

Genetic Variability and Heritability among Sugarcane Genotypes in Plant Crop at First Stage of Advanced Selection for some Agronomic Traits in Ferké, Northern Ivory Coast

Comment [U1]: Modify the title briefly, if possible.

Abstract

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Selection in sugarcane from true seed is recently implemented in Ivory Coast with the aim to increase the genetic variability of crop material used and therefore improve significantly sugar yields with a positive impact on the competitiveness of the Ivorian sugar industry. The study objective was to determine the best performing cane genotypes among 29 clones tested under sprinkler irrigation, in comparison with a check variety (R579). It was carried out on a commercial sugarcane plantation of Ferké 2 sugar estate in northern Ivory Coast.

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The experimental design used was a randomized complete block 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. Based on sugar yields, seven cane 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: RCI14/11, RCI13/136, RCI14/132, RCI12/19, RCI10/133, RCI13/122 and RCI13/126. Their cane yield performances ranged from 134.2 to 160.8 t/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. In contrast, lower and moderate values of heritability were observed for millable stalk number/ha and cane yield, with 1 and 43%, respectively. Regardless the trait considered, the phenotypic coefficient of variation (PCV) was higher than the genotypic one (GCV) suggesting that apparent variations were not only due to genetics but also due to environmental influences. However, differences between PCV and GCV for most traits were small, indicating high prospects for genetic progress through selection under conditions of this study.

Key words. Phenotypic correlation, genotypic correlation, coefficient of variation, Genetic advance, yield trait, juice quality.

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1. Introduction

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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 (Dahlquist, 2013). 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 (Goldemberg, 2008; Waclawovsky et al, 2010). 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 (Altpeter and Karan, 2018). In 2003, the FAO estimated that sugarcane had a worldwide gross production value of \$81.5 billion (FAO, 2013). 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) (FAO, 2014). Sugarcane is ranked third in quantity of plant calories in the human diet (Moore and Botha, 2013). 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 (FAO, 2014). In all cases, increased sugarcane production is linked to expansion of land surface rather than to increases in yield (Jackson, 2005).

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 (Yang et al, 2018).

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 (Wei et al, 2006). 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 (Khan et al, 2009). 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 (Ali et al, 2017).

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 (Rebetzke et al, 2002). Heritability represents the relative importance of genetic and environment factors in the expression of phenotypic and genotypic differences among genotypes within a population (Kang et al, 1983; Dagar et al, 2002 cited by Ehib et al, 2015). Consequently, the knowledge of heritability related to important traits and the correlations among them are key issues to determine the best selection strategy (Hallauer and Miranda, 1988; Falconer, 1989). Genotypic coefficient of variation (GCV) is another measure of relative genetic variation of a trait within a population (Ram and Hemaprabha, 1992). Traits exhibiting relatively high GCV estimates may respond favorably to selection. Chaudhary (2001) 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 (Kimbeng et al, 2002). Studies

in various sugarcane breeding programs have reported significant GxE interactions for cane and sugar yields (Parfitt, 200; Kimbeng et al, 2002; Glaz and Kang, 2008).

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

2. Material and methods

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 (Konan et al a-b, 2017; Péné *et al*, 2012). 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.

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 eRcane Sugarcane Development Centre of Reunion Island 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 virus (SCSMV). Parents of genotypes investigated, as complex polyploids, were

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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 (Tadesse et al, 2014).

Experimental design

The experiment was carried out 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. Field managements in terms of sprinkler irrigation, fertilizer and herbicide applications were done according to usual practices in commercial plantations.

Agronomic traits investigated

Data was 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*.

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 (1970). The recoverable sucrose was calculated as follows (Péné *et al*, 2016; Hugot, 1999):

SE %C = [(0.84 x Pol%C) (1.6 -60/Purity) - (0.05 x Fib %C)] with:

Purity %C = (Pol juice/Brix) x 100 and Pol juice = Pol factor x Pol 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.

