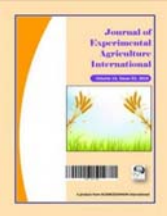

Journal of Experimental Agriculture International

23(3): 1-15, 2018; Article no.JEAI.41862
ISSN: 2457-0591
(Past name: American Journal of Experimental Agriculture, Past ISSN: 2231-0606)

Genetic Diversity of First Sugarcane Accessions of Reunion-Ivorian Origin Preselected at One-Row Stage in Ferké, Ivory Coast

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Authors' contributions

This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JEAI/2018/41862
Editor(s):
(1) Daniele De Wrachien, Professor, State University of Milan, Italy.
Reviewers:
(1) Marcos Siqueira, Sacred Heart University, Brazil.
(2) Asif Mohd Iqbal Qureshi, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir, India.
(3) Meltem Sesli, Manisa Celal Bayar University, Turkey.
Complete Peer review History: http://www.sciencedomain.org/review-history/24852

Original Research Article

Received 14th March 2018
Accepted 24th May 2018
Published 29th May 2018

ABSTRACT

Aims: The overall study objective was to contribute to sugarcane yield improvement in Ivory Coast. Specific objective was to evaluate the genetic diversity of Reunion-Ivorian first sugarcane genotypes preselected at one-row stage for further advanced selection trials of 1st and 2nd steps to be carried out under Ferké commercial field conditions.
Study Design: It was conducted on Ferké 2 experimental station under full covering sprinkler irrigation in northern Ivory Coast. The genotypes were preselected in 1st ratoon among 985 clones planted in single rows of 3 m per clone with 1.5 m of row-spacing following families. Genotypes were not replicated except for the control variety SP70/1006. That one was replicated several times every 5 rows to ease agronomics observations of clones in comparison with the control. Quantitative as well as qualitative traits observed at the age of 10 months were subjected to a series of multivariate analyses.

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Results: It came out that quantitative traits which better explained diversity of genotypes were the following in decreasing order: flowering rate, number of millable stalks/3m, stalk diameter, and stalk height. These phenotypic traits highly contributed to genotypes discrimination into 8 clusters which suggested a good genetic diversity among all 148 preselected accessions. Four best represented clusters (63.5 % of total) comprised 20-30 individuals each, whereas less represented clusters (36.5 %) involved 11-15 individuals each.
Conclusions: Quantitative traits most relevant in variety clustering were high tillering, moderate tillering, erect canopy which were associated respectively with clusters G1, G7 and G2. As for lodging characters, they were associated with 6 clusters all together, namely G2, G3, G4, G5, G6 and G8. The genetic variability as shown was a prerequisite for further advanced selection trials with limited number of accessions to be conducted under commercial field conditions.

Keywords: Visual selection; vigor; one-row stage; phenotypic trait; multivariate analysis; clustering; agro-ecology.

1. INTRODUCTION

Sugarcane has been growing as a commercial crop for milling purpose in Ivory Coast since 1970. Crop yield in the ivorian sugar sector used to be limited to 8 t of sugar/ha until 2010 [1-2]. Crop material of different origins being grown in Ivory Coast and most West African countries was introduced as cuttings of commercial, elites or preselected cane genotypes from quarantine of CIRAD in Montpellier (France). Generally, it was selected in countries of destination for adaptation to local pedo-climatic and phytosanitary conditions. As far as Ferké sugarcane plantations in Ivory Coast were concerned, development of high sugar yielding varieties (9-10 t/ha) contributed significantly to improvement of crop productivity by 25 % from 2010-11 to 2014-15 [3]. Despite that progress in yield, the Ivorian sugar production is still in deficit, with about 200 000 t/yr over a total sugar consumption estimated to 240 000 t/yr [4]. Stem borer (*Eldana saccharina* W) and two endemic diseases economically important, i.e. leaf scald and smut respectively caused by *Ustilago scitaminea* and *Xanthomonas albilieans*, are main biotic constraints currently observed in Ivorian sugarcane plantations. These constraints are increasingly considered among crop yield limiting factors with a cane yield loss reaching sometimes 20 or 30 % due to stem borer damages [5-6].

Breeding has been prioritized in Ivorian sugarcane industry to manage the impact of diseases and pests since at least 5 decades (1967-2018). However, crop material being introduced in the country for screening purpose until 2013-14 showed a limited genetic diversity with therefore a limited adaptation ability [7].

Introducing at yearly basis a great number of sugarcane hybrid seeds from different crosses (about 8000 seeds/yr) allows to maintain a wider genetic diversity among the crop material (seedlings and clones) to be screened.

Selection from cane seedlings and clones produced locally allows to increase the probability to determine new varieties prone to withstand several challenges such as high yield, good adaptation to local agroecological conditions, high fiber content for biofuel production, high tillering ability and erect architecture with easy defoliation trait to minimize cane yield loss and extraneous matter in mechanized harvesting.

The study aimed to characterize the genetic variability of first sugarcane preselected RCI genotypes for next step of the screening procedure to be conducted under commercial field conditions.

2. MATERIALS AND METHODS

2.1 Site Characteristics

The study was carried out at Ferké 2 experimental station in northern Ivory Coast (9°20' – 9°60' N, 5°22' – 5°40' O, 325 m). Prevailing climate is tropical dry with two seasons: one is dry which occurs from early November to April and the other, wet, from May to late October. The dry season is marked by a northern and warm trade wind (*Harmattan*) taking place from mid-November to late January. Rainfall pattern is unimodal and centered over August and September which cumulate almost half of annual average rainfall (1 200 mm) with an average daily temperature of 27 °C, maximum

and minimum values yielding 32.5 and 21°C, respectively. Irrigation water requirements for sugarcane yield to about 650-700 mm/yr [8]. Main soil units (ferralsol or hydromorphic type) are characterized by shallow to moderate depths (30-80 cm) with sand-clay as predominant soil texture where the experiment was located.

