Agricultural Science; Vol. 2, No. 1; 2020
ISSN 2690-5396 E-ISSN 2690-4799
https://doi.org/10.30560/as.v2n1p83

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

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Received: March 15, 2020 Accepted: April 12, 2020 Online Published: April 16, 2020

Abstract

Selection in sugarcane from true seed was 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 objective of study 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 R3-002 commercial sugarcane plantation of Ferké 2 sugar estate, in northern Ivory Coast. The experimental design used was a randomized complete block with 30 cane genotypes in three replications. Each plot comprised 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, four promising genotypes namely RCI12/15, RCI12/19, RCI13/121 and RCI13/136 were equivalent to the check variety which performed 15.6 t/ha. They are due to undergo the advanced selection stage during the 2020-21 cropping season for three more years for determining the first new sugarcane varieties of RCI origin to be tested commercially in Ferké sugar estates. Their yield performances ranged from 12.8 to 13.8 t sugar/ha, i.e. from 134.0 to 144.8 t cane/ha compared to 161.3 t/ha for the control variety. Although a relatively high level of stem-borer infestation rate recorded, with 15.6% on average (almost three times the tolerable threshold value of 5%), reasonable values of sucrose percent obtained with the promising genotypes, ranged from 12.7 to 13.9% over both crop cycles, compared with 13.6% for the check. Higher heritability values ranging from 61 to 80.5% were observed in traits like sugar yield, sucrose content (62.6%), recoverable sucrose (60.6%), fiber content (72%), stem-borer infestation rate (80.5%), number of internodes/stalk (67.7%), and flowering rate (79.6%). In contrast, lower and moderate values of heritability were observed for Pol juice (59.8%), juice purity (50.5%), cane yield (53%), millable stalk number/ha (29.5%), single stalk weight (36.7%), single stalk height (45%), and single stalk diameter (38.7%).

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 approximatively 80% of the world sugar production, greatly exceeding sugar beet as a 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 (Rebettzke 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 & 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 & 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

2.1 Site Characteristics

The study was carried out on a Ferké 2 sugarcane field (R3-002) sprinkler irrigated with center pivot (9°16' N, 5°22' W, 325 m a.s.l), in northern Ivory Coast. 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 Saharan trade wind, which blows over mid-November to late January. The rainfall pattern is unimodal and focussed 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 reach 32.5 and 21 °C, respectively. To meet 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 oxisols 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 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 long 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 magnitude of variability present in the genetic material is therefore of prime importance for breeders to conduct effective selection programs. 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 could be achieved from the material to be investigated (Tadesse et al, 2014).

2.3 Experimental Design

The experiment was carried out from late March 2018 to mid-February 2020 in plant cane and first ratoon, 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.

2.4 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* W).

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 internodes 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, each 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 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 polarimeter SH-M100. Hoarau (1970) reported on methods used in the determination of required technological parameters. The recoverable sucrose was calculated as follows (Hugot, 1999; Péné *et al*, 2016):

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), was 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 each 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 & Davane, 1953 cited by Shitahum et al, 2018):

Genotypic variance (σ^2_g) = ($MS_g - MS_e$)/r

Environmental variance (σ^2_e) = MS_e

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Where MSg and MSe 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 & Chaundary, 1977):

GCV = σ_g x100/grand mean

PCV = σ_p x100/grand mean

Broad sense heritability $h^2 = 100 \times \sigma^2_g / \sigma^2_p$

Genetic advance (GA) and genetic advance as percent mean (GAM): GA = k x h^2 x σ_p and GAM = 100 x 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:

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

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

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

$Cov_p = Cov_g + Cov_e$

2.6 Statistical Analyses

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

Table 1. Analysis of variance calculations in a RCBD involving GxY interactions

Source of variation	Degree of freedom (df)	Mean square (MS)	Expected mean square (EMS)
Replication (R)	y(r-1)	MSr	
Years (Y)	y-1		
Genotypes (G)	g-1	M1=MSg	$\sigma^2_e + r\sigma^2_{gy} + ry\sigma^2_g$
G x Y	(g-1) (y-1)	M2=MSgy	$\sigma^2_e + r\sigma^2_{gy} + ry\sigma^2_g$
Error (G x R)	(r-1) (gy-1)	M3=MSe	σ^2_e
Total	gyr-1		

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^2g, σ^2r, σ^2y and σ^2e stand for variances due to genotypes, replicates, years and error, respectively.

