
Evaluation of Sugarcane Genotypes Under Irrigation Based on Genetic Variations and Heritability for Agronomic Traits at Early Selection Stage in Ferké, Ivory Coast

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Abstract: The objective of the study was to determine the best performing sugarcane genotypes tested at early selection stage under sprinkler irrigation, in comparison with a check variety (R579). The experiment was designed following a randomized complete block (RCB) with 21 cane genotypes in three replications. Each plot consisted of five dual rows of ten meters with 0.5 and 1.90 m of inter-row spacing, i.e. 95 m² per plot and about 6,000 m² for the whole experiment. It was carried out on a commercial sugarcane plantation of Ferké 2 located in the northern part of the country, over two seasons (plant cane and first ratoon) as an early-season crop from, November 18, 2016 to November 15, 2018. Over each micro-plot, data based on different agro-morphological traits were collected at harvest from three central dual rows. The study showed that most relevant traits in genotype clustering were related to juice quality (recoverable sucrose, sucrose content, purity), yields and yield components (millable stalk number/ha, stalk height, stalk diameter, internode number). Based on sugar yields, four genotypes equivalent to the check (R579), namely KQ228, R97-6177, R99-4064 and KQ236, were found promising for the next advanced selection stage with, respectively, 19.2, 17.7, 17.3 and 16.9 t sugar/ha. Their cane yield performances ranged from 147.7 to 170.8 t/ha compared to 170.7 for the check and belong to 3 clusters genotypes over the eight determined. Not only sugar yield, but also flowering rate, stem borer infestation rate and number of tillers per hectare were found as the most relevant agro-morphological traits in the genetic variation of sugarcane genotypes tested.

Keywords: Phenotypic Correlation, Genotypic Correlation, Coefficient of Variation, Genetic Advance, Yield Trait, Juice Quality

1. Introduction

Due to 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 [1]. In all cases, increased sugarcane production is linked to expansion of land surface rather than increase in yield [2].

Commercial sugarcane varieties under cultivation are

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

In Ivory Coast and many tropical countries, sugarcane used to be the major source of sugar production. In the past

time, this crop was cultivated traditionally in the country mainly for chewing purpose by small holder farmers. Commercial sugarcane production in Ivory Coast started in 1974 at Ferké 1 plantations on about 5,500 ha. Nowadays, sugarcane is grown on around 30,000 ha and the four sugar mills located in three different regions of the country produce about 200,000 t sugar per annum [5]. This production does not meet the domestic consumption which is estimated to about 240,000 t. Therefore, the deficit is being offset by imported sugar. To alleviate the gap between supply and demand of sugar, besides expanding the existing sugarcane mill plantations, a productivity improvement and capacity building project has been implemented in the country since 2009 with the assistance of the European Union (EU) [6].

In sugarcane, cane and sugar yields are considered as complex characters which phenotypic and genotypic interrelationship with their component traits would be of importance to breeders. Understanding associations between traits is of great importance in breeding and selection studies, especially for low heritability or hardly measuring traits [7-9]. Genetic relationships between important attributes in studying sugarcane populations through breeding and direct selection is crucial, primarily to understand how changes made by selecting on character may cause changes in others [10-11]. This knowledge can be used when determining effective selection strategies for particular traits in a sugarcane breeding program [12]. Likewise, number of millable stalk, stalk height and stalk diameter were reported to be positively associated with cane yield [13-14]. Similarly, phenotypic associations between yield and its components in sugarcane showed that selecting for stalk number, diameter and length should be emphasized in sugarcane variety development programs where high cane yields were the primary goal [15].

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

2. Material and Methods

2.1. Site Characteristics

The study was carried out on Ferké 2 sugarcane field N1-005, sprinkler irrigated with center pivot, in northern Ivory Coast (9°20' – 9°60' N, 5°22' – 5°40' O, 325 m a. s. l.). 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 northern 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 [16-17]. Both Ferké sugar mill plantations cover around 15500 ha with 10000 ha under irrigation and 3500 ha of rainfed village plantations, lie mainly on shallow or moderately deep soils built up on granites. Main soil units encountered are ferralsols and temporally waterlogged soils in valley bottoms of Bandama and Lokpoho river basins with a sandy-clay texture.

2.2. Cane Genotypes Used

All 21 cane genotypes tested were commercial varieties of four different origins (Australia, Sudan, Reunion and Mauritius). They were provided by the Montpellier sugarcane quarantine of CIRAD (International Centre for Agricultural Research and Development) in France. 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 [18].