2.2 Crop Material

The crop material investigated which comprised 148 RCI accessions (or genotypes) of Reunion and Ivory Coast origin, was preselected in first ratoon sugarcane at one-row screening stage (early selection) among 985 clones. All genotypes were planted following families and compared to a control commercial variety (SP70-1006). Genotypes which came from the first generation of sugarcane hybrid seeds were provided in November 2014 by Reunion Island sugarcane breeding center (eRcane). They resulted from bi-parental crosses of commercial or elite varieties of diversified origins (Reunion, Brazil, Australia, Sudan, Florida, Colombia, South Africa, etc.).

2.3 Experimental Design

The experimental design used at one-row screening stage was a randomized block comprising 985 sugarcane clones, each being planted in single rows of 3 m long with 1.5 m of inter-row spacing. Clones were not replicated apart from the control variety which was replicated many times every 5 rows of clones subjected to visual screening. Clones split into 60 families (or crosses) as well as the control variety were planted in November 2015 following 17 paired sub-blocks of 7 m wide and 30 m long with 3 m spacing, i.e. a total land surface of about 5 000 m². To ease comparison of clones with the control, that one was repeated every 7.5 m (after 5 individuals). To prevent edge effects the field trial was surrounded by a buffer zone of 3 m wide and 30 m long planted with a commercial variety (R579).

2.4 Quantitative and Qualitative Traits

Agro-morphological, phytosanitary and technological traits observed over the vegetation stage for clone preselection at one-row stage were the following: number of millable stalks, millable stalk diameter, crop architecture, millable stalk height, flowering rate, symptoms of endemic diseases (smut, leaf scald, pokkah boeng), severe stem borer attacks, brix (soluble dry matter content in cane juice).

The above observations which allowed to determine clone vegetative vigor were subjected to ratings ranging from 0 to 4 for every clone tested in comparison with the control variety. Details of ratings were as follows:

0 to 1: non-adapted genotypes to be eliminated;
1.5: recovered genotypes, with some missing traits;
2 to 4: best genotypes, provided with good traits (3: very good ability; 4: exceptional ability)

All 148 preselected genotypes scored higher than 2 and therefore were free of endemic diseases. At the age of 10 months, the following quantitative traits were observed for determining their genetic diversity: number of millable stalks per row of 3 m long, stalk diameter, millable stalk eight, flowering rate and brix. Qualitative traits involved tillering ability and crop architecture (Table 1).

2.5 Statistical Analysis

Excel 2013, Statistica 7.1 and R 2.2 software packages were used for data processing which was based on clone phenotypic traits observed. To do so, data were firstly recorded as a database and processed on Excel following a dynamic crossed table. Relevant traits involved in data processing were as follows: number of millable stalks, millable stalk diameter, crop architecture, millable stalk height, flowering rate, brix. A series of 3 multivariate analyses using R software, i.e. principal component analysis (PCA), cluster analysis (CA) and correspondence factor analysis (CFA), were performed. The data were computed for applying Mahalanobis4s D^2 statistics among all possible combinations of genotypes grouped into different clusters following canonical root method reported by Rao [9].

3. RESULTS

3.1 Dispersion of Quantitative Traits Observed at Harvest

Flowering rate and number of millable stalks per row were most dispersed quantitative traits with respectively 86 and 22 % as variation coefficients suggesting that these traits highly contributed to the genotypic diversity of cane accessions investigated. The other three quantitative traits

Table 1. Agro-morphological and technological traits used to preselect the best clones at one-row screening stage in Ferké 2, northern Ivory Coast

Traits	Methods of observation
Agro-morphological	
Number of millable stalks/3m	Counting of millable stalks at the age of 10 months.
Tillering	Density of tillers observed at the age of 3-4 months (low, fair, very good).
Crop architecture	Appreciation of crop architecture at the age of 8 months.
Stalk diameter (mm)	Measuring of stalk medium internode diameter over a sample of 10 millable cane stalks using a slide rule.
Stalk height (m)	Measuring the average height of sample of 10 millable cane stalks at 10 months of age.
Flowering rate (%)	Counting the number of flowered stalks over the total number of stalks per row at 10 months of age.
Phytosanitary	
Endemic diseases and pests	Counting of smut whips, infected shoots by leaf scald and pokkha boeng. Indication of severe stem borer attacks (*E*. *saccharina*).
Technological	
Brix	Measurement of soluble dry matter in cane juice using a portable refractometer.

Table 2. Mean of agro-morphological and technological traits observed at harvest on 148 genotypes of RCI origin and their respective dispersion

Variables	Mean	Minimum	Maximum	CV (%)
Nb of stalks/3m	59	32	100	22,6
Diameter (mm)	24,9	18,7	31,7	10,9
Height (m)	2,7	2,1	3,6	10,8
Brix	20,5	14,2	24,4	8,7
Flowering rate (%)	34,5	0,0	94,4	86,0

observed, i.e. stalk diameter, stalk height and brix, showed a variation coefficient of 10% for each of them (Table 2). Therefore, they might have contributed fewer in the genetic diversity of accessions.

3.2 Principal Component Analysis (PCA)

Three couples of traits most correlated are Stalk diameter-Stalk number, Brix-Stalk number and Flowering rate-Brix with correlation coefficients of -0.78, -0.58 and 0.59 respectively (Table 3). Poorly correlated traits were, in ascendant order of absolute value, Flowering rate-Stalk diameter (-0.08), Brix-Stalk height (-0.26) and Stalk height-Stalk diameter (0.31).

It came out from PCA that phenotypic traits allowing to better explain the diversity of preselected genotypes were, in descendant order, flowering rate, stalk number/row, stalk diameter and stalk height. Brix was the quantitative trait explaining the less the diversity of preselected genotypes (Figs.1 and 2, Table 4).