3. Results and Discussion

3.1 Climatic Conditions Over Plant Cane and First Ratoon Crop

The total amount of rainfall recorded in plant cane was similar to that in first ratoon, with 1311 and 1303 mm, respectively. However, total rainfall during in the hottest period (from April to July) decreased by 51.4% in the first ratoon compared to that of plant cane, with 352.7 and 726.2 mm respectively. In contrast, the amount of rainfall recorded over the cloudy and per-humid period (from August to October) increased by 59%, with 554.6 and 880.7 mm respectively in plant cane and first ratoon (Fig 1). Total crop water deficit over the dry season to be met with irrigation water reached 571 and 565 mm, respectively, in plant cane and first ratoon. The average daily temperature over the entire crop cycle yields 27.8 and 26.8 °C, respectively.

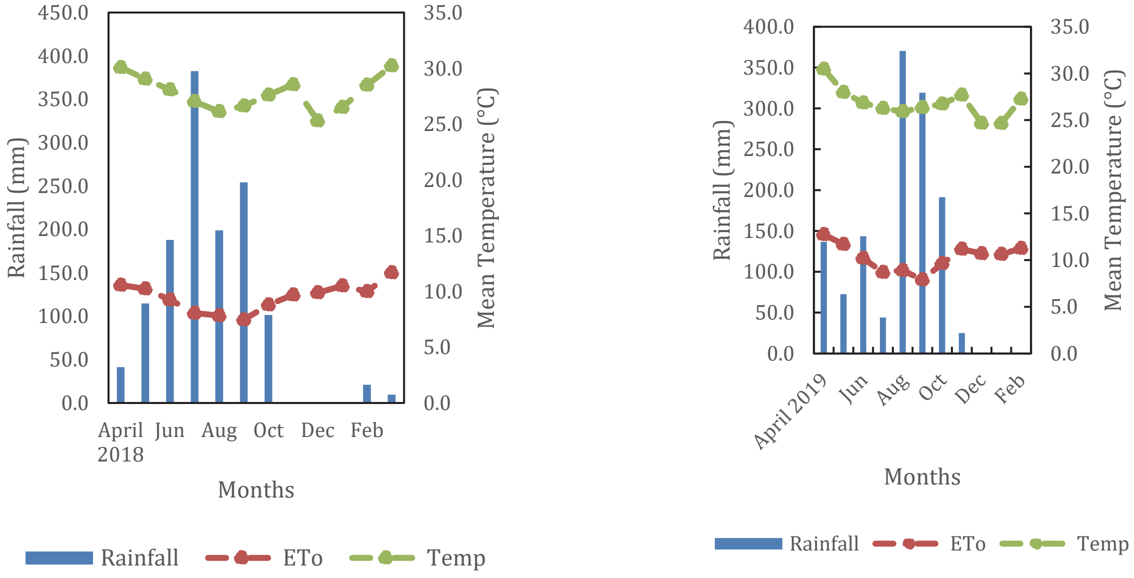

Fig 1a. Climate over plant cane. Fig 1b. Climate over first ratoon crop.

Figure 1. Prevailing climate on experimental site over both crop cycles in Ferké 2 sugar estate, Ivory Coast

3.2 Multivariate ANALYSES

It came out from the principal component analysis (Figure 2) that most relevant traits in genotype clustering were related to juice quality (recoverable sucrose, sucrose content, purity, fiber content), and some yield components like stalk diameter and average stalk diameter. The dendrogram deduced from the hierarchical ascendant classification analysis (Figure 3) exhibits six different cluster genotypes, which average agronomic characteristics are displayed in Table 2.