2.3. Experimental Design

The experiment was carried out over two consecutive years, as early-season trial in plant and first ratoon crops, from November 18, 2016 to November 15, 2018 following a randomized complete block design (RCBD) with 21 different genotypes, including the check (R579), in 3 replicates. A plot comprised 5 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. NKP fertilizer (16-8.5-23) was applied mechanically at the routine rates of 700 kg/ha in plant cane and 720 kg/ha in first ratoon. Pre-emergence chemical weeding based on pendimethalin combined with clorimuron-ethyl (3.5 l/ha) was achieved mechanically two day after planting.

2.4. Agronomic Traits Investigated

Data were collected at harvest from three central dual rows for millable stalk number/ha, cane yield, agro-morphological traits (stalk weight, stalk diameter, stalk height, number of internodes, flowering rate), juice quality traits (sucrose, purity, and recoverable sucrose), fiber content, and damaged internodes by stem borer *Eldana saccharina* W. (Lepidoptera: Pyralidae).

At harvest, burned cane fresh production of the three 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 crushing 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 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). 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 [19]. The recoverable sucrose was calculated as follows [6, 20]:

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

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

$$Pol\%C = Factor n \times Pol \text{ juice}$$

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 crushing operation of every sample of cane stalks.

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

The phenotypic and genotypic variances for each trait were estimated from the RCBD analysis of variance (Table 1). The expected mean squares under the assumption of random effect model were determined from linear combinations as follows (Burton and Davane [21], cited by Shitahum et al [22]):

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

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

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

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

Genotypic and phenotypic coefficients of variation (GCV, PCV) were computed as follows [23]:

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

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

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

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

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

Phenotypic and genotypic correlation coefficients *r_p* and *r_g* between particular pairs of traits A and B are defined as [24]:

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

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

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

Phenotypic correlations between traits were determined following the Pearson correlation coefficient calculated from means of observed traits for each cane genotype [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 [28-30]. Consequently, the knowledge of heritability related to important traits and the correlations among them are key issues to determine the best selection strategy [31-32]. 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 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 [35]. Studies in various sugarcane breeding programs have reported significant G x E interactions for cane and sugar yields [36-37].

2.6. Statistical Analyses

The quantitative data recorded in this study were subjected to the analysis of variance using statistical procedures described by Gomez and Gomez [38] and reported by Shitahum et al [39] with the assistance 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 RCBD.

Source of variation	Degree of freedom	Mean square	Expected mean square
Replication	r-1	MS _r	$\sigma_e^2 + g\sigma_r^2$
Genotypes	g-1	MS _g	$\sigma_e^2 + r\sigma_g^2$
Error	(r-1)(g-1)	MS _e	σ_e^2

R: number of replicates; g=number of genotypes; MS_r mean square due to replicates; MS_g=mean square due to genotypes; MS_e 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

3.1. Climatic Conditions Over Plant and First Ratoon Crops

Total amount of rainfall recorded in first ratoon increased by 37.5% compared to that of plant cane (Figure 1). In absolute values, it varied from 991.4 to 1363.1 mm, respectively. In contrast, variations of reference evaporation (ETo) and average daily air temperatures were almost negligible from one crop cycle to the other, with -0.7 and -1.4% respectively. In absolute values, total ETo varied on average from 1317.3 to 1308.2 mm, whereas the average daily temperature from 28.1 to 27.7°C. Lower total ETo and mean daily temperature obtained in first ratoon were explained by higher total rainfall recorded compared to that of plant crop. Total water deficit over the dry season (from November to June or July depending on the year) to be fulfilled with irrigation water gave 560 mm in plant cane and 320 mm in first ratoon.

