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Genetic diversity and coefficient of kinship among potential genitors for obtaining cultivars of energy cane[1]

Diversidade genética e coeficiente de parentesco entre genitores potenciais para obtenção de cultivares cana energia

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ABSTRACT - The aim of this study was to evaluate the genetic diversity and coefficient of kinship in 50 sugarcane genotypes, in addition to identifying potential parents for obtaining cultivars of energy cane. Diversity analysis was carried out based on the evaluation of morphological and agronomical characteristics. The coefficient of kinship was obtained from information on pedigree. According to analyses carried out, genotypes were separated into two groups. Group G1 consisted of 13 genotypes from the species *Saccharum spontaneum* and *Saccharum robustum*. The other 37 genotypes were from back-crosses with *Saccharum officinarum*, and were allocated to group G2. The genotypes displayed low values for genetic similarity and coefficient of kinship, indicating broad genetic variability in the population. Carrying out crosses involving genotypes from group G1, especially those with a fibre content of over 17% (IJ76-293, 57NG12, IN84-82, IN84-88, IM76-228 and UM69/001), with genotypes from group G2 which have high stalk yield (RB92579, RB83102, RB047232, RB867515, RB971723, RB937570, RB011941, RB75126, MEX68-200, Co62175 and CP691052), should be explored, with the aim of developing energy cane cultivars. Analyses of diversity and of the coefficient of kinship made it possible to identify two heterotic groups. Moreover, it was possible to identify two potential parent groups for obtaining energy cane cultivars. Genetic distances which are based on both morpho-agronomical data and on pedigree, should be used in a complementary way, with a view to having more information when choosing the best parents.

Key words: *Saccharum* spp. Germplasm. Biomass. Breeding.

RESUMO - O objetivo dessa pesquisa foi avaliar a diversidade genética e a relação de parentesco entre 50 genótipos de cana-de-açúcar, além de identificar genitores potenciais para a obtenção de cultivares cana energia. A análise de diversidade foi realizada a partir da avaliação de caracteres morfológicos e agronômicos. O coeficiente de parentesco foi obtido a partir das informações de pedigree. De acordo com as análises realizadas os genótipos foram separados em dois grupos. O grupo G1 foi formado por 13 genótipos descendentes das espécies *Saccharum spontaneum* e *Saccharum robustum*. Os outros 37 genótipos descendem de retrocruzamentos com *Saccharum officinarum* e foram alocados no grupo G2. Os genótipos apresentaram baixos valores de similaridade genética e de coeficiente de parentesco, indicando ampla variabilidade genética na população. A condução de cruzamentos envolvendo genótipos do grupo G1, principalmente aqueles com teor de fibra acima de 17% (IJ76-293, 57NG12, IN84-82, IN84-88, IM76-228 e UM69/001), com os genótipos do grupo G2, que apresentam elevada produtividade de colmos (RB92579, RB83102, RB047232, RB867515, RB971723, RB937570, RB011941, RB75126, MEX68-200, Co62175 e CP691052), devem ser explorados com a finalidade de desenvolver cultivares cana energia. As análises de diversidade e do coeficiente de parentesco permitiram a identificação de dois grupos heteróticos. Além disso, foi possível identificar nos dois grupos genitores potenciais para a obtenção de cultivares cana energia. A utilização das distâncias genéticas com base em dados morfo-agronômicos e do pedigree devem ser usadas de forma complementar, visando agregar maior conhecimento na escolha dos melhores genitores.

Palavras-chave: *Saccharum* spp. Germoplasma. Biomassa. Melhoramento genético.

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INTRODUCTION

Sugarcane (*Saccharum* spp.) is one of the most efficient crops in the conversion of solar energy into chemical energy (TEW; COBILL, 2008). From the beginning, breeders have taken full advantage of the high potential this crop has for sucrose yield, by means of breeding programs.

In Brazil, the sucrose obtained from sugarcane has been widely used in the production of sugar and ethanol. In turn, the bagasse, traditionally used by power plants only in the cogeneration of electricity, has gained importance in the production of second-generation ethanol (HOFSETZ; SILVA, 2012; RABELO *et al*., 2011). Recently, with the prohibition on the use of burning for the removal of straw prior to harvesting, other sugarcane residue, such as the leaves and tips (straw), are also gaining importance due to their economic potential (CAPAZ; CARVALHO; NOGUEIRA, 2013; SEABRA *et al*., 2010).

With the realisation of the feasibility of using straw to produce ethanol (second-generation ethanol) and electricity (combustion), mainly due to the high yield of biomass and low production costs (CARDONA; QUINTERO, PAZ, 2010; DIAS *et al*., 2013), new lines of research which aim at the development of cultivars with greater fibre content, known as energy cane, are starting to be carried out by different sugarcane breeding programs.

However, as the metabolic pathways for the synthesis of sucrose and fibre are incompatible (MING *et al*., 2006), the development of energy cane cultivars should include crosses between genotypes of *Saccharum spontaneum* and *Saccharum officinarum*. This is because the species *S. spontaneum* has a higher fibre content compared to other species of the genus Saccharum; but its stalk production is low (TEW; COBILL, 2008). On the other hand, the species *S. officinarum* has greater productivity. A combination of these two species would therefore appear to be ideal for the development of cultivars of energy cane.