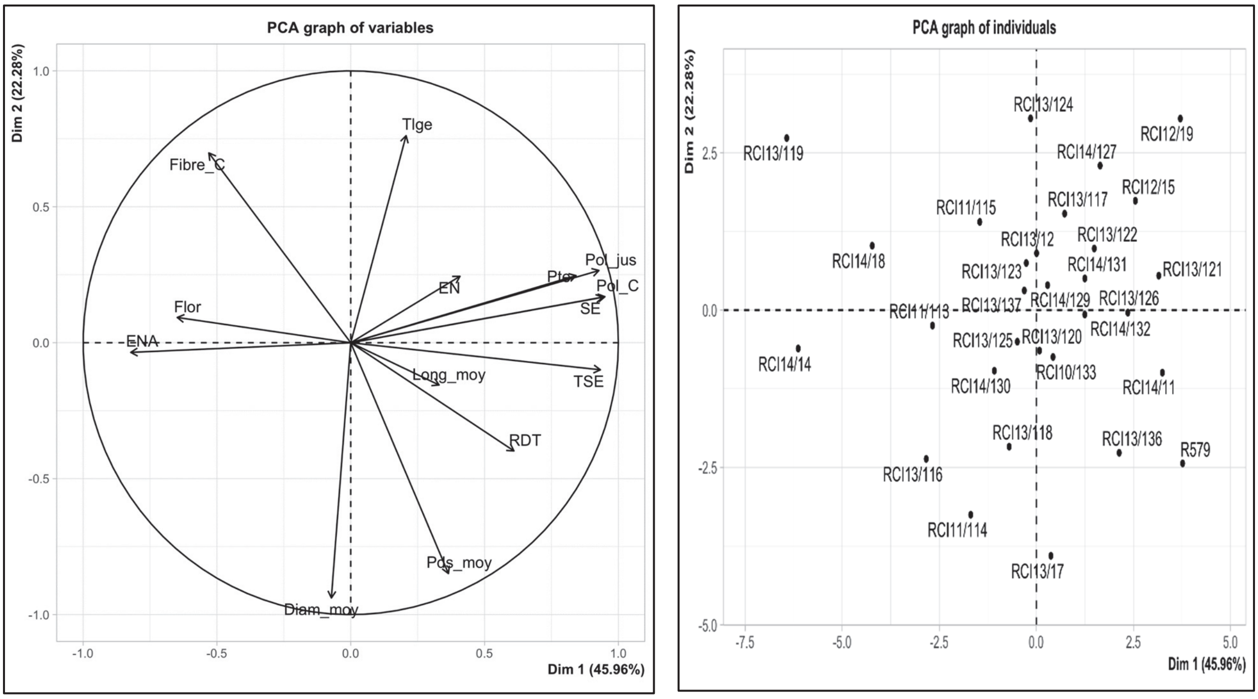

Figure 2a. Correlation circle of agronomic traits investigated in 1-2 factor plane. Figure 2b. Projection of sugarcane genotypes in 1-2 factor plane.

Figure 2. Results of Principal Component Analysis regarding aggregate data of both plant and first ratoon crops