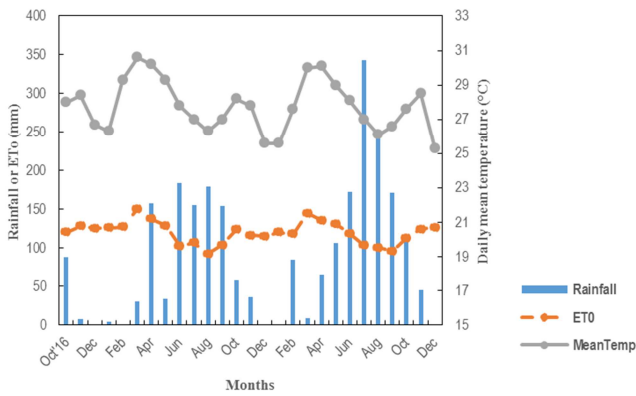
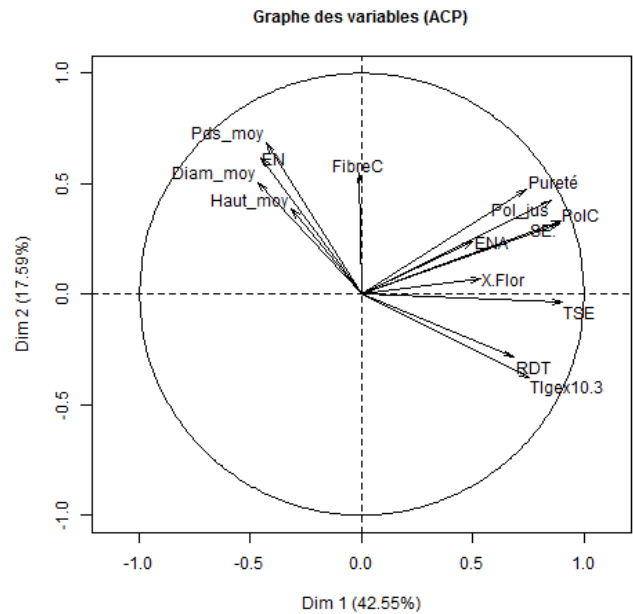


Figure 1. Prevailing climate of the experimental site over crop cycle (plant and 1st ratoon crops) in Ferké 2, Ivory Coast.

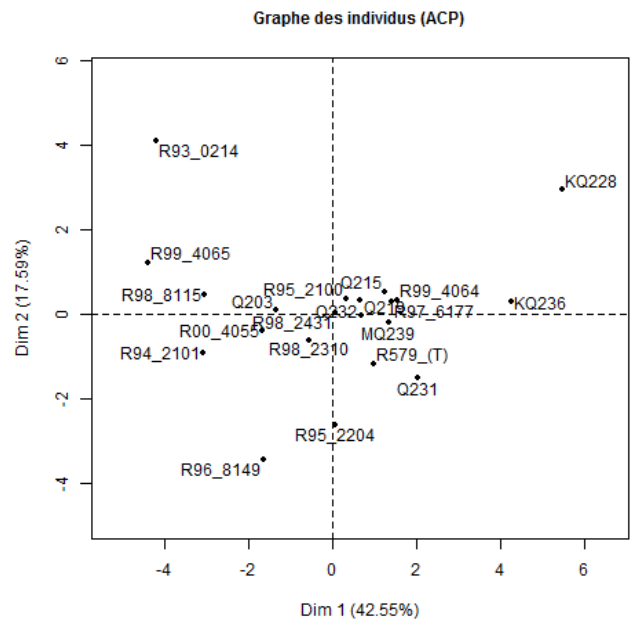
3.2. Multivariate Analyses

It came out from the principal component analysis (Figure 2, Table 2) that most relevant traits in genotype clustering were related to juice quality (recoverable sucrose, sucrose content, purity), yields and yield components (millable stalk number/ha, stalk height, stalk diameter, internode number). Particularly, variety KQ228 from cluster 8 performed better juice quality and higher sugar yield, while R93-0214 from cluster 2 was the least productive with higher fiber content and lower millable stalk number, higher stalk weight and higher stalk diameter. The dendrogram deduced from hierarchical ascendant classification analysis (Figure 3)

exhibits 8 different cluster genotypes which average agro-morphological characteristics are shown in Table 3.



2a: Correlation circle of agronomic traits investigated in 1-2 factor plane.



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.

Table 2. Sugarcane cluster genotypes determined and their main agro-morphological characteristics (aggregate data of both plant and first ratoon crops).

Clusters	Genotypes	Main characteristics
C1 (n=1)	R99-4065	Lower juice quality, very high stalk height, higher internode number, high stalk weight
C2 (n=1)	R93-0214	Lower juice quality, lower stalk number/ha, higher stalk weight, lower cane and sugar yields, larger stalk diameter, higher fiber content
C3 (n=3)	Q203, R94-2101, R98-8115	Lower juice quality, lower stalk weight, larger diameter
C4 (n=2)	R99-2204, R96-8149	Lower stalk height, lower internode number, lower height
C5 (n=2)	Q232, R00-4055	Lower juice quality, higher stalk, higher internode number
C6 (n=6)	Q215, R579, R95-2100, R97-6177, R98-2310, R98-2431	Higher cane and sugar yields, moderate height, moderate juice quality, lower to moderate fiber content

Clusters	Genotypes	Main characteristics
C7 (n=4)	MQ239, Q219, Q231, R99-4064	Higher juice quality, Higher stalk number/ha, higher cane and sugar yields, taller stalk, higher fiber content
C8 (n=2)	KQ228, KQ236	Very High juice quality, higher cane and sugar yields, higher flowering rate, higher stem borer infestation

Table 3. Mean values of clusters genotypes determined following different agronomic traits investigated in Ferké 2, Ivory Coast (aggregate data of both plant and first ratoon crops).

