nb	Bored internode
Juice sucrose	-	0.23	0.26	-0.09	0.01	0.25	0.20	0.68	-0.18
Juice purity	0.92**	-	0.24	-0.07	-0.01	0.23	0.17	0.68	-0.15
Sucrose	0.99**	0.91**	-	-0.12	0.05	0.26	0.22	0.60	-0.19
Fiber	-0.09	-0.08	-0.22*	-	-0.26	-0.12	-0.22	0.39	0.15
Cane yield	0.16	0.17	0.22**	-0.52**	-	0.04	0.12	-0.53	-0.12
Recov. sucrose	0.99**	0.95**	0.99**	-0.22*	0.22*	-	0.21	0.75	-0.19
Sugar yield	0.77**	0.76**	0.81**	-0.42**	0.73**	0.82**	-	0.01	-0.19
Stalks nb	0.09	0.06	0.08	0.00	0.21	0.07	0.15	-	-0.39
Bored internode	-0.48**	-0.36**	-0.52**	0.41**	-0.29**	-0.50**	-0.49**	-0.02	-

*, **: significant at 5 and 1%, respectively

Table 3a. Analysis of variance regarding sugar yields

Source of variation	df	Sum of squares	Mean squares	F	P (prob)
Block	2	5.5	2.728	0.52	0.597
Genotypes	29	643.2	22.181	4.23	0.0000
Error	58	304.1	5.244		
Total	89				

Table 3b. Analysis of variance regarding cane yields

Source of variation	df	Sum of squares	Mean squares	F	P (prob)
Block	2	482	241.2	0.78	0.462
Genotypes	29	28756	991.6	3.22	0.0000
Error	58	17872	308.1		
Total	89				

Table 3c. Analysis of variance regarding recoverable sucrose

Source of variation	df	Sum of squares	Mean squares	F	P (prob)
Block	2	2.03	1.014	0.802	0.453
Genotypes	29	214.49	7.396	5.851	0.0000
Error	58	73.32	1.264		
Total	89				

highly significant differences were observed in cane yields ($P < 0.01\%$), the environmental variance was higher than the genotypic variance which could be explained by moderate values of heritability (43%) and genotypic coefficient of variation (11.6%).

3.5 Genotypic and Phenotypic Coefficients of Variation (GCV, PCV)

As stated by Shivasubramanian and Menon [48] cited by different investigators [16,24,49-50], PCV and GCV values are ranked as low, medium and high with 0 to 10%, 11 to 20% and higher than 20% respectively (Table 5). Based on that statement, all PCV and GCV values determined which ranged from 9.3 to 57.6% on the one hand, and from 1.7 to 53.0% on the other hand, varied from low to high. As reported by different authors [51-52], high GCV and PCV indicated that selection might be effective on traits investigated and their expression be relevant to the genotypic potential. Particularly, agronomic traits exhibiting relatively high GCV estimates may respond favorably to selection [29]. Regardless the trait considered in this study, the phenotypic coefficient of variation was higher than the genotypic one suggesting that apparent variations were not only due to genetics but also to environmental influences. However, differences between PCV and GCV for most traits were small in line of observations made by

different investigators [24,53-54], indicating high prospects for genetic progress through selection under conditions of this study.

3.6 Heritability and Genetic Advance

Estimates of broad-sense heritability (h^2) are categorized according to Robinson [55] cited by different authors [16,41,47] as low (<30%), moderate [30-60%] or high ($\geq 60\%$). Higher heritability values ranging from 61 to 85% were observed on traits like juice sucrose, recoverable sucrose, sucrose percent, fiber content and stem borer infestations (Table 5). In contrast, moderate values (43-52%) were observed for sugar yield, juice purity and cane yield. Estimates of mean genetic advance (GAM) are categorized similarly to GCV and PGV according to Falconer and Mackay [23] cited by several authors [48-49, 53-55]. Therefore, higher values of genetic advance were observed for stem borer infestations (100%), sugar yield (33%), recoverable sucrose (28%) and sucrose content (20%). Moderate values were recorded on traits like fiber content (14%), cane yield (16%) and juice sucrose (19%). Lower data were obtained on millable stalk number (0%) and juice purity (7%). Higher values of GAM suggest that a significant proportion of the total variance might be heritable and selection of corresponding traits would be effective. Similar values were reported by several authors in sugarcane on single stalk

Table 4. Mean values of agronomic traits in plant cane for different genotypes tested in Ferké, Ivory Coast (1st stage of advanced screening)