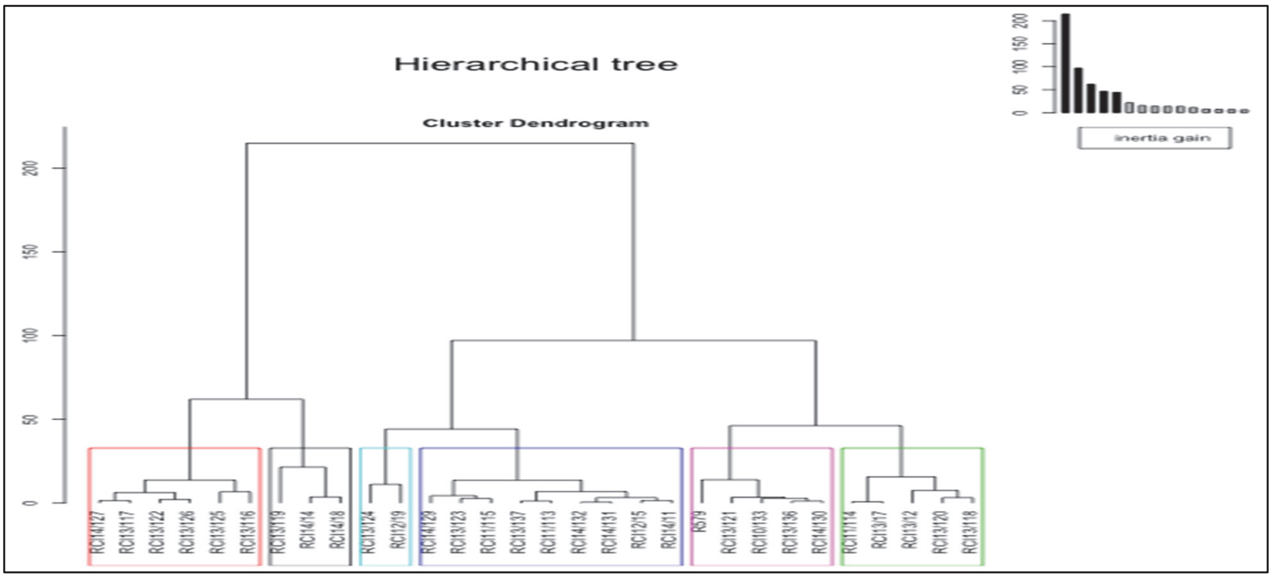

Figure 3. Dendrogram deduced from cluster analysis of all 30 cane genotypes tested in Ferké 2 sugar estate, Ivory Coast

Table 2. Mean values of clusters genotypes determined following different agronomic traits investigated in Ferké 2 sugar estate, Ivory Coast (aggregate of plant cane and first ratoon)

Agronomic traits	Cluster 1 (n=3)	Cluster 2 (n=5)	Cluster 3 (n=6)	Cluster 4 (n=9)	Cluster 5 (n=2)	Cluster 6 (n=5)
Pol juice (%)	11.8	16.1	14.0	14.9	16.1	15.5
Purity (%)	77.1	83.8	80.1	82.2	81.9	83.4
Sucrose (Pol%C)	9.3	12.9	11.4	12.0	12.8	12.7
Fiber content (%)	15.6	14.3	13.4	14.1	14.8	13.3
Cane Yield (t/ha)	95.8	108.5	130.7	128.5	133.5	146.8
Recov Sucrose (%)	5.7	8.9	7.5	8.1	8.6	8.7
Sugar Yield (t/ha)	5.5	9.7	9.8	10.4	11.6	12.8
StalkNbx1000	143.9	145.1	132.2	157.6	182.8	148.2
%BIN	27.7	11.9	16.7	15.4	8.5	13.9
Avg Weight (kg)	0.8	1.0	1.1	1.0	0.9	1.2
Avg Diam (mm)	2.3	2.4	2.4	2.4	2.5	2.5
Avg Height (cm)	21.6	21.8	23.4	21.6	19.6	22.7
Nb Internode	20.0	24.0	20.9	21.2	24.4	21.9
Flowering rate (%)	25.3	3.6	12.4	8.3	2.2	6.2

C1: RCI13/119, RCI14/14, RCI14/18; **C2**: R579, RCI13/121, RCI0/133, RCI13/136, RCI14/130 ; **C3** : RCI14/127, RCI13/117, RCI13/122, RCI13/126, RCI13/125, RCI13/116 ; **C4** : RCI/14/129, RCI13/123, RCI11/115, RCI13/137, RCI11/113, RCI14/132, RCI14/131, RCI12/15, RCI14/11; **C5**: RCI13/124, RCI12/19; **C6**: RCI11/14, RCI13/17, RCI13/12, RCI13/120, RCI13/118

3.3 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 -0.29 to -0.42. Higher and positive correlation coefficients were obtained between sugar yield and juice quality traits, with values ranging from 0.78 to 0.86. A strong and positive correlation was also observed between yield traits (r=0.80) as well as juice quality traits, with coefficients ranging from 0.80 to 0.99. Except for fiber content, juice quality and yield traits were negatively correlated to stem borer infestation rate (r= -0.40 to -0.73). The stalk fiber content and single stalk weight were, respectively, positively and negatively correlated to stem borer infestation rate (r=0.34, -0.68). Moreover, sugarcane flowering rate affected negatively all juice quality and yield traits (r= -0.33 to -0.53).

3.4 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 -0.42 to -0.81. As expected, strong and positive correlations were observed not only between juice quality traits but also between yield traits, with coefficients ranging from 0.83 to 0.99. Strong and positive correlations were also obtained between sugar yield and juice quality attributes like pol juice, purity, sucrose content and recoverable sucrose (r= 0.79 to 0.89). Similarly to phenotypic correlations previously discussed, juice quality and yield traits were negatively correlated to stem borer infestation rate (r= -0.42 to -0.81). The stalk fiber content and single stalk weight were, respectively, positively and negatively influenced by stem borer infestation rate (r=0.36, -0.40). Moreover, sugarcane flowering rate affected negatively all juice quality and yield traits (r= -0.44 to -0.62).

