Genetic Variation and Heritability for Juice Quality and Yield Traits in Selection of Sugarcane Genotypes under Irrigation at Early Stage in Ferké 2 Sugar Estate of Northern Ivory Coast

By Crépin B. Péné, Yavo Michael Béhou & Marcel Silué

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Keywords: early season, phenotype, genotype, environmental influence, multivariate analysis, genetic advance.

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Keywords: early season, phenotype, genotype, environmental influence, multivariate analysis, genetic advance.

1. Introduction

For its high biomass production, and its well-established farming system and processing technologies, sugarcane is a top-ranking candidate for bio energy production and an important source of bio fuel for bio-refineries. Nevertheless, productivity improvements in sugarcane have been almost nil in the past three decades, and production statistics exhibit decreased yields globally [1]. In most cases, increased sugarcane production used to be explained by the expansion of land surface rather than increase in yield [2, 3].

Commercial sugarcane varieties under cultivation are complex polyploids, which heterozygous nature has resulted in generations of higher genetic variability. Information about the nature and magnitude of variability present in genetic materials is of prime importance for breeders to conduct effective selection programs[3-4]. Genotypic and phenotypic coefficients of variation, together with heritability and genetic advance, are key elements to improve any agronomic trait of sugarcane, as this would help in knowing whether or not specific objectives targeted could be achieved from a given crop material [3-5].

Sugarcane used to be the major source of sugar production in Ivory Coast and many tropical countries, where this crop used to be traditionally cultivated mainly for chewing purpose by smallholder farmers. Commercial sugarcane production in Ivory Coast started in 1974 at Ferké 1 plantations on about 5,500 ha[3]. Nowadays, sugarcane is grown on around 30,000 ha and the four sugar mills located in three different regions of the country produce, on yearly basis, about 200,000 t sugar [3, 6]. This production does not meet the domestic consumption, which is estimated to around 240,000 t. The production deficit is being offset by imported sugar, to alleviate the gap between supply and demand of sugar. Besides the expansion of existing sugar mill plantations, a productivity improvement and capacity-building project was implemented in the
country from March 2009 to June 2016, with the assistance of the European Union (EU) [7].

Cane and sugar yields are considered as complex characters in sugarcane, which phenotypic and genotypic interrelationships with their component traits would be of prime importance to breeders. Understanding associations between traits is of great importance in breeding and selection studies, particularly for low heritability or hardly measuring attributes [6, 8-10], like cane and sugar yields, recoverable sucrose, number of tillers/ha, and number of attacked internodes by stem borer. Genetic relationships between important attributes in studying sugarcane populations through breeding and direct selection are crucial to understand how changes made by selecting one character may affect the others [3, 6, 11-12]. This knowledge can be used when determining effective selection strategies for particular traits in a sugarcane breeding program [6, 13]. Likewise, the number of millable stalks/ha, single stalk height and single stalk diameter were reported to be positively associated with cane yield [6, 14-15]. Moreover, phenotypic associations between yields and their components in sugarcane showed that selecting for juice quality traits, number of tillers/ha, single stalk diameter and height, should be emphasized in variety development programs where high cane and sugar yields were the primary goal [3, 6, 16].

The objective of present study was to determine the best performing sugarcane genotypes under irrigation at early selection stage for different agromorphological traits, based on their genetic variations and heritability.

II. MATERIAL AND METHODS

a) Site characteristics

The experiment was conducted on a small portion (0.6 ha) of 80 ha-sugarcane plantation (V4-043) at Ferké 2 sugar estate, under a center pivot irrigation system, in northern Ivory Coast (9°20' - 9°60' N, 5°22' - 5°40', 325 m a.s.l.). The climate of the region is tropical dry, with two different seasons: one, occurring from November to April, is dry and the other, from May to October, is wet. The rainfall pattern is unimodal and centered on August and September which total amount of precipitation reaches almost half of the average annual rainfall (500 mm over 1200 mm/yr). The average daily air temperature yields 27°C, ranging from 21 and 32.5°C as average minimum and maximum daily air temperatures, respectively[18]. Irrigation water requirements in this area for sugarcane reaches 650-700 mm/cycle [19]. Both Ferké sugar mill plantations cover nearly 17,000 ha with 11,500 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[18-19].

b) Cane genotypes tested

Except for the control, all genotypes tested were pre-selected sugarcane clones in Ferké-agaropedological environment at the third stage, i.e., at one genotype per row stage. As genotypes of Reunion Island and Ivorian origin, they resulted from crosses made in Reunion Island, and selection under way at Ivorian sugar estates of Ferké.

c) Assessment of irrigation water requirement

The irrigation water requirement (I), over a given period, was calculated following the climatic water balance method as the difference between maximum evapotranspiration (ETm) and rainfall (R) collected from the closest rain-gauge to the Ferké 2 sugarcane plantation V4-043 subjected to the field experiment, as follows[19].:

\[ I = ETm - R \] (1)

\[ ETm = Kc \times ETo \] (2)

Where:

- Values of crop coefficient Kc were equal to 0.5, 0.8 and 1.0 over tillering, early stem elongation, and late stem elongation stages, which last two, one and half and 8 months, respectively.