Appropriate characterisation of the genotypes available in germplasm banks is essential for the selection of genotypes having a potential for use as parents in crosses to generate cultivars of energy cane (BARBOSA *et al*., 2012; SANTOS *et al*., 2012).

To this effect, studies into genetic divergence as well as information on pedigree are extremely important for defining the best combinations for crosses between parents (PETERNELLI *et al*., 2009). Based on pedigree, useful information can be generated, which can be used to prevent crossings of related genotypes, avoiding the effects of endogamic depression (HALLAUER; CARENA; MIRANDA FILHO, 2010).

The aim of this study was to evaluate the genetic diversity and kinship between sugarcane genotypes of the Active Germplasm Bank (AGB) of the Inter-University Network for the Development of the Sugar-Energy Industry (RIDESA), with a view to their use in the development of cultivars of energy cane through reciprocal recurrent selection (RRS).

MATERIAL AND METHODS

This study evaluated 50 sugarcane genotypes at the ratoon stage, ten months after first harvest (Table 1). The genotypes under evaluation were divided into plots of one row, 3 m long, spaced 1.4 m apart, at the AGB of RIDESA, located at the Federal University of Alagoas (UFAL) in the town of Murici, in the state of Alagoas, Brazil, at latitude 9º13' S and longitude 35º50' W and an altitude of 450 m (BARBOSA *et al*., 2002).

For the 50 genotypes, the following morphological characteristics were evaluated in five stalks per plot: flowering index (FI); flowering (FL); physiological withering (PW); toppling due to development (TD); detrashing (DS); presence of aerial roots (AR); cracks (CR); lateral budding (LB); presence of pilosity (PL); bud prominence (BP); tillering (TL) and growth habit (GH) (Table 2).

Using ten stalks per plot, the agronomical characteristics evaluated were: mean stalk weight (MSW); straw weight (SW); mean stalk diameter (DS) and mean stalk length (SL); juice purity (PUR); fibre content (FIB); cane sucrose content (PC); reducing sugars (RS); total recoverable sugar (TRS) and cane dry weight (DW) (Table 2). The variables PUR, FIB, PC, RS, TRS and DW were obtained from analyses carried out on two samples of 500 g (chopped cane), using technological analysis methodology (FERNANDES, 2003). Finally, the lignin content of the fibre (LC) was quantified. To this end, samples of dry matter were subjected to NIR analysis (Near Infrared Reflectance).

Analysis of genetic diversity was carried out following the Ward Modified Location Model (Ward-MLM) (FRANCO *et al*., 1998), using the phenotypic averages of the quantitative characteristics together with the category modes of the qualitative characteristics evaluated in the 50 sugarcane genotypes. In the Ward-MLM procedure, genetic distance is estimated using the Gower algorithm (GOWER, 1971). Recently, the Ward-MLM strategy has been widely used in studies into genetic diversity in sugarcane (BRASILEIRO *et al*., 2014), the castor bean (OLIVEIRA *et al*., 2013), the jatropha (BRASILEIRO *et al*., 2013), the banana (PEREIRA *et al*.,

2012; PESTANANA *et al*., 2011) and the common bean (BARBÉ *et al*., 2009; CABRAL *et al*., 2010).

Analysis of the coefficient of kinship (CK) was carried out considering all the generations present in the pedigree, which corresponded to 189 known parents over 6 generations. In performing the analysis, the R Software was used (R Development Core Team, 2013), with functions developed by Peternelli *et al*. (2009), based on expressions presented by Kempthorne (1973), where the coefficient of endogamy is given by (1):

Table 1 - Identification, pedigree, coefficient of endogamy (F) and origin of the 50 genotypes evaluated at the Active Germplasm Bank of RIDESA/UFAL, Brazil

Genotype	----------Pedigree----------		F	Origin
	Female Parent	Male Parent		
57NG12	*S. robustum*	?	0,0000	Índia
C90178	?	?	0,0000	Cuba
IJ76-293	*S. robustum*	?	0,0000	Java
IM76-228	*S. robustum*	?	0,0000	Indonesia
IM76-229	*S. robustum*	?	0,0000	Indonesia
IN84-58	*S. spontaneum*	?	0,0000	Indonesia
IN84-82	*S. spontaneum*	?	0,0000	Indonesia
IN84-88	*S. spontaneum*	?	0,0000	Indonesia
KRAKATAU	*S. spontaneum*	?	0,0000	Indonesia
UM69/001	*S. spontaneum*	?	0,0000	Mauritius
US74-103	L65-69	SES205A	0,0000	USA*
US76-14	NCo310	TAINAN	0,0015	USA
US85-1008	*S. spontaneum*	US60-313	0,0000	USA
B70710	28NG288	S. spontaneum	0,0000	Barbados
B74125	B62118	?	0,0000	Barbados
B76734	BTN143	SES567	0,0000	Barbados
CB38-22	CP27-139	?	0,0000	Campos Brasil, Brazil
Co285	STR.MAURITIUS	S. spontaneum	0,0000	India
Co453	BLACK CHERIBON	Co285	0,0000	India
Co617	POJ2878	Co285	0,0038	India
Co62175	Co951	Co419	0,0522	India
CP69-1052	CP62-374	CP56-59	0,0052	Canal Point, USA
CTC5	SP82-1176	?	0,0024	CTC, Brazil
CTC9	SP81-3491	?	0,0000	CTC, Brazil
F150	NCo310	PT43-52	0,0015	Formosa
IAC50/134	Co419	Co285	0,0000	IAC, Brazil
IAC86-2210	CP52-58	Co798	0,0043	IAC, Brazil
IAC87-3396	Co740	SP70-1143	0,0039	IAC, Brazil
IANE48-21	POJ2878	Co285	0,0038	IAGN, Brazil
MEX68-200	B35187	Co617	0,0008	Mexico
RB011941	BJ7504	RB72454	0,0001	RIDESA, Brazil
RB01623	RB835867	?	0,0000	RIDESA, Brazil
RB01649	Co62175	RB72454	0,0173	RIDESA, Brazil