3.5 Performance of Cane Genotypes Tested

Except for stalk number/ha, highly significant differences within genotypes were observed for all agronomic traits investigated (Table 3). Significant or highly significant differences within crop cycles were observed for all traits except for Pol juice, recoverable sucrose, single stalk weight and the average number of internodes per stalk. In contrast, genotype by crop cycle interactions were non-significant except for stem-borer infestation rate, average number of internodes per stalk and flowering rate. Based on sugar yields, four genotypes, namely RCI12/15, RCI12/19, RCI13/121 and RCI13/136 were equivalent to the check variety R579 which performed 15.6 t/ha. Their sugar yields ranged from 12.8 to 13.8 t/ha, while their cane yields from 134.0 to 144.8 t/ha compared with 161.3 t/ha for the control variety. Although a relatively high level of stem-borer infestation rate recorded, with 15.6% on average (almost three times the tolerable threshold value of 5%), reasonable values of sucrose percent obtained with the promising genotypes ranged from 12.7 to 13.9% over both crop cycles, compared with 13.6% for the check.

3.6 Phenotypic, Genotypic and Environmental Variance

Regardless the trait considered, phenotypic variances obtained were higher than the genotypic ones. This shows a greater influence of the environment on genetic variations in line of observations made by different authors (Tadesse et al, 2014; Ehib et al, 2015). Moreover, except for traits like stalk number/ha, average stalk weight, height and diameter, genotypic variances calculated were higher than environmental ones, suggesting significant variations among genotypes (Table 4). 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 7.3 and 29.5% respectively.

3.7 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 (Table 4). 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 & 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 5 to 94%, on the one hand, and from 3.5 to 83.9%, on the other hand, ranged from low to high. As reported by different authors (Tadesse et al, 2014; Singh et al, 1994, Péné & Béhou, 2019a,b), high GCV and PCV indicated that selection might be effective on traits investigated and their expression be relevant to the genotypic potential.

3.8 Heritability and Genetic Advance

Higher heritability values (Table 4) ranging from 61 to 80.5% were observed in traits like sugar yield, sucrose content (62.6%), recoverable sucrose (60.6%), fiber content (72%), stem-borer infestation rate (80.5%), number of internodes/stalk (67.7%), and flowering rate (79.6%). In contrast, lower and moderate values of heritability were observed for Pol juice (59.8%), Juice purity (50.5%), cane yield (53%), millable stalk number/ha (29.5%), single stalk weight (36.7%), single stalk height (45%), and single stalk diameter (38.7%). This distinction was made following heritability scale as stated by Robinson et al (1949) and cited by Tadesse et al, 2014. In line of the scale used by Teklu et al (2014), higher values of genetic advance (GAM) were observed for sugar yield (36.2%), recoverable sucrose (24.3%), and flowering rate (154%), suggesting that a significant proportion of the total variance was 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 (GAM) 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, single 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 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, number of tillers, hand refractrometer brix, cane diameter and millable cane height, which were associated with moderate to high genetic advance (23-190%). Findings indicated that these characters could be improved through selection.

Table 2. Phenotypic and genotypic correlation matrix of agronomic traits investigated regarding aggregate data of both plant and first ratoon crops (respectively below and above diagonal)