- Reference evapotranspiration ETo is computed as follows[19].:

\[ ETo = \Delta/(\Delta + \gamma) \times Rn \]

\[ \Delta/(\Delta + \gamma) = 0.51 + 0.009 \times Ta \]

Rn: Net radiation = a Rg + b, a linear function of global radiation (Rg), which is measured as the average air temperature (Ta = (Tmax+Tmin)/2) in the local automatic weather station.

- Psychrometric constant = 0.66 mb/°C

- Δ: slope of the moisture saturation curve at air temperature E(Ta).

From the equation (1), irrigation water (I) is defined when positive (I > 0), otherwise there is no need of watering because of rainfall excess compared to maximum evapotranspiration (ETm), particularly during the period of heavy rainfall from mid-July to mid-October.

d) Experimental design

The study was conducted over two consecutive years, as early-season trial in plant and first ratoon crops, from November 29, 2018 to November 17, 2019 and October 26, 2020 (i.e. 11.5 month-crop cycle), following a randomized complete block design (RCBD) with 30 different genotypes, including the check (R579), in 3 replicates. An experimental plot was made of 5 dual rows of 5 m long with narrow and wide spacings of 0.50 m and 1.90 m, respectively. Cropping operations, like sprinkler irrigation, fertilizer and herbicide applications...
were performed following usual practices in commercial plantations. NKP fertilizer (16-8.5-23) was applied mechanically at the routine rates of 700 and 720 kg/ha in plant cane and first ratoon, respectively. Pre-emergence chemical weeding based on pendimethalin mixed with chlorimuron-ethyl (3.5 l/ha) was also achieved mechanically, two days after planting or harvest.

e) Agronomic traits investigated
At harvest, burned cane fresh production of the three central dual rows of each plot was weighed in situ, separately, to determine cane 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 Eldanasaccharina W. (Lepidoptera: Pyralidae) [7].

Thirty millable cane stalks were also sampled per plot, on random basis, for juice quality analyses in the laboratory, to determine the recoverable sucrose content and therefore calculate the sugar yield with regard to the cane yield obtained. Prior to sample crushing operations in the laboratory for sucrose analyses, every stalk was cut into 3 pieces of almost equal length while separating them in basal, medial 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 initial cane stalks. Eventually, only one batch of 10 reconstituted stalks over 30 (1/3 of initial sample) were crushed 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) [6, 7]. 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 juice qualit,ytraits were reported by Hoarau [20]. The recoverable sucrose was calculated as follows [6-7, 21):

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

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

Pol%C = Factor n × Pol juice %

Sugar Yield (t/ha) = SE%C x Cane Yield (t/ha).

f) Determination of genetic parameters
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 effect model were determined from linear combinations as follows (Burton and Davane [22], cited by Shitahum et al [23], Péné and Béhou [3, 6]):

Genotypic variance \((\sigma^2_g) = (MS_g - MS_e)/r\)

Environmental variance \((\sigma^2_e) = MS_e\)

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

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 [3, 6, 24]:

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

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

According to Shivasubramanian and Menon [25], cited by different investigators [26-29], PCV and GCV values are ranked as low, medium and high with 0 to 10%, 11 to 20% and higher than 20% respectively.

Broad sense heritability \(h^2 = 100 \times \sigma^2_g / \sigma^2_p\).

Estimates of broad-sense heritability \((h^2)\) are categorized according to Robinson [30] cited by different authors [25, 31, 38, 42] as low (<30%), moderate (30 ≤ -<60%) or high (≥60%).

Genetic advance (GA) and genetic advance as percent mean (GAM):

\[ \text{GA} = k \times h^2 \times \sigma^2_p \text{ and } \text{GAM} = 100 \times \text{GA}/X. \]

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 [24]:

\[ r_p = \frac{\text{Cov}_{p}(A,B)}{\sigma_p \times \sigma_p} \]

\[ r_g = \frac{\text{Cov}_{g}(A,B)}{\sigma_g \times \sigma_g} \]

where, \(\text{Cov}_p\) and \(\text{Cov}_g\) 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 [25].

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 [26-27]. Heritability represents the relative importance of genetic and
environment factors in the expression of phenotypic and genotypic differences among genotypes within a population [3, 6, 28-30]. Therefore, the knowledge of heritability related to important traits and the correlations among them are key issues to determine the best selection strategy [31-32, 38]. Genotypic coefficient of variation (GCV) is another measure of relative genetic variation of a trait within a population [33]. Chaudhary [34] reported high GCV for single stalk weight and millable cane number per unit area. Genotype versus environment interactions (GxE) are a serious concern in breeding programs as they affect decision making in selection. When the ranking of genotypes changes across environments, it requires their evaluation environment-wise to determine their accurate performance [35, 38]. Studies in various sugarcane breeding programs have reported significant G×E interactions for cane and sugar yields [36-38].

g) Statistical analyses
Juice quality and yield traits recorded in this study were subjected to the analysis of variance, using statistical procedures described by Gomez and Gomez [39], and reported by Shitahum et al [23]. Calculations were made by means of R software package version 3.5.1 (Table 1). Differences between means of treatments were determined from Duncan test.