Table 1 Continued

RB0442	?	?	0,0000	RIDESA, Brazil
RB047232	RB865520	SP91-1049	0,0000	RIDESA, Brazil
RB04813	RB745464	RB92524	0,0000	RIDESA, Brazil
RB04823	RB931013	RB72910	0,0004	RIDESA, Brazil
RB72910	?	?	0,0000	RIDESA, Brazil
RB75126	C278	?	0,0000	RIDESA, Brazil
RB83102	NA56-79	SP70-1143	0,0002	RIDESA, Brazil
RB867515	RB72454	?	0,0001	RIDESA, Brazil
RB92579	RB75126	RB72199	0,0000	RIDESA, Brazil
RB928064	SP70-1143	?	0,0000	RIDESA, Brazil
RB93509	RB72454	?	0,0001	RIDESA, Brazil
RB937570	SP70-1143	RB72454	0,0001	RIDESA, Brazil
RB946022	RB855511	RB855077	0,0007	RIDESA, Brazil
RB96524	RB75126	?	0,0000	RIDESA, Brazil
RB971723	H64-1881	RB8491	0,0000	RIDESA, Brazil
RB98710	SP81-3250	RB93509	0,0007	RIDESA, Brazil
SP81-3250	CP70-1547	SP71-1279	0,0000	Copersucar, Brasil

*USA = United States of America; CTC = *Centro de Tecnologia Canavieira* [Centre for Sugarcane Technology]; IAC = *Instituto Agronômico de Campinas* [Agronomic Institute of Campinas]; RIDESA = *Rede Interuniversitária para o Desenvolvimento do Setor Sucroalcooleiro* [Inter-University Network for the Developement of the Sugar-Energy Industry]; IANE = *Instituto Agrônomo do Nordeste* [Agronomic Institute of the Northeast]; Copersucar = *Cooperativa de Produtores de Cana-de-Açúcar, Açúcar e Álcool do Estado de São Paulo* [Cooperative of Sugarcane, Sugar and Alcohol Producers of the State of Sao Paulo]

Table 2 - Descriptors used to characterise genotypes of the Active Germplasm Bank of RIDESA/UFAL, Brazil

Characteristic[a]	Category	Characteristic[a]	Description
FI	1 = Absent, 2 = < 30%, 3 = 30 to 50%, 4 = > 50%	MSW	Mean stalk weight (kg)
PW	1 = Absent, 2 = Low, 3 = Medium, 4 = High	SW	Weight of straw (kg)
TD	1 =Absent, 2 = < 30 o from vertical, 3 = 30 to 60º from vertical	DS	Mean stalk diameter (cm)
DS	1 = Easy, 2 = Normal, 3 = Difficult	SL	Mean stalk length (m)
AR	1 = Absent, 2 = Little, 3 = Normal, 4 = High	PUR	Juice purity (%)
CR	1 = Absent, 2 = < 20%, 3 = 20 to 40%, 4 = > 41%	FIB	Fibre content (%)
LB	1 = Absent, 2 = < 20%, 3 = > 20%	PC	Cane sucrose content (%)
PL	1 = Absent, 2 = Little, 3 = Normal, 4 = High	RS	Reducing sugars (%)
BP	1 = 1 mm, 2 = 2 mm, 3 = 3 mm	TRS	Total recoverable sugar (kg t^{-1})
TL	1 = Low, 2 = Medium 3 = High	DW	Cane dry weight (%)
GH	1 = Erect, 2 = Semi-decumbent, 3 = Decumbent	LC	Lignin content (%)
FL	1 = Absent, 2 = Differentiated germ, 3 = Budding phase, 4 = Panicle		

[a] FI = flowering index; FL = flowering; PW = physiological withering; TD = toppling with development; DS = detrashing; AR = presence of aerial roots; CR = cracks; LB = lateral budding; PL = presence of pilosity; BP = bud prominence; TL = tillering; GH = growth habit

$$F_x = \frac{1}{2k-1}\left[kr_{(A,B)} + \frac{(k+1)}{2}(F_A + F_B)\right], k = 4 \quad (1)$$

for an octaploid organism, and the coefficient of kinship is (2):

$$r_{xx} = \frac{1}{2k}\left[1 + (2k-1)F_x\right] \text{ and } r_{xy} = r_{(AB,Y)}\frac{1}{2}\left[r_{AY} + r_{BY}\right] \quad (2)$$

where: *X* is the offspring of *A* and *B*, and *Y* is any individual of unknown parents.