3.3 Cluster Analysis

The dendrogram resulting from cluster analysis based on Ward method shows 8 clusters at 16 % level of truncation (Fig. 3), suggesting a good genetic diversity among the 148 preselected RCI sugarcane accessions.

Discriminant factor analysis shows that all clusters of genotypes determined (n=8) were significantly different highly ($p<0.000001$), (Tables 5 and 6). Table 7 shows number and nominative list of genotypes within each cluster. Clusters G4, G6 and G3 were the most represented (63.5 %) with respectively 30, 23, 21 and 20 individuals. Clusters G7, G5, G8 and G2 remaining were the less represented (36.5 %) with respectively 15, 15, 13 and 11 individuals. Mean and standard deviation regarding

Table 3. Correlation matrix of quantitative traits observed at harvest regarding 148 preselected genotypes at one-row screening stage in Ferké, Ivory Coast

Traits	Nb stalk/3m	Stalk Diameter	Stalk height	Brix	%Flowering
Nb stalk/3m	1,00				
Stalk diameter	**-0,78**	1,00			
Stalk height	-0,49	0,31	1,00		
Brix	**0,59**	-0,26	0,22	1,00	
%Flowering	-0,48	-0,08	0,47	**-0,58**	1,00

In bold, correlation coefficients higher than 0.5 in absolute value

Table 4. Index of preselected genotypes at one-row screening stage for PCA

N°	Genotypes	N°	Genotypes	N°	Genotypes	N°	Genotypes	N°	Genotypes
1	RCI14/11	31	RCI14/131	61	RCI14/161	91	RCI12/191	121	RCI13/1121
2	RCI13/12	32	RCI14/132	62	RCI11/162	92	RCI12/192	122	RCI13/1122
3	RCI13/13	33	RCI10/133	63	RCI11/163	93	RCI13/193	123	RCI13/1123
4	RCI14/14	34	RCI11/134	64	RCI10/164	94	RCI13/194	124	RCI13/1124
5	RCI12/15	35	RCI11/135	65	RCI11/165	95	RCI13/195	125	RCI14/1125
6	RCI13/16	36	RCI13/136	66	RCI11/166	96	RCI13/196	126	RCI14/1126
7	RCI13/17	37	RCI13/137	67l	RCI11/167	97	RCI13/197	127	RCI14/1127
8	RCI14/18	38	RCI13/138	68	RCI11/168	98	RCI13/198	128	RCI11/1128
9	RCI12/19	39	RCI13/139	69	RCI11/169	99	RCI14/199	129	RCI11/1129
10	RCI13/110	40	RCI13/140	70	RCI11/170	100	RCI14/1100	130	RCI12/1130
11	RCI14/111	41	RCI13/141	71	RCI14/171	101	RCI14/1101	131	RCI13/1131
12	RCI11/112	42	RCI13/142	72	RCI13/172	102	RCI14/1102	132	RCI13/1132
13	RCI11/113	43	RCI13/143	73	RCI13/173	103	RCI14/1103	133	RCI13/1133
14	RCI11/114	44	RCI13/144	74	RCI13/174	104	RCI14/1104	134	RCI13/1134
15	RCI11/115	45	RCI13/145	75	RCI13/175	105	RCI14/1105	135	RCI13/1135
16	RCI13/116	46	RCI14/146	76	RCI13/176	106	RCI14/1106	136	RCI13/1136
17	RCI13/117	47	RCI14/147	77	RCI13/177	107	RCI14/1107	137	RCI14/1137
18	RCI13/118	48	RCI14/148	78	RCI13/178	108	RCI14/1108	138	RCI14/1138
19	RCI13/119	49	RCI12/149	79	RCI13/179	109	RCI14/1109	139	RCI14/1139
20	RCI13/120	50	RCI13/150	80	RCI13/180	110	RCI11/1110	140	RCI14/1140
21	RCI13/121	51	RCI13/151	81	RCI13/181	111	RCI11/1111	141	RCI14/1141
22	RCI13/122	52	RCI13/152	82	RCI13/182	112	RCI11/1112	142	RCI14/1142
23	RCI13/123	53	RCI13/153	83	RCI13/183	113	RCI11/1113	143	RCI14/1143
24	RCI13/124	54	RCI14/154	84	RCI13/184	114	RCI11/1114	144	RCI14/1144
25	RCI13/125	55	RCI14/155	85	RCI13/185	115	RCI12/1115	145	RCI14/1145
26	RCI13/126	56	RCI14/156	86	RCI13/186	116	RCI12/1116	146	RCI11/1146
27	RCI14/127	57	RCI14/157	87	RCI13/187	117	RCI13/1117	147	RCI14/1147
28	RCI14/128	58	RCI14/158	88	RCI14/188	118	RCI13/1118	148	RCI13/1148
29	RCI14/129	59	RCI14/159	89	RCI14/189	119	RCI13/1119		
30	RCI14/130	60	RCI14/160	90	RCI11/190	120	RCI13/1120		

PCA : Principal Component Analysis

each quantitative trait observed at harvest are shown in Table 8. This table shows also that genotypes from cluster G1 have the highest number of cane stalks/row whereas those from cluster G7 have the lowest number of stalks/row, with on average respectively 75 and 47 stalks/4.5 m² i.e. about 167 000 and 104 000 stalks/ha. High flowering rate genotypes derived from cluster 8 whereas lower flowering ones from cluster G3 with respectively 70 and 4% on average. However, that low flowering rate was particularly variable among genotypes from cluster G3 with 138 % as coefficient of variation compared to 33 % for high flowering genotypes (cluster G8). Other clusters with highly versatile traits were G4 and G1. Potentially high sucrose performing genotypes belonged to clusters G5 and G7 whereas shorter cane stalk genotypes to cluster G1 with on average about 3 and 2.4 m of height, respectively.