Table 1: Analysis of variance calculations regarding a Randomized Complete Block Design (RCBD)

| Source of variation | Degree of freedom | Mean square | Expected mean square |
|---------------------|-------------------|-------------|---------------------|
| Replication         | r-1               | MSr         | σ²r + γ²r           |
| Genotypes           | g-1               | MSG         | σ²g + γ²g           |
| Error               | (r-1)(g-1)        | MSe         | σ²e                 |

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; σ²r, σ²g, and σ²e stand for variances due to genotypes, replicates and error respectively.

III. Results and Discussion

a) Climatic conditions over plant cane and first ratoon
Total rainfall recorded in first ratoon decreased by 29% compared to that of plant cane (Figure 1), i.e. it varied from 936.4 to 762.4 mm, respectively. Total reference evaporation (ETo) decreased by 5% from plant cane to first ratoon, i.e. it varied from 1334 to 1267 mm, and the average daily temperature, from 27.5 to 26.3°C (-4%), respectively. Total water deficit over the dry season (from November to June) to be met by irrigation water gave 664 mm in plant cane and 561 mm in first ratoon. Total irrigation water applied reached 554 and 454 mm in plant cane and first ratoon, respectively.

Figure 1: Climate of the experimental site over crop cycle (plant and 1st ratoon) in Ferké 2, Ivory Coast. Total rainfall and irrigation water requirement: plant cane (R: 936.4, I: 664 mm), first ratoon (R: 762.4, I: 561 mm)
b) Performance of cane genotypes tested

Highly significant differences (P<0.01) were observed for all agro-morphological traits investigated, not only for the first ratoon but also for the aggregate data of both crop cycles (Tables 3 and 4). Based on sugar yields, three genotypes, namely RCI14/128, RCI11/112, and RCI11/190 performed better than the control variety (R579), with 16.4, 15.8 and 15.0 sugar/ha, respectively, compared to 13.2 t/ha. Their cane yield performances reached 151.5, 164.2 and 132.6 t/ha, respectively, compared to 146.1 t/ha for the check. Higher juice quality traits, like purity, sucrose content, and recoverable sucrose percent were obtained with genotype RCI11/190, while the higher cane yield with moderate quality traits were observed with RCI11/112. Genotype RCI14/128 was a good compromise with higher juice quality and yield traits.

Table 2: Mean values of sugarcane juice quality and yield traits at first ratoon in Ferké 2 Sugar estate