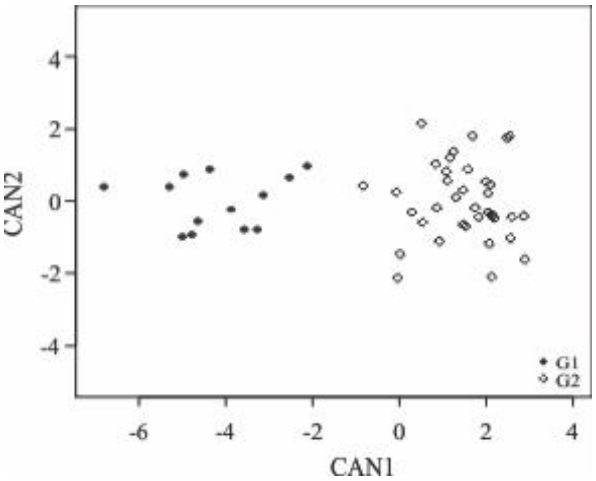
Clustering of the 50 genotypes was by the UPGMA method (SNEATH; SOKAL, 1973), using the inverse of the kinship matrix (1-(2 x r_{xy})). Cluster validation was determined with the cophenetic correlation coefficient (CCC) (SOKAL; ROHLF, 1962).

The Pearson correlation between the genetic similarity (GS) (1 - Gower distance) and the coefficient of kinship (CK) was obtained as a way of evaluating the association between the two strategies for estimating genetic variability.

RESULTS AND DISCUSSION

According to the Ward-MLM analysis, the 50 genotypes were separated into two groups (G1 and G2). Formation of the groups can be seen in the graphical representation of the first two canonical variables (CAN1 and CAN2), which explained 100% of the observed variation, allowing a clear understanding of the genetic variability among the genotypes under evaluation (Figure 1).

Figure 1 - Distribution of the first two canonical variables (CAN1 and CAN2) showing the formation of two groups (G1 and G2) with the Ward-MLM procedure



Group G1 consisted of 13 genotypes, while the other 37 genotypes were allocated in group G2 (Table 3). A greater dispersion of genotypes can be seen in group G1 (Figure 1). This may be explained by the fact that the genotypes in this group descend from two species: *Saccharum spontaneum* and *Saccharum robustum*. The result had been expected, since these species have high levels of fibre and low sucrose content (Table 3).

Twenty-seven genotypes in group G2 are from Brazilian programs, with 19 of these from RIDESA (Tables 1 and 3). Most of the genotypes of this group are hybrid descendants of biparental crosses between genitors used in different breeding programs in Brazil, especially the cultivars SP70-1143 and RB72454; these two being the genitors respectively of 4 and 5 genotypes (Table 1). The cultivars, SP70-1143 and RB72454 are the principal genitors in the RIDESA breeding program, and of the 78 cultivars released by the program, 17 are the offspring of SP70-1143 and RB72454. Of these 17 cultivars, 10 are descended from crossings between the two principal genitors.

Current sugarcane cultivars were developed from interspecific hybridisation involving *S. officinarum* and *S. spontaneum*, followed by successive backcrosses with *S. officinarum*, in order to develop cultivars with high sugar content, high tillering and a greater tolerance to pests and diseases (TEW; COBILL, 2008). Due to these successive backcrosses, approximately 90% of the composition of the genome of the G2 genotypes descends from *S. officinarum* (MING *et al*., 2006).

Among the quantitative traits evaluated in this study, lignin content (LC) contributed least to the diversity analysis. This can be seen from the correlation of LC with the first canonical variable (CAN1) (Table 4). However, LC is one of the most important characteristics in the generation of electrical energy through combustion (RABELO *et al*., 2011).

The largest contributions to the diversity analysis were made by mean stalk diameter (DS), mean stalk weight (MSW), fibre content (FIB), cane pol percentage (PC) and straw weight (SW), demonstrating the importance of these characteristics in studies into genetic diversity, and consequently in the choice of parents and crosses that may optimize the development process in varieties of energy cane (Table 4).

The genotypes of group G1 displayed higher mean values relative to G2, but only for LC, RS and FIB. The mean fibre content of group G1 was higher than the mean value of the principal cultivars currently in use in Brazil (Table 4), especially in genotypes 57NG12 and IM76-228, which showed a fibre content of over 19%.