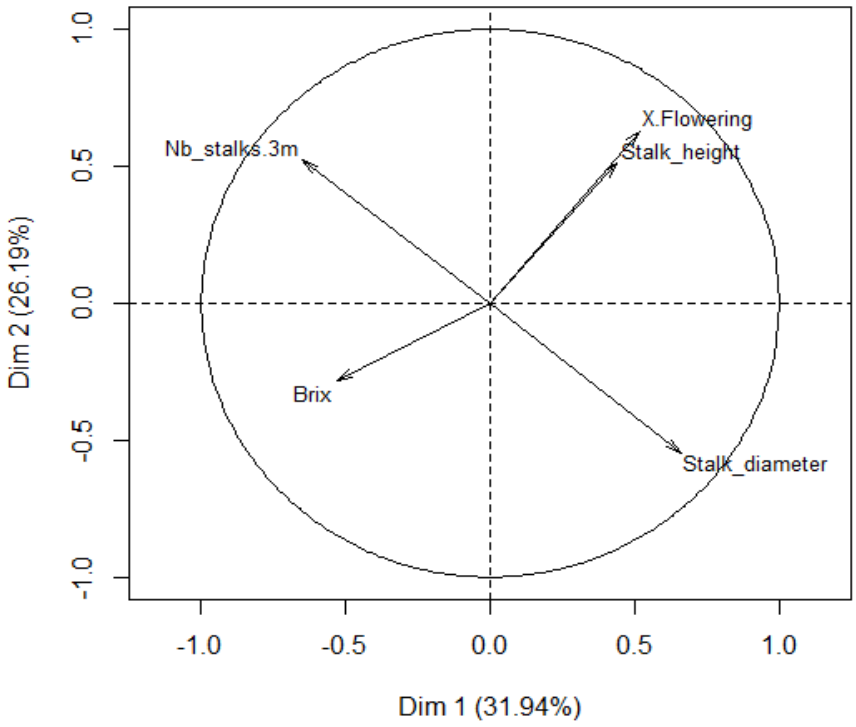

Fig. 1. Correlation circle resulting from projection of RCI genotypes and agro-morphological traits observed in 1-2 factor plane following Principal Component Analysis (PCA)

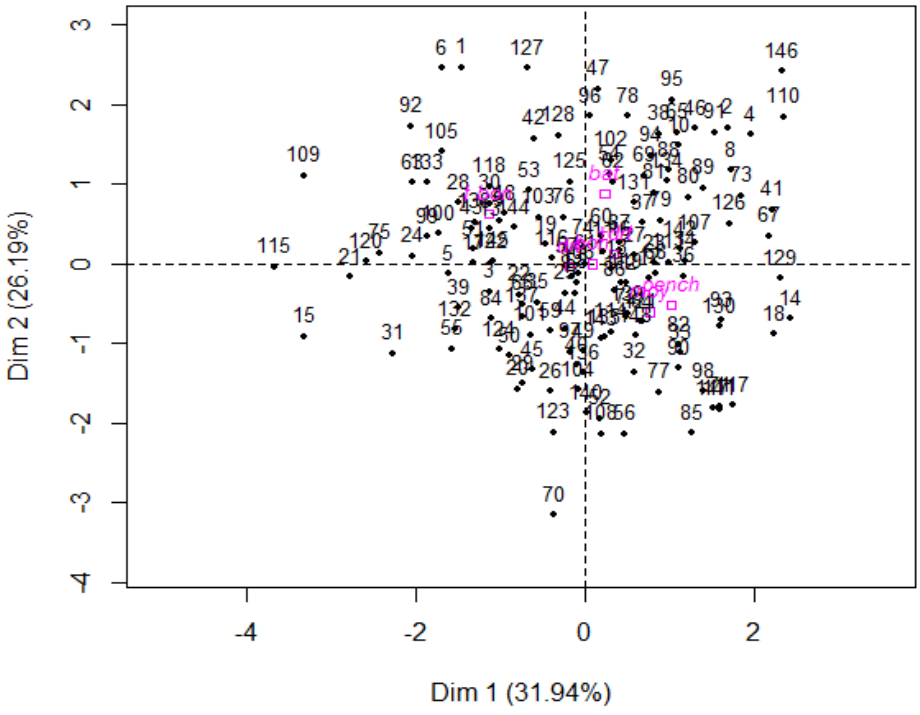

Fig. 2. Projection of 148 preselected RCI genotypes in 1-2 facto plane following PCA based on variance of quantitative traits observed at harvest

It came out from correspondence factor analysis (CFA) that cluster G1 genotypes have a very high tillering ability, a trait known as being associated with high cane yield and a good ratooning ability (Fig. 4). Those from cluster G7 showed a moderate tillering and a crop architecture more or less erect. Genotypes from cluster G2 were prone to an erect architecture which is required for mechanized harvesting in sugarcane as being partly practiced in Ferké sugar mills (Ivory Coast) ten years ago over about 30% of irrigated sugarcane plantations (3 600 ha). Moderately erect or lodging genotypes which highly contributed to clustering seemed to be associated simultaneously with 6 groups (G2, G3, G4, G5, G6 and G8).

Among all 148 preselected genotypes, families F62 and F31 were the most represented with respectively 36 and 18 individuals. Both families were also most represented in cluster G4 with respectively 11 genotypes out of 36 (30.5 %) and 9 genotypes out of 18 (50 %). Family F62 was also well represented in cluster G3 with 12 genotypes out of 26 i.e. 33 % (Table 9). That family was also the most diversified for being represented in 7 clusters (G4, G3, G6, G7, G1, G2 and G5). It is followed by families F59 and F29 each being represented in 6 clusters. Third was the prolific Family F31 with 5 clusters (G4, G1, G3, G5 and G6).

Among the 8 clusters determined, G6 seemed to be the most genetically diversified with 16 different families, followed by cluster G1 with 11 families and cluster G5 with 10 families. Each of clusters G2 and G4 was composed of 8 families. Two clusters with the lowest number of families (n=6) were G3 and G8. Eight families associated with a single cluster were F06, F07, F09, F27, F37, F44, F52 and F55. Families associated with 2 clusters were F05, F02, F11, F15, F21, F24, F36 and F58 (n=6).