Agronomic traits	Different cluster genotypes							
	C1	C2	C3	C4	C5	C6	C7	C8
Pol juice	15,7	17,2	16,1	16,4	16,7	17,2	17,6	19,6
Purity	86,8	89,8	88,7	87,8	88,3	89,8	90,1	92,3
Pol%C	12,7	13,5	13,2	13,4	13,4	14,1	14,2	15,9
Fiber%	13,7	15,5	13,0	13,0	14,4	13,0	14,3	13,7
CYield	135,5	95,0	124,2	137,2	149,9	155,1	152,7	150,4
RSucrose	9,0	9,8	9,6	9,7	9,6	10,4	10,4	12,0
SYield	12,1	9,3	11,8	13,3	14,4	16,1	15,8	18,1
SNbx103	104,3	73,7	99,8	114,8	112,7	114,4	129,7	125,2
%BIN	6,6	6,7	8,2	5,0	9,3	7,9	8,1	11,3
AvWeight	1,6	1,6	1,4	1,2	1,4	1,4	1,2	1,3
AvDiam	22,1	25,5	24,3	21,4	21,9	23,3	21,3	22,0
AvHeight	3,9	3,1	2,9	2,8	3,3	3,0	3,1	2,9
NbInternode	30,3	28,2	24,2	20,5	24,3	23,0	24,2	22,7
Flowering	5,3	9,0	18,8	25,0	57,8	32,1	24,3	57,4

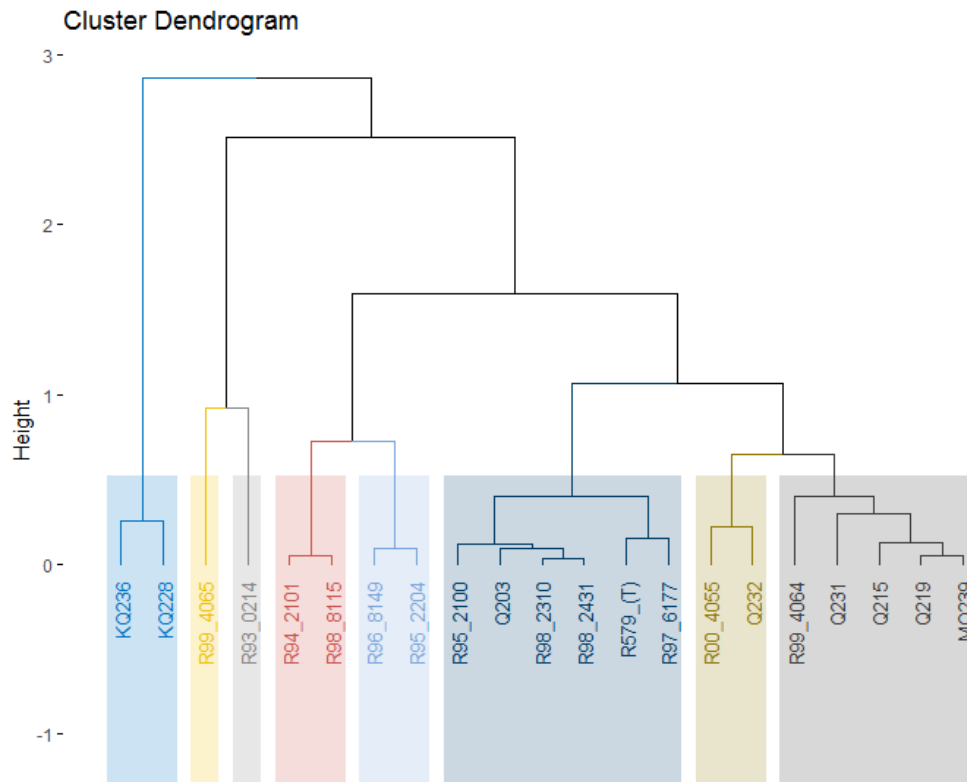


Figure 3. Dendrogram deduced from cluster analysis of all 21 sugarcane genotypes tested in Ferké (Ivory Coast), the check variety (R579) included (aggregate data of both plant and first ratoon crops).