| Genotypes   | Purity% | Sucrose% | Fiber% | Recoverable sucrose% | Internode bored% | Cane (t/ha) | Sugar (t/ha) |
|-------------|---------|----------|--------|----------------------|------------------|------------|-------------|
| R579_(T)   | 87.2 ab | 13.3 ab  | 12.7 e | 9.6 abc               | 4.7 ab           | 123.1 abc  | 11.7 bc     |
| RCI11/112  | 88.1 ab | 13.6 ab  | 13.4 bcde | 9.8 ab               | 4.1 ab           | 164.5 a   | 15.9 ab     |
| RCI11/134  | 86.7 ab | 12.5 b   | 13.2 bcode | 8.9 bc              | 3.1 ab           | 148.8 ab  | 13.2 abc    |
| RCI11/135  | 86.7 ab | 12.0 b   | 13.0 bcode | 8.5 bc              | 3.8 ab           | 130.5 ab  | 11.1 bc     |
| RCI11/162  | 87.9 ab | 13.5 ab  | 13.8 bcode | 9.7 ab              | 3.8 ab           | 127.6 ab  | 12.4 bc     |
| RCI11/165  | 85.3 a  | 12.1 b   | 13.4 bcode | 8.4 bc              | 6.0 ab           | 137.7 ab  | 11.6 bc     |
| RCI11/166  | 89.3 ab | 13.8 ab  | 13.7 bcode | 10.0abc             | 5.6 ab           | 133.3 abc | 13.4 abc    |
| RCI11/190  | 91.5 a  | 15.7 a   | 13.8 bcode | 11.8 a              | 2.5 ab           | 119.6 abc | 14.1 ab     |
| RCI12/191  | 87.7 ab | 13.2 ab  | 14.2 abc | 9.4 abc             | 1.9 b            | 115.5 abc | 10.8 bc     |
| RCI12/192  | 86.6 ab | 14.8 ab  | 14.8 a  | 10.5 abc             | 1.7 b            | 116.1 abc | 12.1 bc     |
| RCI13/110  | 87.9 ab | 13.1 ab  | 12.9 de  | 9.5 abc             | 3.1 a            | 146.5 ab  | 13.9 abc    |
| RCI13/13   | 88.8 ab | 13.9 ab  | 13.6 bcode | 10.1 abc            | 3.9 ab           | 132.3 abc | 13.3 abc    |
| RCI13/139  | 87.0 ab | 12.5 b   | 13.8 bcode | 8.9 bc              | 4.2 ab           | 157.7 abc | 10.3 bc     |
| RCI13/16   | 87.3 ab | 13.0 ab  | 13.6 bcode | 9.3 bc              | 3.0 ab           | 156.5 abc | 14.5 abc    |
| RCI13/173  | 88.0 ab | 13.6 ab  | 13.7 bcode | 9.8 abc             | 4.3 ab           | 130.7 abc | 12.8 abc    |
| RCI13/174  | 84.1 b  | 12.1 b   | 13.7 bcode | 8.3 bc              | 2.3 ab           | 60.3 d    | 5.1 d       |
| RCI13/177  | 89.5 ab | 14.4 ab  | 13.3 bcode | 10.6 abc            | 2.2 ab           | 99.8 bcd  | 10.5 bc     |
| RCI13/179  | 87.9 ab | 13.3 ab  | 13.8 bcode | 9.6 abc             | 3.0 ab           | 115.7 abc | 11.1 bc     |
| RCI13/180  | 86.8 ab | 13.0 ab  | 13.2 bcode | 9.3 bc              | 3.6 ab           | 130.0abc  | 12.3 bc     |
| RCI13/187  | 87.4 ab | 13.2 ab  | 13.1 bcode | 9.5 abc             | 3.4 ab           | 150.1 ab  | 14.3 abc    |
| RCI13/193  | 87.7 ab | 13.3 ab  | 13.3 bcode | 9.5 abc             | 3.2 ab           | 115.8 abc | 11.1 bc     |
| RCI13/194  | 87.6 ab | 13.8 ab  | 12.9 cde  | 10.0abc             | 4.0 ab           | 142.6 abc | 14.1 abc    |
| RCI13/195  | 83.7 b  | 12.1 b   | 14.3 cde  | 8.2 c               | 3.4 ab           | 129.7 abc | 10.6 bc     |
| RCI13/196  | 88.1 ab | 14.2 ab  | 13.5 bcode | 10.3 abc            | 2.1 ab           | 119.9 abc | 12.3 bc     |
| RCI14/111  | 88.1 ab | 13.3 ab  | 13.2 bcode | 9.6 abc             | 4.3 ab           | 147.7 ab  | 14.1 abc    |
| RCI14/128  | 90.9 a  | 14.6 ab  | 13.4 bcode | 10.8 ab             | 6.7 a            | 167.7 a   | 18.2 a      |
| RCI14/159  | 87.6 ab | 13.5 ab  | 13.2 bcode | 9.7 abc             | 3.3 ab           | 123.1 abc | 12.0 bc     |
| RCI14/171  | 86.5 ab | 12.8 b   | 13.7 bcode | 9.1 bc              | 5.6 ab           | 107.2 abc | 9.6 bc      |
| RCI14/188  | 90.1 ab | 13.8 ab  | 14.0abcde | 10.1 abc            | 2.4 ab           | 82.5 cd   | 8.3 cd      |
| RCI14/189  | 86.9 ab | 12.8 b   | 12.9 de  | 9.2 bc              | 6.2 ab           | 94.5 bcd  | 8.7 cd      |

Mean: 87.6 13.3 13.5 9.6 3.7 126.2 12.1
CV (%): 2.7 8.5 4.2 10.7 54.0 22.5 24.7
Replications: * ns ns * *** ns *
Genotypes: * *** *** *** *** *

CV: coefficient of variation. ns: non-significant *: significant ** or ***: highly significant
Table 3: Mean values of sugarcane juice quality and yield traits regarding plant cane and first ratoon on aggregate, in Ferké 2 Sugar estate