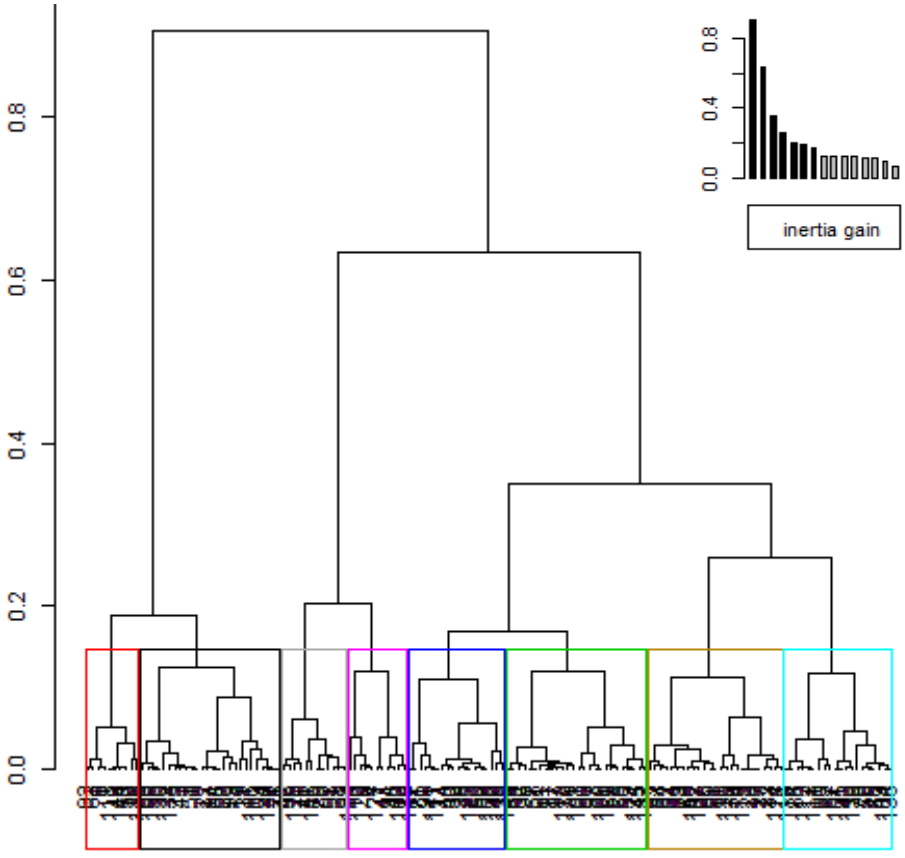

Fig. 3. Dendrogram resulting from cluster analysis regarding the 148 RCI genotypes split in 8 separate clusters

Table 5. Involvement of quantitative traits observed in clustering of RCI cane genotypes

Traits	Wilks (Lambda)	Partiel (Lambda)	F d'exc. (7,136)	Probab. (p)	Toler.	1-Toler. (R^2)
Nb_stalk.3m	0,023503	0,660153	10,00183	0,000000	0,973429	0,026571
Diameter	0,027883	0,556457	15,48619	0,000000	0,981933	0,018067
Height	0,041463	0,374199	32,49181	0,000000	0,981809	0,018191
Brix	0,035094	0,442120	24,51556	0,000000	0,992174	0,007826
%Flowering	0,042251	0,367219	33,47881	0,000000	0,978525	0,021475