3.3. Performance of Cane Genotypes Tested

Except for the average stalk weight with significant differences within genotypes ($P < 0.05$), highly significant differences ($P < 0.01$) were observed for all agromorphological traits investigated (Table 4). Based on sugar yields, three genotypes, namely KQ228, R97-6177 and R99-4064 were equivalent to the check variety R579 with

respectively 19.2, 17.7 and 17.3 t sugar/ha. Their cane yield performances ranged from 153 to 170.8 t/ha compared to 170.7 for the check. Although a relatively high level of stem borer infestation recorded on KQ 228 and KQ236 genotypes, with respectively 10 and 12%BIN due to high rate of nitrogen fertilizer applied in plant cane, their sucrose content were kept high (16.5 and 15.3 Pol%C). The later genotype KQ236 which gave 16.9 t sugar/ha was equivalent to one of

the promising one indicated previously (R99-4064).

Table 4. Mean values of agronomic traits regarding plant and first ratoon crops on aggregate for different sugarcane genotypes tested in Ferké 2, Ivory Coast.

Genotypes	Pol juic %	Purity %	Pol%C	Fiber %C	CYield (t/ha)	RSucrose %C	SYield (t/ha)
KQ228	20.9	92.9 f	16.5 c	14.0bc	153.1 f	12.5 c	19.2 j
KQ236	19.9	91.7 e	15.3 b	13.4 b	147.7 f	11.5 c	16.9gh
MQ239	18.0	89.9de	14.4ab	14.2 c	144.5 e	10.5 b	15.1 f
Q203	18.2	87.9bc	13.9ab	12.8ab	125.8bc	10.1ab	12.5 c
Q215	19.1	90.4de	14.7ab	13.2 b	142.2de	10.9bc	15.4 fg
Q219	17.5	89.9de	14.1ab	14.0 c	150.1 f	10.4 b	15.5 fg
Q231	17.2	89.9de	13.9ab	14.0 c	151.2 f	10.2 b	15.3 fg
Q232	17.5	89.6 d	13.5ab	14.3 c	156.8 g	9.8ab	15.4 fg
R00-4055	17.8	87.0 b	13.2 a	14.5cd	143.0 e	9.4ab	13.4 cd
R579	18.1	88.7bc	14.3ab	12.5 a	170.7hi	10.5 b	17.9 ij
R93-0214	17.5	89.8de	13.5ab	15.5 e	95.0a	9.8ab	9.3 a
R94-2101	15.7	88.5bc	12.7 a	12.9ab	127.6 c	9.2ab	11.7 bc
R95-2100	18.0	89.4cd	13.9ab	13.4 b	150.5 f	10.2 b	15.2 fg
R95-2204	18.1	89.1cd	13.7ab	13.1 b	139.6de	10.0ab	13.9 d
R96-8149	17.0	86.4 a	13.2 a	12.9ab	134.7d	9.4ab	12.7 c
R97-6177	17.7	90.7de	14.0ab	13.1 b	170.8hi	10.4 b	17.7 i
R98-2310	16.9	88.8 c	13.8ab	12.8ab	145.5ef	10.1 b	14.7 e
R98-2431	16.2	90.5de	13.8ab	12.9ab	151.1 f	10.2 b	15.6 fg
R98-8115	16.4	89.7de	13.0 a	13.2 b	119.3 b	9.5ab	11.2 b
R99-4064	18.8	90.7de	14.3ab	14.9de	165.2 h	10.5 b	17.3 hi
R99-4065	17.0	86.8ab	12.7 a	13.7bc	135.5 d	9.0 a	12.1 bc
Mean	17.1	89.4	13.9	13.6	143.8	10.2	14.7
CV (%)	6.6	1.7	6.7	5.0	12.1	8.2	14.2
Replications	**	***	**	Ns	Ns	***	Ns
Genotypes	***	***	***	***	***	***	***
Crop cycles	**	***	***	***	***	***	ns

Table 4. Continued.