| Genotypes       | Juice quality criteria | Yield traits (t/ha) |
|-----------------|------------------------|--------------------|
|                 | Purity% | Sucrose% | Fiber% | Recoverable sucrose% | Internode bored % | Cane | Sugar |
| R579 (T)        | 86.1 cd  | 12.9 bcde| 12.2 e | 9.2 cdef            | 4.9 ab | 146.1 ab | 13.2 abcde |
| RCI11/112       | 87.9 abcd| 13.5 bcde| 13.1 cde| 9.7 bcdef | 5.7 a | 164.2 a | 15.8 ab |
| RCI11/134       | 85.9 cd  | 12.3 efg | 12.8 cde| 8.6 efg            | 3.7 ab | 153.5 ab | 13.2 abcde |
| RCI11/135       | 87.0 bcd | 12.4 defg| 12.9 cde| 8.9 defg          | 3.9 ab | 145.1 ab | 12.9 abcde |
| RCI11/162       | 86.2 cd  | 13.1 bcde| 12.6 cde| 9.1 cdef           | 3.5 ab | 136.9 ab | 12.7 abcde |
| RCI11/165       | 85.1 d   | 12.3 fde| 13.0 cdeo| 8.6 efg           | 5.6 a | 117.4 bc | 10.1 efg |
| RCI11/166       | 87.0 bcd | 13.2 bcdef| 13.0 cdeo| 9.4 bcdef         | 5.5 a | 149.3 ab | 14.0 abcde |
| RCI11/190       | 90.4 a   | 15.3 a  | 13.3 bcde| 11.4 abc          | 3.2 ab | 132.6 ab | 15.0 abc |
| RCI12/191       | 85.0 d   | 11.8 fg  | 13.8 bcde| 8.2 fg            | 2.0 ab | 140.4 ab | 11.2 cdefg |
| RCI12/192       | 87.5 abcd| 14.5 ab  | 14.1 ab  | 10.4 abcd         | 1.4 b | 121.1 abc | 12.6 abcde |
| RCI13/110       | 86.8 cd  | 12.9 bcde| 12.2 e  | 9.2 cdef           | 3.4 ab | 157.0 ab | 14.4 abcde |
| RCI13/13        | 87.5 abcd| 13.4 bcde| 12.9 cde| 9.7 bcdef         | 4.2 ab | 134.6 ab | 13.0 abcde |
| RCI13/139       | 86.7 cd  | 13.1 bcde| 13.0 cde| 9.3 cdef           | 3.6 ab | 131.2 ab | 12.4 abcde |
| RCI13/16        | 85.6 cd  | 12.6 cdef| 13.3 bcde| 8.9 cdefg        | 2.9 ab | 153.9 ab | 13.7 abcde |
| RCI13/173       | 87.8 abcd| 13.8 bcd | 13.3 bcd| 10.0 bcdef        | 3.2 ab | 136.1 ab | 13.6 abcde |
| RCI13/174       | 84.9 d   | 12.6 cde| 13.1 cde| 8.8 defg          | 2.1 ab | 92.5 c  | 8.4 g |
| RCI13/177       | 88.9 abc | 14.2 abc | 12.9 cde| 10.4 abc          | 3.0 ab | 120.0 bc | 12.5 abcde |
| RCI13/179       | 87.0 bcd | 13.0 bcde| 13.5 bcd| 9.3 cdef          | 4.2 ab | 132.0 ab | 12.2 bcde |
| RCI13/180       | 85.8 cd  | 12.7 cde| 13.3 bcd| 9.0 cdef          | 3.3 ab | 141.2 ab | 12.8 bcde |
| RCI13/187       | 86.5 cd  | 13.2 bcd | 12.4 de| 9.4 bcdf         | 3.0 ab | 148.7 ab | 14.0 abcde |
| RCI13/193       | 87.2 bcd | 13.0 bcd | 12.9 cde| 9.3 cdef          | 3.9 ab | 133.4 ab | 12.4 abcde |
| RCI13/194       | 87.2 bcd | 13.8 bcd | 12.1 e | 9.9 bcde        | 5.5 a | 144.5 ab | 14.3 abcde |
| RCI13/195       | 82.1 e   | 11.5 g  | 14.6 a  | 7.7 g            | 3.0 ab | 135.6 ab | 10.4 defg |
| RCI13/196       | 87.7 abcd| 14.0 bcde| 13.0 cde| 10.1 bcde        | 2.8 ab | 137.5 ab | 13.9 abcde |
| RCI13/141       | 87.5 abcd| 13.5 bcde| 13.1 cde| 9.7 bcdef        | 5.4 a | 152.7 ab | 14.8 abc |
| RCI14/128       | 83.2 ab  | 14.6 ab  | 13.0 cde| 10.8 ab          | 6.0 a | 151.5 ab | 16.4 a |
| RCI14/159       | 86.6 cd  | 13.1 bcde| 13.0 cde| 9.4 cdef         | 2.8 ab | 128.1 ab | 12.0 bcdef |
| RCI14/171       | 86.1 cd  | 13.0 bcdef| 13.4 bcd| 9.2 cdef          | 4.9 ab | 123.0 ab | 11.2 cdefg |
| RCI14/188       | 88.2 abcd| 13.4 bcde| 13.6 bc| 9.6 bcdef        | 2.3 ab | 90.3 c  | 8.6 fg |
| RCI14/189       | 86.8 cd  | 13.2 bcde| 12.4 de| 9.5 bcdef        | 5.3 ab | 114.2 bc | 10.9 cdefg |

Mean 86.8 13.2 13.0 9.4 3.8 135.5 12.7
CV (%) 2.7 8.6 6.6 11.0 56.5 20.5 21.9
Replications * * ns * *** ns **
Genotypes *** *** *** *** *** *** ***

CV: coefficient of variation. ns: non-significant *: significant ** or ***: highly significant

