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PLANT BREEDING - Article

Canonical correlation for morphoagronomic and bromatological traits in silage corn genotypes

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ABSTRACT: The aim of this study is to assess whether there is linear dependence between groups of morphoagronomic and bromatological traits in hybrid silage corn. Nineteen topcross hybrids and five checks were assessed in two different environments in Campos dos Goytacazes and Itaocara counties, Rio de Janeiro State, during the growing seasons 2013/2014. The study followed a randomized blocks design with four replicates. The phenotypic and canonical correlations between the groups of seven morphoagronomic and five bromatological traits were assessed. There is linear dependence between the group pairs of morphoagronomic, and bromatological variables. The morphoagronomic trait green mass yield can be adopted in indirect selection processes to indicate the increased bromatological quality of maize silage based on features such as crude protein, neutral detergent fiber, lignin, crude fat and mineral matter. Topcross hybrids UENF-2208 and UENF-2209 presented high potential for silage yield in the North and Northwest Regions.

Key words: *Zea mays* L., topcross, tester, multicollinearity.

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INTRODUCTION

The United States is the biggest corn (*Zea mays* L.) producer in the world. The country is followed by China and Brazil, with estimated production of 386.74, 216.00 and 83.88 million tons, respectively (USDA 2016). The maize crop area estimated for the 2017/2018 growing season in Brazil is 16,969 thousand hectares with yield estimated at 4,967 kg·ha^{-1}, which would result in the production of 82,927.9 thousand tons (Conab 2018). According to estimates, approximately 800,000 hectares in Brazil are planted with maize exclusively grown for silage production (Moraes and Santos 2008); this area has been constantly growing in recent years.

It is worth noticing that most breeding programs developed in the country do not emphasize the development of cultivars for silage production. Often, the best hybrids for grain production are also recommended for silage production (Mendes et al. 2008); therefore the lack of information about agronomic response and nutritional values became a barrier to the selection of hybrid corn for silage production. The morfoagronomic and bromatological traits of genetic materials are of crucial importance for silage (Rosa et al. 2004).

The association between features of economic interest is essential to enable genetic improvement programs, mainly to investigate correlated responses that can help identifying changes in a given trait, which would have resulted from selection processes based on a different trait (Cruz et al. 2012). According to Cruz et al. (2012), although simple correlation coefficients are very useful to quantify the magnitude and direction of factors influencing the determination of complex traits, they do not show the relative importance of the direct and indirect effects resulting from these factors.

It is essential identifying and quantifying the association between morphoagronomic and bromatological traits in order to improve the efficiency of selection processes focused on meeting most aims of maize breeding programs. The canonical correlation analysis allows investigating the association between two groups of variables (Cruz et al. 2012) in order to enable the selection of a more appropriate plant ideotype.

The canonical correlation analysis is an uncomplicated way to reduce the complexity of associating two sets of variables (Trugilho et al. 2003). It can be used to estimate the maximum correlation between two complexes of variables composed by linear combinations of several traits, as well as to enable the evaluation of interrelationships between two complexes determined by an arbitrary number of traits. This analysis is often used in exploratory studies comprising a large number of variables to investigate linear combinations presenting increased correlation (Cruz et al. 2012; Silva et al. 2007; Witten and Tibshirani 2009).

Canonical correlations have been used to elucidate relationships in *Saccharum officinarum* (Silva et al. 2009), *Carica papaya* (Oliveira et al. 2010), guava (Santos et al. 2017), *Spondias purpurea* (Giles et al. 2016), *Ricinus communis* (Brum et al. 2011), *Triticum sativum L.* (Carvalho et al. 2015), *Lolium Multiflorum* (Müller et al. 2012) and *Zea mays* L. (Souza et al. 2015). However there is no information on the associations between groups of traits their simultaneous selection in corn improvement for silage production purposes.

The aim of this study was to investigate whether there is linear dependence between morphoagronomic and bromatological traits in hybrid corn for silage production.