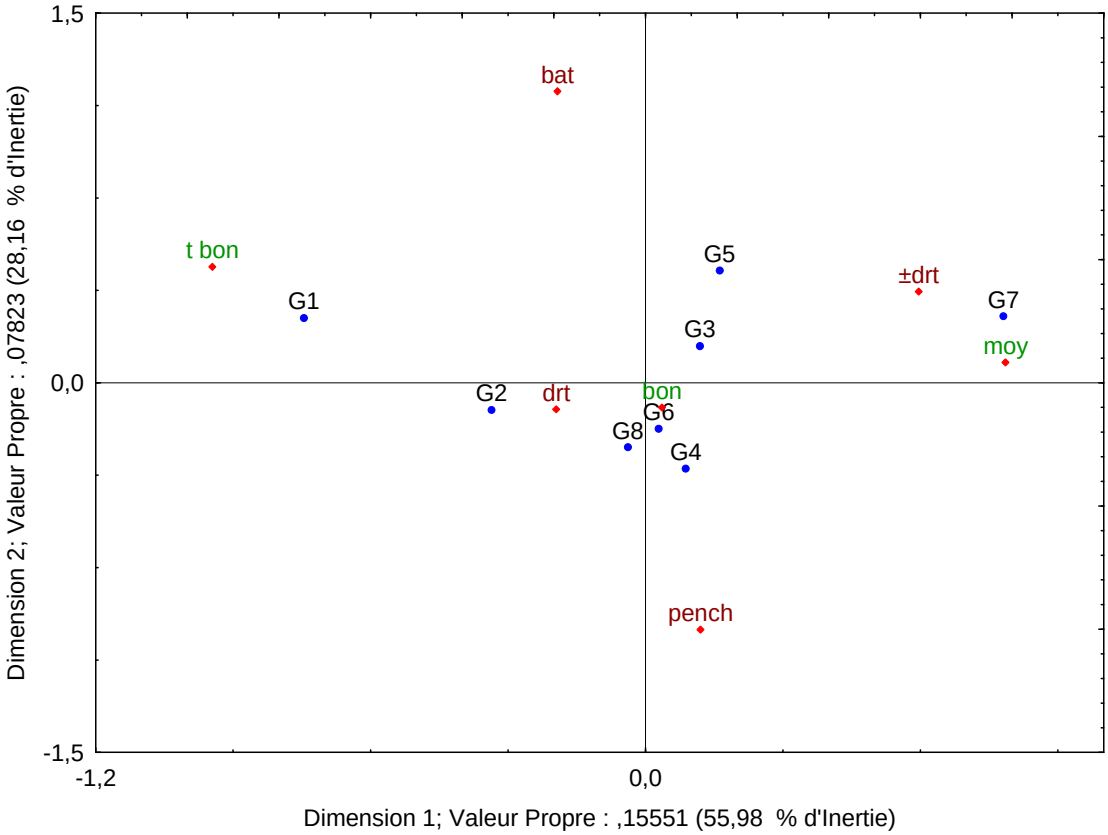

Fig. 4. Projection of different clusters and qualitative traits (tillering, crop architecture) in 1-2 factor plane following correspondence factor analysis (CFA)

***G1**: Cluster 1, **G2**: Cluster 2, …, **G8**: Cluster 8; **t bon**: very high tillering, **bon**: good tillering, **moy**: moderate tillering; **drt**: erect architecture, **±drt**: moderately erect, **pench**: benched architecture, **bat**: lodged architecture.*

4. DISCUSSION

4.1 Quantitative Trait Variability

High dispersion in flowering rate and number of millable stalks on the one hand as opposed to low dispersion in stalk diameter, stalk height and brix on the other hand, observed on preselected genotypes in Ferké were in line of findings of Tadesse et al. [9] in Wonji, Ethiopia. High dispersion in number of millable stalks/ha was also reported by other authors [10-13]. According to Shivasubramanian and Menon [14], phenotypic and genotypic coefficients of variation (PCV, GCV) were ranked as low from 0 to 10%, moderate from 11 to 20% and high more than 20%. Singh et al. [15] showed that higher PCV and GCV meant the relevance of phenotypic traits observed in screening of varieties and suggested their high potential genetic diversity.

Table 6. Mahalanobis square distance (bellow diagonal) between clusters taken 2 by 2 and Fisher values (above diagonal)

Clusters	Cluster 2	Cluster 5	Cluster 3	Cluster 8	Cluster 1	Cluster 4	Cluster 6	Cluster 7
Cluster 2	-	F = 17,64	F = 21,87	F = 28,43	F = 17,92	F = 42,89	F = 18,22	F = 26,40
Cluster 5	14,30488	-	F= 23,70	F = 17,24	F = 48,73	F = 58,70	F = 17,06	F = 17,59
Cluster 3	15,86127	14,22889	-	F = 41,18	F = 18,51	F = 24,70	F = 26,52	F = 23,39
Cluster 8	24,55377	12,73791	26,90228	-	F = 52,27	F = 52,84	F = 15,56	F = 40,98
Cluster 1	12,77522	28,66366	9,30022	33,50342	-	F = 27,46	F = 34,64	F = 42,59
Cluster 4	27,42735	30,21162	10,59433	29,99069	11,44161	-	F = 25,26	F = 29,14
Cluster 6	12,60566	9,66919	12,75838	9,61582	16,24074	9,98844	-	F = 14,57
Cluster 7	21,41264	12,07119	14,04839	30,28743	25,05566	14,99903	8,25805	-

P<0.00000 for all F values

Table 7. Preselected RCI cane genotypes composing the different clusters of genotypes determined

N° cluster	Number of genotypes	List of genotypes
1	21	RCI12/15 ; RCI11/113 ; RCI11/115 ; RCI13/117 ; RCI13/121 ; RCI13/122 ; RCI13/124 ; RCI14/131 ; RCI13/139 ; RCI13/143 ; RCI14/155 ; RCI11/166 ; RCI13/175 ; RCI13/184 ; RCI14/199 ; RCI14/1109 ; RCI12/1115 ; RCI13/1120 ; RCI13/1122 ; RCI13/1132 ; RCI13/1133
2	11	RCI14/11 ; RCI13/16 ; RCI13/119 ; RCI14/128 ; RCI14/148 ; RCI13/153 ; RCI11/163 ; RCI12/192 ; RCI13/1118 ; RCI14/1125 ; RCI14/1144
3	20	RCI13/13 ; RCI12/19 ; RCI13/125 ; RCI14/130 ; RCI11/135 ; RCI13/150 ; RCI13/151 ; RCI14/157 ; RCI14/160 ; RCI14/161 ; RCI13/183 ; RCI13/197 ; RCI14/1100 ; RCI14/1101 ; RCI14/1103 ; RCI14/1105 ; RCI14/1106 ; RCI14/1137 ; RCI14/1138 ; RCI14/1145
4	30	RCI13/17 ; RCI13/120 ; RCI13/126 ; RCI14/129 ; RCI14/132 ; RCI13/140 ; RCI13/144 ; RCI13/145 ; RCI12/149 ; RCI13/152 ; RCI14/156 ; RCI14/159 ; RCI10/164 ; RCI11/170 ; RCI13/177 ; RCI13/182 ; RCI13/185 ; RCI13/198 ; RCI14/1104 ; RCI14/1108 ; RCI11/1114 ; RCI13/1117 ; RCI13/1121 ; RCI13/1123 ; RCI13/1124 ; RCI13/1135 ; RCI13/1136 ; RCI14/1140 ; RCI14/1141 ; RCI13/1148
5	15	RCI13/12 ; RCI13/138 ; RCI13/142 ; RCI14/154 ; RCI11/162 ; RCI11/165 ; RCI11/169 ; RCI13/178 ; RCI13/179 ; RCI13/180 ; RCI12/191 ; RCI13/195 ; RCI13/196 ; RCI14/1102 ; RCI11/1128
6	23	RCI14/111 ; RCI11/114 ; RCI13/116 ; RCI13/123 ; RCI14/127 ; RCI10/133 ; RCI11/134 ; RCI13/136 ; RCI13/137 ; RCI14/158 ; RCI11/168 ; RCI13/172 ; RCI13/173 ; RCI13/176 ; RCI13/181 ; RCI13/187 ; RCI14/188 ; RCI14/189 ; RCI14/1107 ; RCI11/1113 ; RCI13/1119 ; RCI12/1130 ; RCI14/1142
7	15	RCI11/112 ; RCI13/118 ; RCI11/167 ; RCI14/171 ; RCI13/174 ; RCI13/186 ; RCI11/190 ; RCI13/193 ; RCI11/1111 ; RCI11/1112 ; RCI12/1116 ; RCI11/1129 ; RCI14/1139 ; RCI14/1143 ; RCI14/1147
8	13	RCI14/14 ; RCI14/18 ; RCI13/110 ; RCI13/141 ; RCI14/146 ; RCI14/147 ; RCI13/194 ; RCI11/1110 ; RCI14/1126 ; RCI14/1127 ; RCI13/1131 ; RCI13/1134 ; RCI11/1146