Multivariate analyses of agronomic traits observed in sugarcane

The principal component analysis shows that most relevant traits in genotype clustering are related to juice quality (recoverable sucrose, sucrose content, purity), yields and yield components (sugar yield, cane yield, stalk height, stalk weight), (Figure 2, Table 2). The three high yielding genotypes determined are RCI14/128, RCI11/112, and RCI11/190 with 16.4, 15.8 and 15.0 t/ha, respectively (Table 3). They belong to cluster 2, 4 and 1, respectively (Table 4). In contrast, the least relevant traits in genotype clustering are millable cane stalk/ha, number of internodes, fiber content, and bored internode rate. The least productive genotypes are RCI13/174 (8.4 t/ha) on the one hand, and RCI14/188 (8.6 t/ha) and RCI11/165 (10.1 t/ha) on the other hand, which belong to clusters 4 and 3, respectively. The dendrogram deduced from hierarchical ascendant classification analysis exhibits 6 different cluster genotypes (Figure 2), which average agromorphological characteristics are displayed in Table 4.
Figure 1a: Correlation circle of agronomic traits investigated, in 1-2 factor plane

Figure 1b: Projection of sugarcane genotypes following their agronomic performances, in 1-2 factor plan

Figure 1: Results of principal component analysis regarding aggregate data of plant cane and first ratoon crops, obtained in Ferké 2 sugar estate

Figure 2: Dendrogram deduced from the cluster analysis of all 30 cane genotypes tested in Ferké 2 sugar estate, based on different agronomic traits observed in plant cane and first ratoon on aggregate
Table 4: Average juice quality, yield traits of sugarcane cluster genotypes over plant cane, and first ratoon on aggregate, in Ferké 2 Sugar Estate (Ivory Coast)

| Cluster Genotypes | Juice quality traits | Yield traits (t/ha) |
|-------------------|----------------------|---------------------|
|                   | Purity% | Sucrose% | Fiber% | Recoverable sucrose% | Internode bored % | Cane | Sugar |
| Cluster 1         | 83.6    | 11.7     | 14.2   | 8.0               | 2.5              | 138.0 | 10.8  |
| Cluster 2         | 86.3    | 12.9     | 13.0   | 9.1               | 3.8              | 103.6 | 9.5   |
| Cluster 3         | 86.5    | 12.9     | 12.8   | 9.2               | 3.7              | 143.2 | 13.2  |
| Cluster 4         | 87.3    | 13.4     | 13.1   | 9.6               | 4.5              | 141.4 | 13.6  |
| Cluster 5         | 88.9    | 14.6     | 13.6   | 10.6              | 3.7              | 136.3 | 14.5  |
| Cluster 6         | 89.7    | 14.8     | 13.1   | 10.9              | 3.1              | 126.3 | 13.8  |
| Mean              | 87.0    | 13.4     | 13.8   | 9.6               | 3.5              | 131.5 | 12.6  |

d) Phenotypic correlations between pairs of agro-morphological traits

Juice quality traits (pol juice, purity, sucrose content, and recoverable sucrose) were positively, tightly, and highly significantly correlated between pairs with coefficients ranging from 0.80** to 0.99**. Similar correlation was obtained with cane and sugar yields which coefficient (r=0.86**) matches that magnitude. Juice quality traits were also positively, significantly correlated highly, but moderately, to sugar yield with coefficients ranging from 0.31 to 0.39. In contrast, they were loosely correlated negatively and not significantly (P=0.05) to cane yield, with coefficients ranging from -0.16 to -0.11. The millable stalk number per hectare was positively and moderately correlated to cane and sugar yields, with 0.27 and 0.21, respectively, as coefficients. Agro-morphological characters like stalk diameter and stalk height were moderately and significantly correlated to stalk weight with coefficients of 0.27 and 0.37, respectively. The cane Fiber content was correlated positively to internode number (r=0.32), but negatively to cane and sugar yields (-0.25, -0.23) as reported by different investigators [3, 5, 40-41]. It was negatively correlated to stem borer infestation rate (r=-0.18), in contrast of findings of these investigators. More importantly, it was positively correlated to the recoverable sucrose, in line of observations made by Péné and Béhou [42], and in contrast of findings obtained in the same agro-ecological context [43].

e) Genotypic correlations between pairs of agro-morphological traits

Juice quality traits were positively and strongly correlated between pairs with coefficients ranging from 0.89** to 0.98**. Similar correlation was observed not only with cane and sugar yields (r=0.83**). Other strong and positive correlations occurred between cane yield and the average stalk height (r=0.80**), and between single stalk weight and agro-morphological traits like single stalk height (r=0.77**) and single stalk diameter (r=0.70**). In contrast, a negative and strong correlation was observed between the millable stalk number and single stalk diameter(r=-0.71**), indicating that the higher the number of tillers/ha, the smaller stalk diameter was due to competition for light and soil nutrients. As reported by several researchers [27, 30], such tight genotypic correlations indicate that selection based on single stalk weight, and millable stalk number could lead to improvement in agro-morphological traits like stalk diameter, stalk height and yield traits. In the present study, correlations observed between the internode number and other agro-morphological traits were loose, in contrast of findings reported by these researchers.