Genotypes	PolJ%.	Pty%	Pol%	Fiber%	Cane Yield	RSucr.	Sug. Yield	10^3 xNb Tillers	%BIN	AvWeight	AvHeight	AvgDiam	NbIntern.	Flow.%
Pol juice	**1.00**	0.92	0.99	-0.37	0.45	0.99	0.85	0.46	-0.81	0.11	0.21	-0.35	0.40	-0.60
Purity	0.91	**1.00**	0.92	-0.36	0.37	0.95	0.79	0.40	-0.67	0.09	0.00	-0.24	0.29	-0.44
Pol%C	0.99	0.91	**1.00**	-0.47	0.51	0.99	0.89	0.36	-0.80	0.21	0.19	-0.24	0.36	-0.62
Fiber%	-0.31	-0.29	-0.41	**1.00**	-0.72	-0.48	-0.67	0.58	0.36	-0.82	0.02	-0.75	0.13	0.46
CYield	0.36	0.32	0.42	-0.61	**1.00**	0.50	0.83	-0.02	-0.42	0.74	0.32	0.37	-0.01	-0.44
RSucrose	0.99	0.94	0.99	-0.42	0.41	**1.00**	0.89	0.34	-0.78	0.20	0.14	-0.21	0.34	-0.59
SYield	0.83	0.78	0.86	-0.59	0.80	0.86	**1.00**	0.20	-0.71	0.50	0.29	0.04	0.20	-0.59
SNbx103	0.30	0.26	0.25	0.35	0.08	0.23	0.19	**1.00**	-0.30	-0.97	-0.37	-0.99	0.17	-0.23
%BIN	-0.72	-0.58	-0.73	0.34	-0.40	-0.70	-0.66	-0.18	**1.00**	-0.40	-0.61	0.09	-0.58	0.68
AvWeight	0.09	0.07	0.17	-0.68	0.53	0.16	0.38	-0.52	-0.30	**1.00**	0.35	0.80	0.04	-0.40
AvHeight	0.18	0.04	0.18	-0.01	0.32	0.14	0.29	-0.16	-0.48	0.39	**1.00**	-0.06	0.56	-0.18
AvDiam	-0.27	-0.22	-0.18	-0.61	0.20	-0.17	-0.01	-0.74	0.09	0.78	-0.04	**1.00**	-0.53	0.02
NbInternode	0.35	0.23	0.32	0.11	0.01	0.29	0.19	0.17	-0.50	0.14	0.54	-0.33	**1.00**	-0.49
Flowering	-0.50	-0.33	-0.53	0.42	-0.36	-0.49	-0.49	-0.17	0.62	-0.35	-0.14	-0.44	-0.46	**1.00**

Table 3. Mean values of agronomic traits in plant cane and first ratoon (on aggregate) for different genotypes tested in Ferké, Ivory Coast (1rst stage of advanced screening)