Genotypes	SNbx103 (/ha)	BIN (%)	AvWeight (kg)	AvDiam (mm)	AvHeight (m)	NbInternode (-)	Flowering (%)
KQ228	117.5 e	10.2 b	1.4	22.8	2.9	23.5	61.8
KQ236	132.8 g	12.4 c	1.3	21.2	2.9	22.0	53.0
MQ239	118.8 f	8.2 b	1.2	21.2	3.2	22.7	34.5
Q203	111.0 d	9.5 b	1.4	24.2	3.0	25.0	25.0
Q215	113.0 d	8.7 b	1.3	23.0	3.0	23.7	29.2
Q219	123.5 f	6.1ab	1.3	22.1	3.2	24.2	28.2
Q231	137.5gh	12.4c	1.1	20.5	2.9	24.2	34.5
Q232	116.0de	10.7bc	1.4	21.7	3.3	24.3	79.7
R00-4055	109.3cd	8.0 b	1.4	22.1	3.3	24.3	36.0
R579	125.3 f	6.9ab	1.5	22.9	2.9	22.3	0.0
R93-0214	73.7 a	6.7ab	1.6	25.5	3.1	28.2	9.0
R94-2101	92.7 b	7.2ab	1.3	24.1	2.9	24.5	22.5
R95-2100	107.3cd	10.0 b	1.5	23.5	3.1	21.3	52.0
R95-2204	114.5de	5.1 a	1.2	20.9	2.8	20.3	25.7
R96-8149	115.2de	5.0 a	1.2	21.8	2.8	20.8	24.3
R97-6177	127.5fg	7.5 b	1.4	24.0	3.1	24.0	52.5
R98-2310	103.2 c	5.5ab	1.4	23.2	3.1	21.8	42.7
R98-2431	110.0cd	8.5b	1.4	23.2	3.0	24.8	16.3
R98-8115	95.8bc	8.0 b	1.5	24.5	3.0	23.5	8.8
R99-4064	138.8 h	5.6ab	1.3	21.5	3.2	26.2	0.0
R99-4065	104.3 c	6.6ab	1.6	22.1	3.9	30.3	5.3
Mean	113.7	8.0	1.4	22.7	3.1	23.9	30.5
CV (%)	11.8	34.8	17.3	8.2	7.5	10.6	59.1
Replications	***	Ns	**	Ns	Ns	Ns	Ns
Genotypes	***	***	*	***	***	***	***
Crop cycles	**	***	***	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.

3.4. Phenotypic Correlations Between Pairs of Agro-morphological Traits

All juice quality traits (pol juice, purity, sucrose content,

and recoverable sucrose) were positively, strongly and highly significantly correlated between pairs with coefficients ranging from 0.83 to 0.99. Similar correlation was obtained with cane and sugar yields which coefficient (0.83***)

matches that magnitude. All juice quality traits were also positively, moderately and highly significantly correlated to sugar yield with coefficients ranging from 0.51 to 0.60. In contrast, they were loosely correlated and mostly not significantly ($P=0.05$) to cane yield with coefficients ranging from 0.01 to 0.06. The millable stalk number per hectare was positively and moderately correlated to cane and sugar yields, with 0.56 and 0.58***, respectively, as coefficients. Agro-morphological characters like stalk diameter and stalk height were moderately and significantly correlated to stalk weight with coefficients of 0.72 and 0.60, respectively. Sugarcane flowering impacted negatively on stalk internode number as exhibited by a correlation coefficient of -0.32***, while it enhanced cane and sugar yields with values of 0.28*** and 0.27*** respectively. The cane fiber content was correlated positively to internode number (0.42***) and stem borer infestations rate (0.30***), but negatively to cane yield (0.21***) as reported by different investigators [5, 40-41]. More importantly, it was not negatively correlated to the recoverable sucrose in contrast of findings obtained in the same agro-ecological context [42].

3.5. Genotypic Correlations Between Pairs of Agro-morphological Traits

Juice quality and sugar yield traits were positively and strongly correlated between pairs with coefficients ranging

from 0.86 to 0.98. Similar correlation was observed not only with cane and sugar yields ($r=0.96$), but also between sugar yield other characters like sucrose content (0.82), recoverable sucrose (0.85), and millable stalk number per plot (0.85). Such strong and positive genotypic correlation was observed also between millable stalk number per plot and traits like cane and sugar yields ($r=0.89$ and 0.85 respectively). It was still observed, on the one hand, between the number of internodes and single stalk weight and height ($r=0.75$ and 0.81 respectively), and on the other hand, between single stalk weight and height (0.98). In contrast, strong negative correlation was observed between millable stalk number per plot and single stalk weight and diameter ($r=-0.84$ and -0.83 respectively). As reported by several researchers [30, 43], such strong and positive genotypic correlations indicate that selection based on single stalk weight, internode number and millable stalk number could lead to improvement in agro-morphological traits like stalk diameter, stalk height and yield traits. The flowering ability was negatively correlated moderately or loosely with agro-morphological traits like stalk number of internodes (-0.42), stalk weight (-0.22), stalk diameter (-0.23) and stalk height (-0.06). In contrast, this character was positively and moderately or loosely correlated with stem borer infestation rate (0.67), juice quality traits ($r=0.38 - 0.44$), cane and sugar yields ($r=0.34$ and 0.43 respectively), and millable stalk number per plot (0.23).