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, 1953 cited by Shitahum *et al*, 2018):

Genotypic variance (σ_g^2) = (MS_g - MS_e)/r

Environmental variance (σ_e^2) = MS_e

Phenotypic variance (σ_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 (Singh and Chaundary, 1977):

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

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

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 A and B traits are defined as:

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

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

where similarly to the phenotypic variance equation, the phenotypic covariance Cov_p is expressed as:

$$\text{Cov}_p = \text{Cov}_g + \text{Cov}_e$$

Statistical analyses

The quantitative data recorded in this study was subjected to the analysis of variance using statistical procedures described by Gomez and Gomez (1984) using with the assistance of R software package version 3.5.1 (Table 1).

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.

3. Results and discussion

Phenotypic correlations within 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 (Gravois et al, 1992, Tena et al, 2016, Dumont et al, 2019). Fiber content was negatively correlated with yields and juice quality traits like juice sucrose, purity, sucrose percent and recoverable sucrose with coefficients ranging from -0.02 to -0.18. All traits were positively correlated,

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although poorly, with stalk number with coefficients ranging from 0.00 to 0.11. Higher correlation coefficients were expected between stalk number and yields traits, instead of 0.11 and 0.10 values. Moderate and positive correlation coefficients were obtained between sugar yield and juice quality traits like juice sucrose, purity, sucrose percent and recoverable were obtained, with coefficients ranging from 0.32 to 0.40, instead of high values expected. Similarly, moderate and positive correlations were observed between yield traits on the one hand and between sugar yield and juice quality traits were obtained with values ranging from 0.32 to 0.34, instead of higher values expected.

Genotypic correlations within agronomic traits

Similarly with phenotypic correlations, all yield and juice quality traits were genotypically correlated negatively with stem borer infestations except for fiber content (Table 2), with values ranging from 0.01 to 0.18. Except for 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, all traits were positively correlated to stalk number with 0.01 for sugar yield and values ranging from 0.39 to 0.75 regarding traits like sucrose juice, sucrose percent, recoverable sucrose and fiber content. A much lower coefficient was expected between recoverable sucrose and stalk number, instead of 0.75. In contrast, a stronger correlation was expected between yield traits instead of 0.12. Lower genotypic correlations expected between cane yield and juice quality traits were obtained, with coefficients ranging from -0.01 to 0.12.

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	0.38	-	0.24	-0.07	-0.01	0.23	0.17	0.68	-0.15
Sucrose	0.40	0.37	-	-0.12	0.05	0.26	0.22	0.60	-0.19
Fiber	-0.02	-0.02	-0.06	-	-0.26	-0.12	-0.22	0.39	0.15
Cane yield	0.07	0.08	0.09	-0.18	-	0.04	0.12	-0.53	-0.12
Recov. sucrose	0.40	0.39	0.40	-0.06	0.10	-	0.21	0.75	-0.19
Sugar yield	0.32	0.32	0.33	-0.13	0.32	0.34	-	0.01	-0.19
Stalks nb	0.05	0.02	0.05	0.00	0.11	0.02	0.10	-	-0.39
Bored internode	-0.17	-0.12	-0.18	0.14	-0.10	-0.17	-0.17	-0.01	-

Performance of cane genotypes tested

Except for stalk number/ha, highly significant differences within genotypes were observed for all agronomic traits investigated (Table 3). Based on sugar yields, a number of 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: RCI14/11, RCI13/136, RCI14/132, RCI12/19, RCI10/133, RCI13/122 and RCI13/126. 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), reasonable values of sucrose percent obtained with some of the promising genotypes ranged from 13.8 to 14.7 %, compared with 14.1 for the check.

Phenotypic, genotypic and environmental variance

Regardless the trait considered, phenotypic variances obtained were higher than genotypic variances. This shows a greater influence of environment on genetic variations in line of observations made by different authors (Tadesse et al, 2014; Ehib et al, 2015). 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 due to a very lower values of genotypic coefficient of variation and heritability obtained, with 1.7 and 1% respectively. Although significant differences were observed in cane yields, 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%).