Genotypes	PolJ%	Pty%	Pol%	Fiber%	Cane Yield	RSucr%	Sug. Yield	10^3 xNb Tillers	BIN%	AvWeight (kg)	AvHeight (m)	AvgDiam (mm)	NbIntern.	Flow.%
R579	16.5ab	85.7ab	13.6ab	12.7hi	161.3a	9.7ab	15.6a	136.7	13.7de	1.3ab	2.5ab	23.5ab	21.2cd	2.0hi
RCI10/133	15.0ab	83.2ab	12.1ab	14.3cd	140.8ab	8.2ab	11.5bc	150.7	21.0bc	1.1ab	2.5ab	23.1ab	22.0cd	9.7fg
RCI11/113	12.4ef	77.6de	10.0fg	14.2cd	132.1ab	6.2ef	8.2fg	154.5	19.9bc	1.0ab	2.4ab	21.8ab	21.4cd	15.2cd
RCI11/114	12.8de	77.2ef	10.5ef	12.9gh	137.6ab	6.6de	9.0ef	122.3	20.3bc	1.2ab	2.5ab	23.6ab	21.7cd	10.7ef
RCI11/115	14.0ab	79.9ab	11.2cd	14.5bc	122.4bc	7.3bc	9.0ef	158.8	22.1bc	0.9bc	2.2de	20.8bc	21.7cd	0.0i
RCI12/15	17.3a	86.8a	13.9ab	14.1cd	134.0ab	9.9a	13.1ab	154.8	9.5hi	0.9bc	2.3bc	21.0bc	20.6de	12.ef0
RCI12/19	17.0ab	84.6ab	13.6ab	14.5bc	144.8ab	9.5ab	13.8ab	180.2	4.7k	0.9ab	2.6ab	19.2e	26.0ab	3.3hg
RCI13/116	12.3fg	77.6de	10.0fg	13.8de	116.2bc	6.3ef	7.3gh	130.5	18.8bc	1.2ab	2.3ab	24.2ab	21.3cd	9.7ef
RCI13/117	16.2ab	83.4ab	13.1ab	14.2cd	107.4cd	9.0ab	9.7bc	148.7	13.4ef	0.9bc	2.2cd	21.4cd	22.6cd	3.8gh
RCI13/118	14.1ab	81.1ab	11.4bc	13.4fg	136.3ab	7.6ab	10.4bc	135.7	17.5bc	1.1ab	2.1ef	24.1ab	18.7h	6.5ef
RCI13/119	11.8gh	78.0cd	9.2hi	15.7ab	97.1fg	5.7fg	5.5ij	160.8	37.3a	0.7c	2.1f	20.3cd	20.6de	32.0a
RCI13/12	15.5abc	82.9ab	12.2ab	15.3ab	131.5ab	8.2ab	10.7bc	141.7	12.8fg	1.0ab	2.8a	20.9bc	21.9cd	27.4ab
RCI13/120	15.0abc	82.7ab	12.3ab	12.9gh	125.9bc	8.4ab	10.6bc	139.5	13.7de	0.9ab	2.3bc	22.7ab	19.2fg	13.8de
RCI13/121	16.1abc	84.8ab	13.1ab	13.6ef	144.6ab	9.2ab	13.3ab	149.7	10.5hi	1.0ab	2.8a	20.6bc	24.7bc	0.0i
RCI13/122	16.9ab	84.4ab	13.4ab	14.9ab	115.5bc	9.3ab	10.8bc	142.3	16.2cd	1.1ab	2.5ab	21.5ab	23.4cd	4.3gh
RCI13/123	14.5abc	83.8ab	11.7ab	14.1cd	118.9bc	8.0ab	9.6cd	163.3	15.3cd	1ab	2.2cd	22.1ab	21.1cd	8.2ef
RCI13/124	15.1abc	79.2bc	12.0ab	15.1ab	122.1bc	7.7ab	9.4de	185.3	12.4fg	0.9bc	2.4ab	20.0de	22.9cd	1.0hi
RCI13/125	14.0bc	79.2bc	11.1cd	14.7bc	102.9de	7.1cd	7.4fg	135.0	8.9ij	1.2ab	2.7ab	22.5ab	27.2a	1.5hi
RCI13/126	16.3ab	85.1ab	13.3ab	13.8de	114.4bc	9.3ab	10.7bc	145.0	5.8jk	1.1ab	2.4ab	22.8ab	24.2bc	0.8i
RCI13/136	15.4abc	83.6ab	12.7ab	12.7hi	146.9ab	8.8ab	12.8ab	152.7	12.3fg	1.3a	2.4ab	23.9ab	21.0cd	7.7ef
RCI13/137	14.5abc	82.6ab	11.6ab	14.3cd	128.7ab	7.8ab	10.1bc	157.7	16.0cd	1.1ab	2.4ab	22.1ab	22.2cd	15.9cd
RCI13/17	14.3abc	79.3bc	11.9ab	12.4i	136.9ab	7.8b	10.5bc	123.5	17.1bc	1.3a	2.5ab	25.0a	22.7cd	6.3ef
RCI14/11	17.1ab	85.4ab	14.1a	12.9gh	137.7ab	10.0a	13.7ab	146.7	11.5gh	1.2ab	2.6ab	22.9ab	21.6cd	10.8ef
RCI14/127	17.1ab	86.8a	13.9ab	13.8de	102.4de	9.9a	10.2bc	154.7	15.1cd	0.9bc	2.3cd	20.6bc	22.5cd	7.7ef
RCI14/129	15.2abc	80.1ab	12.2ab	14.4cd	133.0ab	8.0ab	10.6bc	165.2	14.1de	1.0ab	2.5ab	22.0ab	20.2ef	3.0gh
RCI14/130	13.1cd	77.6de	10.6de	13.9cd	149.5ab	6.6de	10.0bc	152.7	14.6cd	1.1ab	2.5ab	22.1ab	21.1cd	7.1ef
RCI14/131	15.6abc	82.2ab	12.5ab	14.0cd	131.2ab	8.5ab	11.1bc	152.5	12.7fg	1.1ab	2.6ab	20.8bc	22.4cd	4.8fg
RCI14/132	15.6abc	84.7ab	12.8ab	13.5ef	128.0ab	8.9ab	11.4bc	154.2	14.1de	1.1ab	2.4ab	22.1ab	20.0ef	7.6ef
RCI14/14	11.3h	73.5f	9.0i	15.0ab	90.8g	5.2g	4.8j	130.8	24.2b	0.9ab	2.5ab	22.9ab	18.9gh	22.8bc
RCI14/18	12.5ef	78.9ab	9.7gh	16.0a	99.5ef	6.1ef	6.2hi	140.0	21.6bc	0.9bc	2.5ab	21.7ab	20.6de	21.0bc
Mean	14.8	81.8	12.0	14.0	126.3	8.0	10.2	148.9	15.6	1.0	2.4	22.1	21.8	9.2
SD	2.2	4.9	1.9	1.7	23.7	1.7	3.1	38.5	7.6	0.2	0.3	2.4	2.7	11.5
CV(%)	15.1	6.0	15.7	11.9	18.8	21.6	30.6	26.0	48.6	23.6	11.2	11.0	12.0	125.0
Replications	Ns	Ns	Ns	Ns	**	Ns	Ns	***	**	*	Ns	Ns	**	Ns
Genotypes	***	***	***	***	***	***	***	Ns	***	***	***	***	***	***
Crop cycles	Ns	***	***	***	*	Ns	**	***	***	Ns	***	***	Ns	***
Genotypes x Cycles	Ns	Ns	Ns	Ns	Ns	Ns	Ns	Ns	***	Ns	Ns	Ns	***	***