Cane genotypes	Sucrose (% juice)	Purity (%C)	Sucrose (%C)	Fibre %C	Cane yield (t/ha)	R. Sucrose (%C)	Sugar yield (t/ha)	Nb x10³ (stalks/ha)	% Bored internodes
R579	16.7 ab	85.1 abc	14.1 abcd	11.4 gh	176.0 a	10.0 abc	17.6 a	152.3 a	12.1 cdef
RCI10/133	16,3 abc	83.4 abcd	13.4 abcde	12.9 cdefgh	140.2 abc	9.3 abcde	13.0 abcd	178.0 a	20.6 bc
RCI11/113	12.2 cde	73.9 cde	10.1 efg	12.4 efgh	136.0 abc	6.1 ef	8.3 bcde	157.7 a	18.0 cd
RCI11/114	12.0 de	72.9 de	10.1 efg	11.8 fgh	145.6 abc	6.0 ef	8.7 bcde	139.3 a	15.8 cde
RCI11/115	13.1 bcde	75.8 abcde	10.7 defg	13.1 cdefg	123.8 abc	6.7 cdef	8.4 bcde	172.3 a	18.6 cd
RCI12/15	17.6 a	85.8 ab	14.6 ab	12.2 efgh	112.7 bc	10.4 ab	11.8 abcde	172.3 a	6.5 ef
RCI12/19	17.0 ab	82.6 abcde	14.0 abcd	12.8 cdefgh	135.2 abc	9.6 abcd	13.2 abcd	187.3 a	4.2 f
RCI13/116	12.0 de	74.3 bcde	9.9 fg	12.7 cdefgh	110.2 bc	5.9 ef	6.6 de	135.0 a	18.5 cd
RCI13/117	16.0 abcd	81.5 abcde	13.2 abcdef	12.9 cdefgh	105.7 bc	8.9 abcde	9.7 bcde	156.0 a	14.8 cde
RCI13/118	12.4 cde	77.3 abcde	10.3 efg	12.1 efgh	138.9 abc	6.5 def	9.1 bcde	145.0 a	18.2 cd
RCI13/119	13.2 bcde	77.8 abcde	10.4 efg	15.0 ab	104.2 c	6.5 def	6.8 cde	177.0 a	44.4 a
RCI13/12	16.0 abcd	81.8 abcde	12.9 abcdef	14.3 bcd	126.2 abc	8.6 abcde	10.9 bcde	152.3 a	10.0 def
RCI13/120	15,3 abcde	81.1 abcde	12.9 abcdef	11.7 fgh	135.9 abc	8.7 abcde	11.9 abcde	149.3 a	9.5 def
RCI13/121	16.1 abcd	82.7 abcde	13.3 abcdef	12.7 cdefgh	140.1 abc	9.1 abcde	12.9 abcd	147.7 a	9.3 def
RCI13/122	17.7 a	83.7 abcd	14.3 abc	13.9 bcde	122.6 abc	9.9 abcd	12.2 abcd	164.7 a	12.9 cdef
RCI13/123	15.1 abcde	82.4 abcde	12.5 abcdef	12.6 defgh	123.6 abc	8.5 abcde	10.6 bcde	182.7 a	13.5 cdef
RCI13/124	14.9 abcde	77.3 abcde	12.1 abcdefg	13.7 bcde	128.6 abc	7.7 abcdef	9.9 bcde	221.0 a	12.5 cdef
RCI13/125	14.3 abcde	77.3 abcde	11,7 abcdefg	13.4 cdef	107.9 bc	7.4 abcdef	8.1 cde	151.3 a	7.2 ef
RCI13/126	16.8 ab	85.4 abc	14.0 abcd	12.3 efgh	124.8 abc	9.9 abcd	12.3 abcd	169.0 a	4.5 f
RCI13/136	15.0 abcde	80.9 abcde	12.7 abcdef	11.1 h	160.8 ab	8.6 abcde	13.9 abc	179.7 a	10.4 def
RCI13/137	14.7 abcde	81.5 abcde	12.1 abcdefg	13.2 cdefg	132.5 abc	8.1 abcdef	10.7 bcde	180.0 a	17.5 cd
RCI13/17	14.2 abcde	75.7 abcde	12.0 abcdefg	11.4 gh	130.1 abc	7.6 abcdef	9.9 bcde	137.3 a	17.9 cd
RCI14/11	17.5 a	85.0 abc	14.7 ab	11.5 gh	146.8 abc	10.5 ab	15.4 ab	156.7 a	7.3 ef
RCI14/127	18.0 a	86.9 a	14.9 a	12.7 cdefgh	107.9 bc	10.7 a	11.5 abcde	181.3 a	11.1 def
RCI14/129	13.8 abcde	75.1 bcde	11.3 abcdefg	13.0 cdefg	141.6 abc	7.0 cdef	9.9 bcde	191.0 a	11.2 def
RCI14/130	13.1 bcde	74.9 bcde	10.9 cdefg	12.2 efgh	149.6 abc	6.7 cdef	10.2 bcde	187.3 a	11.2 def
RCI14/131	15.1 abcde	79.0 abcde	12.5 abcdef	12.5 efgh	139.0 abc	8.2 abcdef	11.3 abcde	182.7 a	7.2 ef
RCI14/132	16.7 ab	84.5 abc	13.8 abcd	12.4 efgh	134.2 abc	9.7 abcd	13.1 abcd	178.7 a	12.5 cdef