Table 3 - Groups and phenotypic averages for the 50 genotypes of the Active Germplasm Bank of RIDESA/UFAL, Brazil

Group	Genotype	MSWa	SW	DS	SL	PUR	FIB	PC	RS	TRS	DW	LC
1	57NG12	0.11	0.10	0.90	1.05	48.60	19.20	2.89	1.50	40.21	60.70	27.05
1	C90178	0.38	0.20	2.10	2.11	68.00	14.20	5.25	1.20	59.46	46.40	24.16
1	IJ76-293	0.35	0.40	1.60	1.73	61.40	17.20	4.45	1.30	52.84	46.10	25.58
1	IM76-228	0.28	0.30	1.60	1.77	66.10	19.00	4.30	1.00	49.42	37.90	25.82
1	IM76-229	0.23	0.10	1.50	1.37	66.80	15.10	4.36	1.10	50.96	48.90	25.55
1	IN84-58	0.17	0.10	1.20	1.95	79.70	16.90	6.81	0.80	71.31	40.40	27.66
1	IN84-82	0.19	0.10	1.30	2.44	64.70	18.50	5.31	1.10	59.77	41.30	26.97
1	IN84-88	0.18	0.10	1.10	1.68	80.60	18.50	7.98	0.80	81.48	37.00	26.05
1	KRAKATAU	0.19	0.20	1.40	1.80	75.10	16.70	4.11	1.00	47.31	22.30	23.91
1	UM69/001	0.28	0.20	1.60	1.34	67.10	17.70	6.02	1.10	66.08	51.50	26.13
1	US74-103	0.27	0.10	1.60	1.26	78.10	14.30	10.30	0.90	104.70	46.20	22.36
1	US76-14	0.20	0.10	1.10	1.23	85.60	15.40	9.39	0.70	94.17	46.70	24.27
1	US85-1008	0.12	0.10	1.20	1.15	72.00	14.90	6.03	1.00	65.70	26.10	25.40
2	B70710	0.77	0.40	2.50	2.30	62.70	14.20	4.51	1.30	53.74	47.60	26.84
2	B74125	1.11	0.40	3.20	1.74	75.30	15.20	8.75	1.00	90.43	77.80	22.23
2	B76734	0.83	0.50	2.60	1.82	92.00	12.90	10.20	0.60	101.20	48.50	23.13
2	CB38-22	0.60	0.50	2.70	1.65	70.50	12.90	8.65	1.10	90.81	52.00	24.17
2	Co285	0.46	0.30	1.80	1.85	84.10	14.40	10.20	0.80	102.20	45.80	26.01
2	Co453	0.65	0.30	2.40	1.74	83.40	13.80	9.90	0.80	99.76	47.60	25.80
2	Co617	0.59	0.40	1.90	1.81	81.60	14.40	9.52	0.80	96.49	44.20	22.83
2	Co62175	1.07	0.30	3.00	1.84	85.60	12.70	12.50	0.70	123.20	49.90	24.25
2	CP69-1052	0.81	0.30	2.60	1.84	80.50	13.60	12.80	0.90	127.40	44.00	25.42
2	CTC5	1.05	0.40	2.40	2.29	78.20	12.30	11.50	0.90	115.90	39.50	25.11
2	CTC9	0.66	0.40	2.60	2.23	83.90	14.00	10.60	0.80	106.20	45.40	23.10
2	F150	0.80	0.30	2.70	2.06	75.00	12.80	8.90	1.00	92.27	48.10	25.97
2	IAC50/134	0.57	0.20	2.20	2.02	85.70	14.30	10.80	0.70	107.90	46.40	23.97
2	IAC86-2210	0.84	0.30	2.80	2.01	77.40	11.80	10.10	1.00	102.60	44.30	27.45
2	IAC87-3396	0.98	0.30	2.90	2.25	82.00	13.90	10.90	0.80	109.10	47.00	26.19
2	IANE 48-21	0.65	0.30	2.40	1.50	78.90	12.30	10.40	0.90	105.60	46.90	25.21
2	MEX68-200	0.94	0.30	2.70	1.89	84.30	12.90	12.30	0.80	121.80	46.60	25.90
2	RB011941	1.61	0.50	3.20	1.76	77.10	12.40	10.10	1.00	103.10	55.60	23.39
2	RB01623	1.15	0.50	2.90	1.58	70.50	12.00	6.94	1.10	74.48	51.00	21.60
2	RB01649	0.93	0.40	2.50	1.78	80.10	12.20	11.10	0.90	112.50	58.80	23.74
2	RB0442	0.53	0.40	2.40	1.31	79.60	12.80	8.06	0.90	83.83	49.80	21.92
2	RB047232	0.74	0.20	2.40	1.82	81.70	9.71	12.50	0.90	125.10	48.90	26.03
2	RB04813	0.84	0.20	2.50	1.74	78.30	14.40	10.20	0.90	103.20	63.70	23.38
2	RB04823	0.63	0.60	2.40	1.53	77.90	15.60	9.16	0.90	93.69	46.00	26.77
2	RB72910	1.23	0.60	2.80	2.54	76.00	12.10	7.90	1.00	82.87	41.80	24.77
2	RB75126	1.22	0.40	3.00	1.78	86.20	13.20	11.00	0.70	109.10	47.40	24.17
2	RB83102	0.78	0.30	2.80	1.66	84.00	13.80	12.20	0.80	121.20	46.10	24.66
2	RB867515	1.40	0.40	2.90	2.57	82.70	15.70	12.40	0.80	123.00	57.10	24.41