SNb: millable stalk number/ha; BIN: bored internode; AvWeight: average stalk weight; AvHeight: average stalk height; Ns: non-significant.

*, **,***: significant at 5, 1 and 0.1% levels of probability.

Table 4. Variability and heritability among sugarcane genotypes tested as plant crop and first ratoon (aggregate data) in Ferké, Ivory Coast

Variability	Mean	Variance			Coef. of variation (%)		h² (%)	GA	GAM (%)
		σ^2_p	σ^2_e	σ^2_g	PCV	GCV			
Juice sucrose%	14.8	4.0	1.6	2.4	13.5	10.4	59.8	2.5	16.7
Purity%	81.8	16.7	8.2	8.4	5.0	3.5	50.5	4.2	5.2
Sucrose%	12.0	2.8	1.0	1.7	13.9	11.0	62.6	2.1	18.0
Fiber content%	14.0	1.0	0.3	0.7	7.1	6.0	72.1	1.5	10.6
Cane yield (t/ha)	123.3	426.6	200.6	226.0	16.7	12.2	53.0	22.6	18.3
Recov. sucrose%	8.0	2.4	1.0	1.5	19.4	15.1	60.6	1.9	24.3
Sugar yield (t/ha)	10.2	8.1	3.0	5.1	27.8	22.1	63.0	3.7	36.2
Stalk number/ha	148.9	396.0	279.0	117.0	13.4	7.3	29.5	12.1	8.1
Bored internode	15.6	43.8	8.5	35.3	42.6	38.2	80.5	11.0	10.7
Avg weight (kg)	1.0	0.0	0.0	0.0	19.3	11.7	36.7	0.1	14.6
Avg height (m)	2.4	0.05	0.0	0.0	9.0	6.0	45.1	0.2	8.4
Avg diameter (mm)	22.1	3.3	2.0	1.3	8.2	5.1	38.7	1.4	6.5
Nb Internodes	21.8	4.6	1.5	3.1	9.8	8.0	67.7	3.0	13.7
Flowering rate%	9.2	75.1	15.3	59.8	94.0	83.9	79.6	14.2	154.4

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, four promising genotypes namely RCI12/15, RCI12/19, RCI13/121 and RCI13/136 were equivalent to the check variety R579 which performed 15.6 t/ha. They are due to undergo the advanced selection stage during the 2020-21 cropping season for three more years for determining the first new sugarcane varieties of RCI origin to be tested commercially in Ferké sugar estates. Their yield performances ranged from 12.8 to 13.8 t sugar /ha, i.e. from 134.0 to 144.8 t cane/ha compared with 161.3 t/ha for the control variety. Although a relatively high level of stem-borer infestation rate recorded with 15.6% on average (almost three times the tolerable threshold value of 5%), reasonable values of sucrose percent obtained with the promising genotypes, ranged from 12.7 to 13.9% over both crop cycles, compared with 13.6% for the check. Higher heritability values ranging from 61 to 80.5% were observed in traits like sugar yield, sucrose content (62.6%), recoverable sucrose (60.6%), fiber content (72%), stem-borer infestation rate (80.5%), number of internodes/stalk (67.7%), and flowering rate (79.6%). In contrast, lower and moderate values of heritability were observed for Pol juice (59.8%), Juice purity (50.5%), cane yield (53%), millable stalk number/ha (29.5%), single stalk weight (36.7%), single stalk height (45%), and single stalk diameter (38.7%).

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