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	0.98	0.28	0.39	0.98	0.77
Purity	0.83***	1.00	0.86	0.21	0.34	0.92	0.66
Pol%C	0.98***	0.83***	1.00	0.07	0.45	0.98	0.82
Fiber%	0.36***	0.27***	0.17	1.00	-0.20	0.05	-0.12
CYield	0.01	0.03	0.05	-0.21*	1.00	0.45	0.96
RSucrose	0.97***	0.87***	0.99***	0.14	0.06***	1.00	0.82
SYield	0.54***	0.51***	0.59***	-0.09	0.83***	0.60***	1.00
SNbx103	0.28***	0.19*	0.26***	0.16	0.56	0.25***	0.58***
%BIN	0.21*	0.23***	0.16	0.30***	-0.04	0.16	0.06
AvWeight	-0.31**	-0.27***	-0.32***	-0.08	0.20	-0.31***	-0.01
AvDiam	-0.27**	-0.17	-0.28***	-0.05	-0.16	-0.27***	-0.26***
AvHeight	-0.26***	-0.30***	-0.29***	0.07	0.28***	-0.30***	0.05
NbInternode	0.04	0.05	-0.04	0.42***	-0.23***	-0.05	-0.21
Flowering	0.05	0.11	0.08	-0.12	0.28***	0.10	0.27***

Table 5. Continued.

Genotypes	SNbx103	%BIN	AvWeight	AvDiam	AvHeight	NbInternode	Flowering
Pol juice	0.49	0.49	-0.20	-0.24	-0.20	-0.19	0.43
Purity	0.35	0.53	-0.05	0.00	-0.26	-0.12	0.38
Pol%C	0.52	0.49	-0.23	-0.22	-0.31	-0.32	0.43
Fiber%	-0.06	0.09	0.08	-0.14	0.42	0.52	0.05
CYield	0.89	0.17	-0.38	-0.55	0.06	-0.33	0.34
RSucrose	0.51	0.51	-0.21	-0.19	-0.33	-0.32	0.44
SYield	0.85	0.34	-0.35	-0.45	-0.12	-0.37	0.43
SNbx103	1.00	0.34	-0.84	-0.83	-0.10	-0.34	0.23
%BIN	0.21*	1.00	-0.15	-0.20	-0.15	-0.06	0.67
AvWeight	-0.19*	-0.14	1.00	0.98	0.67	0.75	-0.22
AvDiam	-0.37**	-0.04	0.72***	1.00	-0.08	0.33	-0.23
AvHeight	-0.03	-0.21*	0.60***	0.24	1.00	0.81	-0.06
NbInternode	-0.07	0.21*	0.34***	0.37***	0.44	1.00	-0.42
Flowering	0.03	0.02	0.03	-0.10	0.04	-0.32***	1.00

3.6. Phenotypic and Genotypic Coefficient of Variation (PCV, GCV)

As stated by Shivasubramanian and Menon [43] cited by different investigators [18, 25, 44-45], PCV and GCV values are ranked as low, medium and high with 0 to 10%, 11 to 20% and higher than 20% respectively (Table 5). Based on that statement, all PCV and GCV values determined which ranged from 2.0 to 77.6% on the one hand, and from 1.6 to 664.1% on the other hand, varied from low to high. As reported by different authors [46-47], high GCV and PCV indicated that selection might be effective on traits investigated and their expression be relevant to the genotypic potential. Particularly, agronomic traits exhibiting relatively high GCV estimates like flowering ability, stem borer infestations and sugar yield with values ranging from 16 to 64%, might respond favorably to selection [30]. Regardless the trait considered in this study, the phenotypic coefficient of variation was higher than the genotypic one suggesting that apparent variations were not only due to genetics but also to environmental influences. However, differences between PCV and GCV for most traits were small in line of observations made by different investigators [25, 48-49], indicating high prospects for genetic progress through selection under conditions of this study.

3.7. Phenotypic, Genotypic and Environmental Variance

Regardless the trait considered, phenotypic variance data obtained were higher than the genotypic ones. This shows a greater influence of environment on genetic variations in line of observations made by different authors [18, 30, 43]. Moreover, except stalk borer infestation rate and single stalk weight, genotypic variance data calculated were higher than environmental ones suggesting important variations among genotypes in line of their higher or moderate values of broad sense heritability ($h^2 \geq 53\%$) ranging from 53.6 to 100%. Therefore, agro-morphological traits with lower genotypic variance data like stalk borer infestation rate and single stalk weight suggested limited variations among genotypes and exhibited lower or moderate heritability values of 47.6 and 26.8% respectively.