4.2 Cluster Genotypes Determined

It came out that each cluster determined by multivariate analyses based on observed quantitative traits derived from several families which number ranged from 4 to 16. This suggested that every cluster was genetically diversified enough. Number of clusters composing each family of genotypes varied from 4 to 7 suggesting that it was phenotypically diversified. The relatively high diversity observed among each cluster was in line of the fact that parents of families investigated covered up to 9 geographical origins worldwide where sugarcane was subjected to hybridizations (South Africa, Reunion, Australia, Florida, Brazil, Guadeloupe, Philippines, Barbados and India). Genitors themselves were commercial or elite varieties (heterozygotes hybrids) deriving from crosses which parents covered also different geographic origins. Genetic recombination across hybridizations allowed to maintain a diversity enough wide to consider that of targeted local sugarcane growing areas as reported by several.

Table 8. Means of clusters regarding RCI cane genotypes determined following quantitative traits observed at harvest

Different clusters	Nb_stalks/3m		Diameter (mm)		Height (m)		Brix		%Flowering	
	Mean	CV (%)	Mean	CV (%)	Mean	CV (%)	Mean	CV (%)	Mean	CV (%)
Cluster 1	75	15.1	23.2	8.4	2.44	7.7	21.7	5.8	13.3	109.0
Cluster 2	66	17.1	20.7	6.8	2.65	7.5	22.0	4.3	61.4	21.0
Cluster 3	60	16.2	23.2	6.9	2.87	4.6	20.8	5.9	4.1	138.1
Cluster 4	49	16.3	30.0	6.4	2.49	7.1	20.2	6.7	11.6	106.8
Cluster 5	62	17.0	24.2	6.8	3.19	5.7	20.2	3.8	57.0	35.0
Cluster 6	53	13.8	26.1	7.5	2.71	5.6	19.8	3.8	56.7	31.8
Cluster 7	47	17.7	27.7	7.1	3.00	5.0	22.1	4.3	43.2	57.8
Cluster 8	64	19.4	25.0	8.0	2.83	7.7	16.9	8.3	70.0	33.2

CV : coefficient of variation

Table 9. Number of preselected RCI cane genotypes in Ferké following families and clusters determined by multivariate analysis

	Clusters								
Families	**G1**	**G2**	**G3**	**G4**	**G5**	**G6**	**G7**	**G8**	**Total**
NCo376 x N27 (F61)	1	2	-	-	1	1	-	-	5
R575 x Q140 (F36)	-	1	-	-	-	-	1	-	2
R579 x BT92/3586 (F31)	5	-	2	9	1	1	-	-	18
R579 x R585 (F62)	3	2	12	11	1	4	3	-	36
R579 x R97/0434 (F37)	-	-	-	-	-	1	-	-	1
R582 x R01/6043 (F27)	-	-	-	-	-	1	-	-	1
R582 x R570 (F52)	-	-	-	-	-	1	-	-	1
R582 x SP70/1143 (F58)	-	-	-	-	-	1	-	1	2
R89/2042 x R97/2332 (F11)	-	-	-	-	-	2	-	-	2
R92/2210 x R91/2069 (F24)	-	1	-	-	-	1	-	-	2
R92/2401 x R 98/6092 (F13)	1	-	-	2	-	-	-	-	3
R92/6545 x R93/6683 (F09)	-	-	-	-	1	-	-	-	1
R93/0136 x N27 (F50)	1	1	1	1	-	-	-	-	4
R93/4255 x CP81/1405 (F42)	-	-	-	-	1	-	2	-	3
R93/6480 x FG04/517 (F63)	-	1	-	-	2	-	-	2	5
R94/0142 x R98/6092 (F05)	-	-	-	-	-	1	1	-	2
R94/6113 x R93/6885 (F04)	1	-	-	-	-	1	3	-	5
R94/6113 x R97/6375 (F02)	-	-	-	1	-	1	-	-	2
R96/0216 x R93/6776 (07)	-	-	1	-	-	-	-	-	1
R 96/2116 x Q 213 (F32)	-	1	-	-	-	1	-	6	8
R96/2569 x R585 (F59)	2	-	3	2	2	-	1	1	11
R97/2335 x CP92/1641 (F30)	-	-	-	2	4	1	-	1	8
R97/4004 x R95/4053 (F44)	-	-	-	-	1	-	-	-	1
R97/6055 x R96/6422 (F21)	-	-	-	-	-	2	-	-	2
R99/2162 x R01/2221 (F15)	1	-	-	-	-	-	1	-	2
R99/2162 x R585 (F56)	2	-	1	-	-	-	-	2	5
SP70/3225 x R585 (F55)	-	-	-	-	-	-	1	-	1
VMC93/282 x R01/6043 (F29)	3	2	-	2	1	3	2	-	13
VMC93/282 x R97/2335 (F06)	1	-	-	-	-	-	-	-	1
Total (29)	21	11	20	30	15	23	15	13	148

authors [16-19]. They are phenotypically expressed through the number of agro-morphological, technological and pathological traits influencing cane yield, sucrose content and sugar recovery. However, different studies showed that the number of clusters determined by multivariate analyses could vary highly depending on crop species, number of accessions and type or number of traits observed [20-24].