Juice quality traits were also positively correlated, but moderately, to sugar yield with coefficients ranging from 0.49 to 0.63, in line of findings obtained by Péné and Béhou [3, 42] in the same agro-ecological context.
Table 5: Phenotypic and genotypic correlation matrix of agro-morphological traits investigated (respectively below and above diagonal) regarding aggregate data of both plant and first ratoon crops

| Genotypes   | Pol juice | Purity | Pol%C  | Fiber% | CYield | RSucrose | SYield |
|-------------|-----------|--------|--------|--------|--------|----------|--------|
| Pol juice   | 1.00      | 0.89** | 0.99** | -0.03  | -0.07  | 0.97**   | 0.49   |
| Purity      | 0.80**    | 1.00   | 0.94** | -0.36  | 0.11   | 0.96**   | 0.63** |
| Pol%C       | 0.98**    | 0.80** | 1.00   | -0.18  | -0.01  | 1.00     | 0.55** |
| Fiber%      | 0.18      | 0.11   | 0.02   | 1.00   | -0.34  | -0.25    | -0.43  |
| CYield      | -0.16     | -0.12  | -0.12  | -0.25  | 1.00   | 0.03     | 0.83** |
| RSucrose    | 0.97**    | 0.87** | 0.99** | 0.00   | -0.11  | 1.00     | 0.59** |
| SYield      | 0.33      | 0.31   | 0.38   | 0.23   | 0.86** | 0.39     | 1.00   |
| SNbx10³     | -0.03     | -0.02  | -0.04  | 0.05   | 0.27   | -0.04    | 0.21   |
| AvWeight    | -0.07     | -0.10  | -0.08  | 0.04   | 0.25   | -0.09    | 0.19   |
| AvHeight    | -0.16     | -0.24  | -0.12  | -0.24  | 0.50*  | -0.13    | 0.39   |
| AvDiam      | -0.05     | 0.04   | -0.02  | -0.10  | 0.19   | -0.01    | 0.16   |
| NbIntemode  | 0.13      | 0.13   | 0.08   | 0.32   | 0.02   | 0.08     | 0.07   |
| BIN%        | -0.09     | -0.04  | -0.06  | -0.18  | 0.24   | -0.05    | 0.21   |

| Genotypes   | SNbx10³ | AvWeight | AvHeight | AvgDiam | NbIntemode | BIN% |
|-------------|---------|----------|----------|---------|-------------|------|
| Pol juice   | -0.13   | -0.14    | -0.22    | 0.03    | -0.03       | 0.05 |
| Purity      | -0.26   | -0.22    | -0.28    | 0.17    | -0.14       | 0.34 |
| Pol%C       | -0.17   | -0.13    | -0.24    | 0.09    | -0.09       | 0.14 |
| Fiber%      | 0.20    | 0.06     | 0.21     | -0.29   | 0.44        | -0.59|
| CYield      | 0.41    | 0.51*    | 0.80**   | 0.23    | 0.13        | 0.44 |
| RSucrose    | -0.19   | -0.15    | -0.26    | 0.11    | -0.12       | 0.20 |
| SYield      | 0.23    | 0.34     | 0.50     | 0.24    | 0.05        | 0.50 |
| SNbx10³     | 1.00    | -0.22    | 0.31     | -0.71** | -0.44       | -0.29|
| AvWeight    | -0.01   | 1.00     | 0.77**   | 0.70**  | 0.41        | -0.18|
| AvHeight    | 0.15    | 0.37     | 1.00     | 0.23    | 0.32        | 0.09 |
| AvDiam      | -0.19   | 0.27     | 0.29     | 1.00    | 0.32        | 0.30 |
| NbIntemode  | -0.12   | 0.17     | 0.10     | 0.18    | 1.00        | -0.01|
| BIN%        | -0.14   | 0.10     | 0.07     | 0.01    | -0.03       | 1.00 |

f) Phenotypic and Genotypic Coefficient of Variation (PCV, GCV)

All PCV and GCV values determined, which ranged from 4.8 to 89% on the one hand, and from 4.4 to 80.5% on the other hand, varied from low to high (Table 6). As far as PCV is concerned, higher values were observed for traits like cane yield, sugar yield, recoverable sucrose, millable stalk number/ha, single stalk weight, single stalk height, and stem borer infestation rate. Moreover, higher GCV values were observed for traits like cane yield, sugar yield, recoverable sucrose, millable stalk number, single stalk weight, and stem borer infestation rate. In line of findings reported by different investigators [44 -45], higher GCV and PCV values indicated that selection might be effective on traits investigated and their expression be relevant to the genotypic potential. Agronomic traits exhibiting relatively high GCV, with values ranging from 29 to 80.5%, might respond favorably to selection, as reported by Ebid et al [46].