3.8. Heritability and Genetic Advance

Estimates of broad-sense heritability (h^2) are categorized according to Robinson [50] cited by different authors [18, 41, 43] as low ($<30\%$), moderate ($30 \leq <60\%$) or high ($\geq 60\%$). Higher heritability values ranging from 60.6 to 100% were observed on traits like flowering rate, millable stalk number, cane yield and sugar yields, fiber content, internode number, single stalk weight and juice quality (Pol juice, purity,

sucrose content) - (Table 6). In contrast, moderate values (47.6 - 53.6%) were observed for stem borer infestation rate and stalk diameter. The lowest value of heritability was obtained on single stalk weight (26.8%). Estimates of mean genetic advance (GAM) are categorized similarly to GCV and PGV according to Falconer and Mackay [24] cited by several authors [43-44, 48-50]. Therefore, higher values of genetic advance were observed for flowering rate (109.2%), sugar yield (29.0%), millable stalk number (21.0%) and stem borer infestation rate (33.3%). Moderate values were recorded on number of internodes (14.1%), fiber content (11.7%), recoverable sucrose (12.5%) and single stalk height (12.1), while lower values on traits like juice quality (2.7 - 10.0%), single stalk weight (7.4%), and stalk diameter (7.8%). Higher values of GAM suggest that a significant proportion of the total variance might be heritable and selection of corresponding traits would be effective. Similar values were reported by several authors in sugarcane on single stalk 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 [54-55].

Higher levels of mean genetic advance observed for cane and sugar yields, millable stalk number, stem borer infestation rate and flowering rate were the result of moderate or high broad sense heritability combined with high GCV for these traits in line of findings reported by Bakshi [56]. According to this author, 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 [57]. Patel et al [58] 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, 40, 59]. 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 (%)		H ² (%)	GA (-)	GAM (%)
		σ^2_e	σ^2_g	σ^2_p	GCV	PCV			
Pol juice	17.1	0.54	1.04	1.59	5.96	7.35	65.8	1.71	10.0
Purity	89.5	1.10	2.11	3.21	1.63	2.00	65.9	2.43	2.7
Pol%C	13.9	0.29	0.65	0.95	5.81	6.99	68.9	1.38	9.9
Fiber%	13.59	0.00	0.60	0.60	5.69	5.69	100.0	1.60	11.7

Agronomic traits	Mean	Variance			Coefficient of variation (%)		H ² (%)	GA (-)	GAM (%)
		σ^2_e	σ^2_g	σ^2_p	GCV	PCV			
CYield	143.80	108.90	269.23	378.13	11.41	13.52	71.2	28.56	19.9
RSucrose	10.20	0.23	0.54	0.78	7.23	8.64	69.9	1.27	12.5
SYield	14.68	1.70	5.55	7.25	16.04	18.33	76.6	4.25	29.0
SNbx103	113.71	100.00	201.40	301.40	12.48	15.27	66.8	23.93	21.0
%BIN	8.04	3.90	3.54	7.45	23.40	33.93	47.6	2.68	33.3
AvWeight	1.37	0.02	0.01	0.03	6.93	13.39	26.8	0.10	7.4
AvDiam	22.67	1.20	1.39	2.59	5.20	7.09	53.6	1.78	7.8
AvHeight	3.08	0.03	0.05	0.08	7.24	8.93	65.7	0.37	12.1
NbInternode	23.86	2.87	4.42	7.29	8.81	11.31	60.6	3.38	14.1
Flowering	30.52	178.60	383.03	561.63	64.12	77.64	68.2	33.34	109.2

4. Conclusions

The study showed that most relevant traits in genotype clustering were related to juice quality (recoverable sucrose, sucrose content, purity), yields and yield components (millable stalk number/ha, stalk height, stalk diameter, internode number). Based on sugar yields, four genotypes equivalent to the check variety (R579), namely KQ228, R97-6177, R99-4064 and KQ236, were found promising for the next advanced selection stage with respectively 19.2, 17.7, 17.3 and 16.9 t sugar/ha. Their cane yield performances ranged from 147.7 to 170.8 t/ha compared to 170.7 for the check and belong to three clusters genotypes over the eight determined. Not only sugar yield, but also flowering rate, stem borer infestation rate and number of tillers per hectare were found as the most relevant agro-morphological traits in the genetic variation of sugarcane genotypes tested.

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