Cane genotypes	Sucrose (% juice)	Purity (%C)	Sucrose (%C)	Fibre %C	Cane yield (t/ha)	R. Sucrose (%C)	Sugar yield (t/ha)	Nb x10³ (stalks/ha)	% Bored internodes
RCI14/14	11.4 e	71.5 e	9.1 g	14.4 bc	98.3 c	5.1 f	5.1 e	140.7 a	25.2 b
RCI14/18	14.1 abcde	80.5 abcde	11.0 cdefg	15.7 a	100.2 c	7.1 bcdef	7.3 cde	153,7 a	16.5 cd
Mean	14.9	79.9	12.3	12.8	129.3	8.2	10.7	166.0	14.0
SD	2.2	5.2	1.9	1.2	23.0	1.8	3.3	45.3	8.0
CV (%)	14.8	6.5	15.1	9.2	17.8	22.0	30.6	27.3	57.4
Replications	ns	ns	ns	ns	ns	ns	ns	***	*
Genotypes	***	***	***	***	***	***	***	ns	***

(Followed Table 4). Ns: not significant at 5% level; *: significant at 5% level; ***: highly significant at 1% level; CV: coefficient of variation; abcd: means followed by the same letter in same column do not differ significantly following Duncan test at 5% level

Table 5. Variability and heritability among sugarcane genotypes tested as plant crop in Ferké, Ivory Coast

Variability	Mean	Variance			CV (%)		h ² (-)	GA (-)	GAM (%)
		σ^2_p	σ^2_e	σ^2_g	PCV	GCV			
Juice sucrose (%)	14.9	4.97	1.93	3.04	14.9	11.7	0.61	2.81	18.8
Purity (%)	79.9	27.56	13.34	14.22	6.6	4.7	0.52	5.59	7.0
Sucrose (%)	12.3	3.51	1.26	2.25	15.2	12.2	0.64	2.48	20.1
Fibre (%)	12.8	1.41	0.39	1.03	9.3	7.9	0.73	1.78	13.9
Cane yield (t/ha)	129.3	535.93	308.10	227.83	17.9	11.7	0.43	20.30	15.7
Recov. sucrose (%)	8.2	3.31	1.26	2.04	22.2	17.5	0.62	2.32	28.3
Sugar yield (t/ha)	10.7	10.89	5.24	5.65	30.9	22.2	0.52	3.53	33.0
Stalk number/ha	166.0	1166.33	1158.00	8.33	20.6	1.7	0.01	0.50	0.3
Bored internode (%)	14.0	64.86	9.96	54.90	57.6	53.0	0.85	14.06	100.7

CV: coefficient of variation; PCV: phenotypic CV (%); GCV: genotypic CV (%); h²: broad sense heritability; GA: genetic advance; GAM: genetic advance as percent of mean (%)

weight [29,56-57]. As indicated by Vidya et al. [58], knowledge of variability and heritability of characters is essential for identifying those relevant to genetic improvement through selection. Moreover, the effectiveness of selection will depend not only on heritability but also on genetic advance [59-60]. Higher levels of mean genetic advance observed for sugar yield, recoverable sucrose, sucrose content and stem borer infestations were the result of moderate or high broad sense heritability combined with high GCV for these traits in line of findings reported by Bakshi [61]. These findings showed the existence of considerable scope for sugarcane improvement based on some cane yield components like number of millable stalks/ha, stalk weight, stalk diameter and single stalk weight. This author reported that heritability estimates, together with expected genetic gain, were more useful than heritability values alone in predicting the effects of selecting best genotypes. Chaudhary [33] also reported high heritability and genetic gain for single cane weight followed by number of millable cane in a study of 36 clones indicating substantial scope for cane yield improvement. On the other hand, sucrose content recorded low heritability and genetic gain suggesting little scope for improvement in this character [62]. Patel et al [63] also reported high heritability estimates for single cane weight, number of internodes, tiller number, hand refractometer brix, cane diameter and millable cane length, which were associated with moderate to high genetic advance (23-190%). Findings indicated that these characters might be improved through selection. From the literature, findings on heritability, genetic gain, PCV and GCV for the same traits look sometimes controversial depending on locations, crop cycle (plant cane or

ratoon), soil types, water regime (rainfed or irrigated), etc. [21,41-42, 64]. But still, this is all about the scope of experimentation in agronomy, findings being mostly site-specific. Nevertheless, in line of findings reported in the literature, data collection in first ratoon of this study might focus on additional traits like number of internodes per stalk, stalk diameter, average single stalk weight, stalk height and flowering rate.

4. CONCLUSIONS

Based on sugar yields, seven cane genotypes equivalent to the check variety R579 which gave 17.6 t/ha were the following: RC114/11, RC113/136, RC114/132, RC112/19, RC110/133, RC113/122 and RC113/126. Higher heritability values ranging from 52 to 85% were observed in traits like sugar yield, juice purity, juice sucrose, recoverable sucrose, sucrose percent, fiber content and stem borer infestations. Differences between PCV and GCV for most traits were small, indicating high prospects for genetic progress through selection under conditions of this study. Nevertheless, data obtained need to be confirmed over the 2019-20 cropping season in first ratoon crop to determine promising cane genotypes for the advanced selection stage to be similarly conducted under commercial field conditions.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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