Parental varieties used in breeding programs were obtained after several consecutive back-crosses (recurrent selection) between *Saccharum officinarum* genotypes and that of rustic *Saccharum* such as *S. spontaneum* for transfer of sucrose content trait. In that process, the noble parent was not necessarily the same used [25]. However, crosses involved a restricted number of wild clones suggesting that only few of the genetic diversity in genus *Saccharum* was explored so far in sugarcane breeding. This is in line of the fact that different studies on genetic diversity assessment using quantitative as well as qualitative traits on the one hand, and/or molecular markers on the other hand, revealed high genetic similarity between different varieties resulting in limited number of clusters [26-32]. That's why most recent breeding programs are based on new nobilization studies aiming at providing an additional diversity in crop material cultivated.

According to Gouy [33], sugarcane breeding is rather recent as it started with the release of first hybrids obtained in Java early last century. Nobilization as an interspecific breeding technique allowed to obtain high performing varieties resistant to major sugarcane diseases. Since then, hybridization centers make crosses between elite varieties and sugarcane breeding is carried out based on progeny phenotypes. Using molecular information for screening of elites would be a great progress for breeders. Although number of studies on molecular markers were achieved, no marker so far has been used in sugarcane breeding programs. Effects of markers were not estimated accurately enough and must be validated across independent populations. Association between markers and genetic traits requires nowadays new approaches such as genomic breeding and the use of eco-physiological methods in yield prediction.

4.3 Genetic Progress in Yield

Genetic progress is defined as the positive difference between mean of progenies of selected parents and that of progenies of parents chosen randomly [34]. Progress which is also named genetic gain, depends on intensity of selection, heritability of selected trait and phenotypic standard deviation of trait.

The annual genetic progress is therefore defined as the ratio between the genetic progress by generation across the whole population and mean interval between generations.

The FAO reported an average world yield in sugarcane of 50.3 t/ha in 1961 and 70.9 t/ha in 2009 [35]. From these data, sugarcane yields therefore have increased by 41 % over about 50 years, i.e. an average annual yield gain of 0.8 % because of both improvement in agricultural practices and crop breeding efforts. An average annual genetic gain of 0.6% was observed in Barbados between 1940 and 1975 [36]. Hogarth [37] estimated to 1% the average annual yield increase in Queensland, Australia. An assessment of genetic gain over 33 years of experimentation showed that about 70% of gain reported could be explain by breeding efforts [38]. The study showed also that cane and sugar yields did not reach a plateau. Comparing sugarcane cultivars from different generations, it was observed that yield gain resulted mainly from increase in biomass rather than that in sucrose content, which was more enhanced across ratoons [39]. The author explained that by not enough selection pressure in choice of ascendants as well as their progenies for sucrose content trait. Also, the allelic diversity of that trait is narrow in germplasm cultivated. The number of initial crosses is limited i.e. about 30 common parents and modern elite varieties are mainly crossed between one another.

Breeding in sugarcane enhanced an increase in sugar yield and a plateau did not seem to have been reached as far as cane yield is concerned [40-43], suggesting that some improvements were still possible. More knowledge on yield build up and existing relations between yield components should be undertaken to improve breeding of that character [33].

4.4 Investigations in Quantitative Genetics on Yield

Quantitative genetics allows to investigate the variability of traits across populations and know which part is recoverable in progenies. Up to recently, studies on this issue regarding sugarcane yield involved mainly traits such as biomass, sugar yield, stalk height, stalk diameter and number of millable stalks [44-48] gave an insight of strict sense heritability figures obtained from 47 crosses for 24 agronomic traits. These figures ranged from low to moderate (0.02 to 0.67). Jackson [39] investigated morphological and technological yield components (number of stalks/m², stalk weight, fiber content, etc.) on 141 clones from F1 and F2 generations derived from 32 interspecific crosses between *S. officinarum* and *S. spontaneum*. Broad sense heritability

related to these traits ranged from moderate to high (0.42 to 0.75). Quantitative genetics studies allowed to rank traits depending on their heritability coefficients. It came out that sucrose measurements based on degree brix was one of the most inheriting phenotypic traits. Sugar yield was also highly inherited compared to other traits. In contrast, number of stalks/m² and cane yield were poorly inherited. Genetic correlations resulting from different studies were sometimes contradictory. Jackson findings [39] showed that from one generation to another, genetic correlations could reverse between sucrose content and cane yield. However, a positive correlation between tillering and cane yield was maintained over several ratoons. That positive correlation was also shown by Sills *et al* [49] on 44 progenies regarding crosses involving *S. officinarum* and *S. spontaneum*. From his study, Jackson stated that few correlations were observed across all research works carried out.

5. CONCLUSION

It came out from the study that quantitative traits which better explained diversity of preselected genotypes were the following in decreasing order: flowering rate, number of millable stalks/3m, stalk diameter, and stalk height. These phenotypic traits highly contributed to discrimination of genotypes into 8 clusters which suggested a good genetic diversity among all 148 preselected clones. Four best represented clusters (63.5% of total) comprised 20-30 individuals each, whereas less represented clusters (36.5%) involved 11-15 individuals each. Most relevant quantitative traits in variety clustering were high tillering, moderate tillering, erect canopy which were associated respectively with clusters G1, G7 and G2. As for bent and lodging shapes, they were associated with 6 clusters all together, namely G2, G3, G4, G5, G6 and G8. The genetic variability so shown was a prerequisite for further advanced selection trials with limited number of accessions to be conducted under commercial field conditions.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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Peer-review history:
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