Regardless the trait considered in this study, the phenotypic coefficient of variation was higher than the genotypic ones 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 [3, 25, 30,42,47], indicating a good perspective for genetic progress through selection under the agroecological conditions of this study.

g) Phenotypic, Genotypic and Environmental Variances

Regardless the trait considered, phenotypic variance data determined were higher than the genotypic ones. This shows a greater influence of environment on genetic variations, in line of observations made by different authors [19, 27, 46]. No matter the trait considered, genotypic variance calculated was higher than environmental one, suggesting important variations among genotypes, in line of their higher or moderate values of broad sense heritability ($h^2 \geq 56.8\%$) ranging from 53.6 to 87%. Except for the single stalk weight, the heritability observed ranged from 74 to 87%, which values are much higher than the threshold 60%.

h) Heritability and Genetic Advance

Except for the single stalk weight, higher heritability values ranging from 74 to 87% were observed on all traits investigated (Table 6). Estimates of mean genetic advance (GAM) are categorized similarly to GCV and PGV according to Falconer and Mackay [26] cited by several authors [27 -28, 30, 47 -48]. Therefore, except for juice purity (8.5%) and cane fiber content (19.8%), higher values of genetic advance were observed for all traits investigated like cane yield (57%), sugar yield (67%), millable stalk number (52%), single stalk weight (46%), and stem borer infestation rate (150%). Higher values of GAM suggest that a significant proportion of...
the total variance might be heritable and selection of corresponding traits would be effective. In sugarcane, several authors reported similar values on single stalk weight [30, 51-52]. As indicated by Vidya et al [53], 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, as reported by different authors [54-55].

Higher levels of mean genetic advance observed for yield (57%), sugar yield (67%), millable stalk number (52%), single stalk weight (46%), and stem borer infestation rate (150%) were the result of moderate or high broad sense heritability, combined with high GCV for these traits, in line of findings reported by Bakshi [54]. According to this author, cited by Péné and Béhou [55], heritability estimates together with expected genetic gain were more useful than heritability values alone in predicting the effects of selecting best genotypes. Chaudhary [34] 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 [56]. Patel et al [57] 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 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. [6, 22, 41, 58]. But still, this is all about the scope of experimentation in agronomy, findings being mostly site-specific.

Table 6: Variability and heritability among sugarcane genotypes tested in Ferké 2, Ivory Coast (aggregate data of both plant and first ratoon crops)

| Agronomic traits | Mean | Variance | Coefficient of variation (%) | Heritability (%) | Genetic Advance (%) | Estimation |
|------------------|------|----------|-------------------------------|-----------------|---------------------|------------|
|                  |      |          |                               |                 |                     | GAM (%)    |
| Pol juice        | 16.1 | 5.79     | 1.02                          | 15.0            | 16.1                | 86.3       |
| Purity           | 86.8 | 14.88    | 2.85                          | 4.4             | 4.8                 | 86.1       |
| Po%C            | 13.2 | 3.96     | 0.66                          | 15.1            | 16.2                | 86.8       |
| Fiber%           | 13.1 | 1.80     | 0.28                          | 10.3            | 11.0                | 87.1       |
| CYield           | 135.5| 1778.00  | 398.00                        | 31.1            | 34.8                | 80.1       |
| RSucrose         | 9.4  | 3.35     | 0.54                          | 19.4            | 20.8                | 87.1       |
| SYield           | 12.8 | 21.06    | 3.85                          | 36.0            | 39.5                | 83.1       |
| SNbx10³          | 116.3| 1139.90  | 265.80                        | 29.0            | 32.9                | 78.0       |
| AvWeight         | 1.3  | 0.14     | 0.07                          | 29.6            | 39.3                | 56.8       |
| AvHeight         | 260.7| 2468.00  | 510.00                        | 19.1            | 20.5                | 86.6       |
| AvDiam           | 21.9 | 13.05    | 2.63                          | 16.5            | 17.9                | 84.4       |
| NbInternode      | 22.6 | 10.35    | 3.61                          | 14.2            | 16.5                | 74.3       |
| BINC%            | 3.8  | 9.35     | 3.44                          | 80.5            | 89.0                | 81.8       |

IV. Conclusion

The present study showed that most relevant traits in genotype clustering were associated to juice quality (recoverable sucrose, sucrose content, purity), yields and their components like single stalk height, and single stalk weight. Based on sugar yields, three high yielding genotypes compared to the check variety (R579), namely RCI14/128, RCI11/112, and RCI11/190, were determined for the late selection stage, with 16.4, 15.8 and 15.0 t sugar/ha, respectively. Their cane yields reached 151.5, 164.2 and 132.6 t/ha, respectively, compared to 146.1 t/ha for the check, and they belong to two clusters genotypes over six determined. Except for juice purity and cane fiber content, all agromorphological traits investigated have explained the genetic variation of sugarcane genotypes tested, with stem borer infestation rate, cane and sugar yields, and number of tillers/ha as the most important traits in this regard.

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