Table 3 Continued

2	RB92579	1.10	0.40	2.70	2.14	86.40	14.30	13.00	0.70	127.70	52.20	24.14
2	RB928064	1.20	0.30	2.70	1.91	82.90	12.20	9.79	0.80	98.77	48.80	25.04
2	RB93509	0.95	0.30	2.90	1.80	68.00	12.30	9.36	1.20	98.39	34.10	23.84
2	RB937570	1.16	0.50	3.00	1.86	92.10	13.80	11.70	0.60	114.70	54.10	24.61
2	RB946022	1.10	0.40	2.70	1.83	80.10	14.30	10.50	0.90	106.00	51.60	26.17
2	RB96524	0.84	0.40	2.70	1.62	68.60	12.40	7.50	1.20	80.65	50.90	24.82
2	RB971723	1.37	0.50	2.80	2.37	82.30	13.20	11.50	0.80	115.20	54.00	24.02
2	RB98710	0.84	0.40	2.80	1.84	83.80	13.10	11.30	0.80	112.30	42.40	26.27
2	SP81-3250	1.19	0.40	2.60	2.34	71.90	13.30	9.54	1.10	98.93	45.60	25.78

[a] MSW = mean stalk weight (Kg); SW = mean straw weight (Kg); DS = mean stalk diameter (cm); SL = mean stalk length (m); PUR = juice purity (%); FIB = fibre content (%); PC = cane sucrose content (%); RS = reducing sugars (%); TRS = total recoverable sugar (kg t^{-1} cane); DW = cane dry weight (%); LC = lignin content (%)

Table 4 - Mean values, standard deviation (SD), maximum and minimum values for the quantitative characteristics of both groups (G1 and G2), and the correlation coefficient of the characteristics with the first canonical variable (CAN1)

Variables[a]	----------Group (G1)----------			----------Group (G2)----------			CAN1[b]
	Mean ± SD	Max.	Min.	Mean ± SD	Max.	Min.	
MSW	0.22 ± 0.08	0.38	0.11	0.92 ± 0.27	1.61	0.46	0.85
SW	0.16 ± 0.07	0.36	0.06	0.37 ± 0.09	0.57	0.17	0.75
DS	1.39 ± 0.31	2.09	0.88	2.64 ± 0.30	3.24	1.81	0.94
SL	1.60 ± 0.41	2.44	1.05	1.90 ± 0.29	2.57	1.31	0.41
PUR	70.29 ± 9.76	85.61	48.55	79.77 ± 6.38	92.13	62.73	0.53
FIB	16.73 ± 1.82	19.24	14.20	13.26 ± 1.18	15.73	9.71	-0.80
PC	5.94 ± 2.17	10.32	2.89	10.21 ± 1.79	12.96	4.51	0.76
RS	1.03 ± 0.20	1.47	0.70	0.88 ± 0.15	1.29	0.55	-0.40
TRS	64.87 ± 18.95	104.70	40.21	103.54 ± 15.86	127.66	53.74	0.77
DW	42.41 ± 10.19	60.70	22.29	49.22 ± 7.25	77.82	34.14	0.37
LC	25.45 ± 1.46	27.66	22.36	24.67 ± 1.41	27.45	21.60	-0.25

[a]MSW = mean stalk weight (Kg); SW = mean straw weight (Kg); DS = mean stalk diameter (cm); SL = mean stalk length (m); PUR = juice purity (%); FIB = fibre content (%); PC = cane sucrose content (%); RS = reducing sugars (%); TRS = total recoverable sugar (kg t^{-1} cane); DW = cane dry weight (%); LC = lignin content (%); [b]CAN1 = first canonical variable

In both groups, the predominant genotypes are those of erect growth habit, high flowering index and expanded panicles, as well as the absence of toppling, cracks, aerial roots and pilosity (Table 5).

All the genotypes of group G1 display flowering at the expanded-panicle stage and a high level of withering; both undesirable characteristics in commercial crops. However, it should be remembered that the genotypes were evaluated at the RIDESA breeding station, where the climatic conditions favour flowering in sugarcane (BARBOSA *et al.*, 2002). A germ with a thickness of less than, or equal to 1 mm, high tillering, difficult detrashing and stalks without lateral budding are also notable characteristics of this group. In group G2, most genotypes have a lower fibre content and higher sucrose levels, as well as a germ of approximately 2 mm, medium tillering, normal detrashing and stalks with little lateral budding (Table 5).