Genotypic and phenotypic coefficients of variation (GCV, PCV)

GCV is another measure of relative genetic variation of a trait in a population (Ram and hemaprabha, 1992). Traits exhibiting relatively high GCV estimates may respond favorably to selection (Ebid et al, 2015). Regardless the trait considered, the phenotypic coefficient of variation was higher than the genotypic one suggesting that apparent variations were not only due to genetics but also due to environmental influences. However, differences between PCV and GCV for most traits were small in line of observations made by Ram (2005), indicating high prospects for genetic progress through selection under conditions of

this study. As stated by Shivasubramanian and Menon (1973) cited by Tadesse et al (2014), PCV and GCV values are ranked as low, medium and high with 0 to 10 %, 11 to 20% and > 20% respectively. 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 (Tadesse et al, 2014; Singh et al, 1994), high GCV and PCV indicated that selection may be effective on traits investigated and their expression would be relevant to the genotypic potential.

Heritability and genetic advance

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. In contrast, lower and moderate values of heritability were observed for millable stalk number/ha and cane yield, with 1 and 43%, respectively. This distinction was made following heritability scale as stated by Robinson et al (1949) and cited by Tadesse et al, 2014. In line of scale used by Teklu et al (2014), higher values of genetic advance (GA) were observed for cane yield as well as stem borer infestations, with 20.3 and 14.0%, respectively, suggesting that a significant proportion of the total variance is heritable and selection of these traits would be effective. Similar values were reported by different authors in sugarcane on single stalk weight (Nair et al, 1980; Singh et al, 1994; Ebid et al, 2015). As indicated by Vidya et al (2002), knowledge of variability and heritability of characters is essential for identifying those relevant to genetic improvement through selection. Moreover, the effectiveness of selection depends not only on heritability but also on genetic advance (Butterfield and Nuss, 2002; Shba et al, 2009). Higher levels of genetic advance (GA) observed for cane yield and stem borer infestations were the result of broad sense heritability and high GCV for these traits in line of findings reported by Bakshi (2005). The results suggest 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. Heritability estimates, together with expected genetic gain, are more useful than heritability values alone in predicting the effects of selecting best genotypes. Chaudhary (2001) 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

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heritability and genetic gain suggesting little scope for improvement in this character (Pandey, 1989). Patel et al (2008) also reported high heritability estimates for single cane weight, number of internodes, tiller number, hand refractrometer brix, cane diameter and millable cane length, which were associated with moderate to high genetic advance (23-190%). Findings indicated that these characters could be improved through selection.

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Table 3. 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 x10 ³ (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 bcdefg	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
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	***

Table 4. Variability and heritability among sugarcane genotypes tested as plant crop in Ferké, Ivory Coast.

Variability	Mean	Variance			Coef. of variation (%)		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

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

4. Conclusions

Based on sugar yields, seven cane 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: RCI14/11, RCI13/136, RCI14/132, RCI12/19, RCI10/133, RCI13/122 and RCI13/126. Their cane yield performances ranged from 134.2 to 160.8 t/ha compared to 176 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. In contrast, lower and moderate values of heritability were observed for millable stalk number/ha and cane yield, with 1 and 43%, respectively. Regardless the trait considered, the phenotypic coefficient of variation was higher than the genotypic one suggesting that apparent variations were not only due to genetics but also due to environmental influences. However, differences between PCV and GCV for most traits were small, indicating high prospects for genetic progress through selection under conditions of this study. Data obtained need to be confirmed over the 2019-20 cropping season in first ratoon crop to determine promising cane genotypes for the second and final advanced selection stage to be similarly conducted under commercial field conditions.

Comment [U11]: Rewrite the conclusion in brief and with clear recommendations.

Comment [U12]: ??

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Comment [U13]: Reference should be written as per the journal guidelines