To increase the probability of obtaining superior genotypes, carrying out crosses of contrasting parents is recommended (HALLAUER; CARENA; MIRANDA FILHO, 2010), it being essential to take the degree

Table 5 - Number of genotypes for each category of morphological characteristics in the two groups (G1 and G2) formed following the Ward-MLM strategy

Caracteristic	Group		Caracteristic	Group	
	G1	G2		G1	G2
Flowering index			Cracks		
absent	0	4	*Absent*	11	26
reduced	1	1	*Little*	2	6
normal	2	3	*Normal*	0	4
high	10	29	*High*	0	1
Flowering			Lateral budding		
absent	0	3	*Absent*	8	15
differentiated germ	0	3	*Little*	5	20
budding phase	0	4	*abundant*	0	2
expanded panicle	13	27	Pilosity		
Withering			*Absent*	6	17
absent	0	8	*Little*	0	11
low	0	12	*Médium*	2	7
medium	0	9	*High*	5	2
high	13	8	Bud prominence		
Toppling			*1 mm*	9	14
absent	8	23	*2 mm*	4	16
inclination less than 30º	5	13	*3 mm*	0	7
between 30ºand 60º	0	1	Tillering		
Detrashing			*Low*	1	5
easy	0	4	*Médium*	1	24
normal	1	20	*High*	11	8
difficult	12	13	Growth habit		
Aerial roots			*Erect*	8	26
absent	7	33	*semi-decumbent*	5	11
few	6	4	*decumbent*	0	0

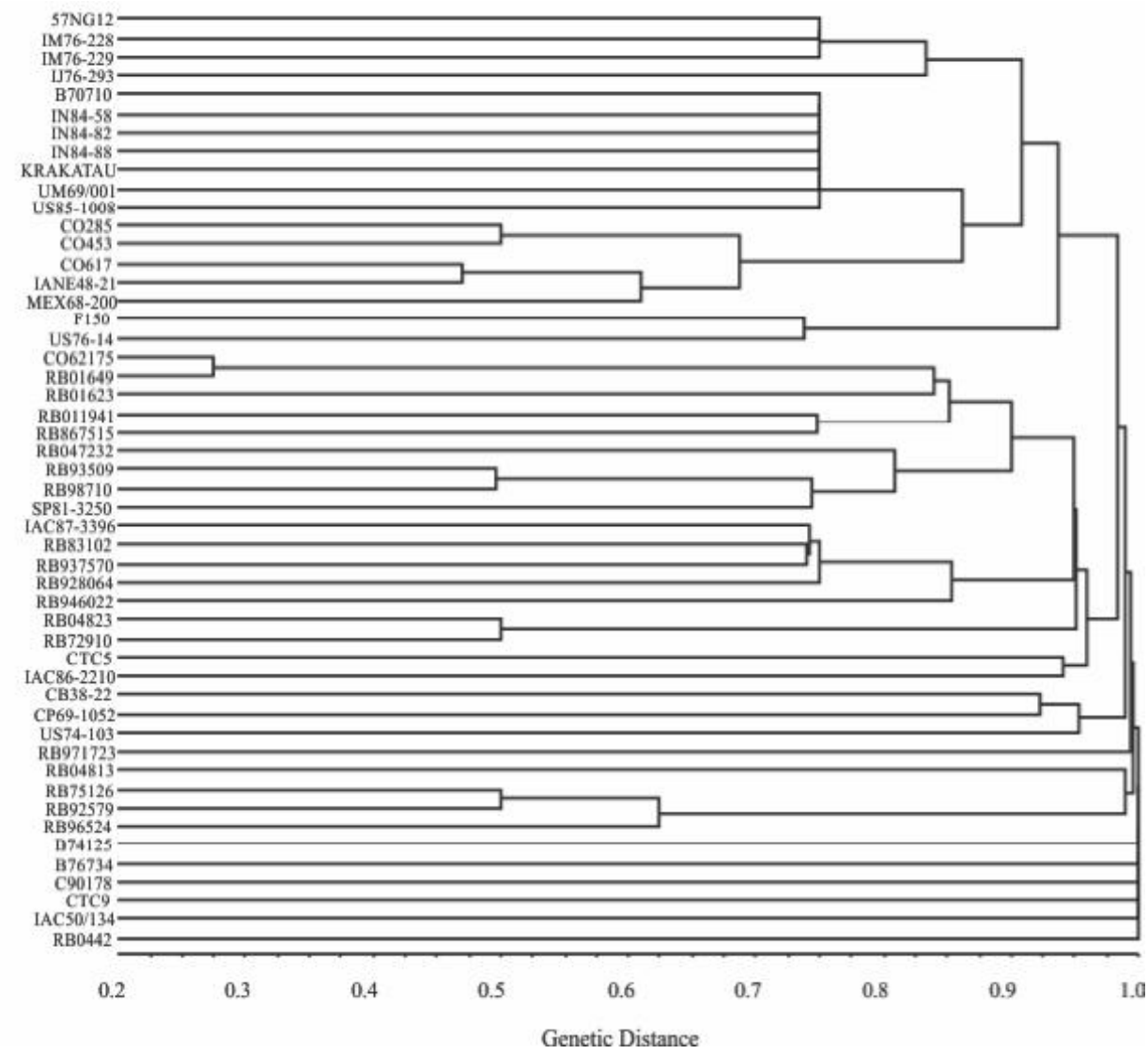
of kinship between parents into consideration. The UPGMA method of grouping (SNEATH; SOKAL, 1973), using the kinship matrix obtained from the pedigree data, contributed in identifying the relationship between genotypes (Figure 2).

The correlation between the cophenetic matrix of the UPGMA hierarchical clustering and the inverse of the kinship matrix was satisfactory (cophenetic correlation coefficient = 0.88), with little distortion of the generated graph (Figure 2).

In the dendrogram, only genotypes C90178, US74-103 and US76-14 were not located close to the other genotypes of group G1 (Figure 2). This was due to a lack of information on the genitors of genotype C90178, and because genotypes US74-103 and US76-14 are directly descended from *S. robustum* or *S. espontaneum* (Table 1). However, the close relationship of these genotypes with group G1, as seen from the morphological and agronomical characteristics under evaluation, suggests that their parents were descendants *of S. spontaneum* or *S. robustum*.

The Pearson correlation coefficient (r) between genetic similarity (GS) and the coefficient of kinship (CK) was only 0.08, demonstrating the low association between the two strategies for estimating genetic variability (Figure 3).

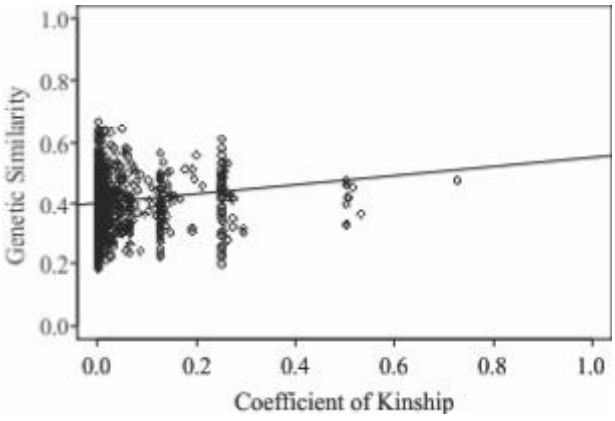
Figure 2 - Dendrogram generated using the UPGMA method from the inverse of the kinship matrix (1-(2 x r_{xy})) between 50 genotypes of the Active Germplasm Bank of UFAL/RIDESA (cophenetic correlation coefficient = 0.88)



The low correlation between GS and CK in sugarcane was also observed by Lima *et al.* (2002). Although these authors used data from AFLP markers, the correlation found between GS and CK was only 0.42. Duarte Filho *et al*. (2010) also found a low correlation between GS and CK (r = 0.17) when evaluating sugarcane genotypes using data from SSR markers. These results confirm the need for further use of differing analyses of genetic diversity, so as to have increasing knowledge of the germplasm which is available to sugar-cane breeding programs.

While most of the values for genetic similarity (GS) were between 0.3 and 0.6, the majority of the coefficients of kinship (CK) were between 0 and 0.2 (Figure 3). These figures show the existence of genetic variability among the genotypes involved in this study, which can be exploited in breeding programs. However, it is noteworthy that low values for CK may in part be related to a lack of information on the genealogy of some genotypes (Table 1). On the other hand, it should be considered that sugarcane is octaploid by nature, which makes numerous allelic combinations possible at a single locus during fertilisation. As a result, there is great phenotypic variability among the descendants of crosses between contrasting parents. In many ways this was evident in the results obtained wih this study. Of all the possible combinations of genotype pairs (1,225), in only ten was the value for CK greater than 0.4 (Figure 3). The only relatively high value (0.72) was observed

Figure 3 - Plot of the correlation between kinship coefficient(2 x r_{xy}) and genetic similarity (1 - Gower distance) among 1,225 pairs of sugarcane genotypes



between a female parent (Co62175) and the female offspring (RB01649). The coefficient of endogamy was also low in all genotypes, varying between 0 and 0.05 (Table 1), showing the high heterozygosity of the sugarcane genotypes evaluated.

According to Tew and Cobill (2008), sugarcane currently being cultivated has approximately 12% fibre, 13% sugar and 75% water. According to the same authors, breeding programs for obtaining energy cane should be aiming to develop cultivars with 30% fibre, 5% sugar and 65% water. It should be remembered that the road to achieving genotypes with these characteristics is relatively long. Moreover, considering that production plants are not yet ready to process sugarcane with a fibre content of over 20%, the development of cultivars with a fibre content of around 17% and which maintain approximately 13% sugar, would answer the current needs of the sugar-energy industry. This type of cane would increase the capacity for biomass production by increasing the percentage of fibre, without resulting in losses in sugar production.

Carrying out crosses involving genotypes from group G1, particularly those with a fibre content of more than 17% (IJ76-293, 57NG12, IN84-82, IN84-88, IM76-228 and UM69 / 001), with genotypes of group G2 which display high stalk productivity (RB92579, RB83102, RB047232, RB867515, RB971723, RB937570, RB011941, RB75126, MEX68-200, Co62175 and CP691052) (Table 3), as well as crosses between the best genotypes within each group, should be explored with the aim of developing energy cane cultivars by means of reciprocal recurrent selection (RRS).

CONCLUSIONS

1. Analyses of diversity and of the coefficient of kinship identified two heterotic groups of potential genitors of energy cane cultivars;
2. The use of genetic distances based on morpho-agronomic and pedigree data, should be used in a complementary way to obtain greater knowledge on potential genitors for the generation of energy cane cultivars.

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