MATERIALS AND METHODS

The genotypes used came from the corn collection of Universidade Estadual do Norte Fluminense Darcy Ribeiro – UENF. Nineteen genotypes were selected, all of them belonging to the heterotic group Dent. Each genotype was crossed with a tester – Piranão 12, which is a broad-based tester also belonging to the heterotic group DENT – in order to generate heterotic group DENT topcross hybrids (Table 1). Topcross hybrids were obtained in an isolated field of Barra do Pomba Island Experimental Station in Itaocara County, Northern Region of Rio de Janeiro State, in March 2013.

Tester Piranão 12 resulted from interpopulation crossings between Cimmyt and Piranão populations, which were already subjected to the 16th reciprocal recurrent selection cycle in the Plant Genetics and Breeding Program of UENF.

Each genotype was cultivated in 10.0 m-long rows (1.0 m spacing between rows). Five seeds were sown per linear meter, thus totaling 50 plants per row. Rows were placed 0.20 m from each other. Female genitor detasseling was performed during the flowering phase – before the spike could release the style-stigma – in order to avoid contamination. The style-stigma only received pollen from the tester (Piranão 12). Harvest was performed 120 days after sowing.

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Table 1. Description of the 19 topcross hybrids, 5 checks and 1 tester used in the experiments.

Identification	Hybrids	Grain type	Origin	Genetic basis
1	UENF-2194*	Dent	UENF	Lines
2	UENF-2195*	Dent	UENF	Lines
3	UENF-2199*	Dent	UENF	Lines
4	UENF-2205*	Dent	UENF	Population
5	UENF-2198*	Dent	UENF	Lines
6	UENF-2203*	Dent	UENF	Population
7	UENF-2192*	Dent	UENF	Lines
8	UENF-2206*	Dent	UENF	Population
9	UENF-2207*	Dent	UENF	Population
10	UENF-2208*	Dent	UENF	Lines
11	UENF-2209*	Dent	UENF	Lines
12	UENF-2210*	Dent	UENF	Population
13	UENF- 2200*	Dent	UENF	Population
14	UENF-2202*	Dent	UENF	Population
15	UENF-2201*	Dent	UENF	Population
16	UENF-2204*	Dent	UENF	Population
17	UENF-2193*	Dent	UENF	Lines
18	UENF-2191*	Dent	UENF	Lines
19	Piranão 13*	Dent	UENF	Population
20	AG 1051**	Dent	Commercial	Hybrid double
21	UENF-2197**	Semi-dent	UENF	Lines
22	UENF-2196**	Semi-dent	UENF	Lines
23	Br 106**	Semi-dent	Commercial	Population
24	UENF 506-11**	Semi-dent	UENF	HIP
	Piranão 12***	Dent	UENF	Population

*Topcross hybrids; **Checks; HIP = Híbrido interpopulacional. ***Tester; Genotypes from 1 to 19, 21, and 22 were crossed with Piranão 12.

The trials to assess topcross hybrids were simultaneously installed in two different environments: Escola Técnica Estadual Agrícola Antônio Sarlo, in Campos do Goytacazes, Rio de Janeiro State, and Barra do Pomba Island Experimental Station, in Itaocara, Rio de Janeiro State, in the growing seasons 2013/2014.

These environments are located at 21°24’48” S, 41°44’48” W, 14 m altitude, with mean rainfall 108.6 mm and mean temperature 27.27 °C; and at 21°40’09” S, 42°04’34” W, 60 m alt, with mean rainfall 183.25 mm and mean temperature 25.32 °C, respectively (INMET 2017).

The study followed a randomized blocks design with four replicates, each of them with 24 treatments, 19 topcross hybrids and 5 checks (Table 1).

The experimental unit comprised one 5.0 m-long row with 1.0 m spacing between rows. Each unit had 25 plants per plot with 0.20 m spacing between pits. Three seeds were sown in each pit (5 cm down in the pit). Trimming was conducted 21 days after emergence and only one plant was left in each pit.

The experiments were structured based on conventional planting system. Crop management was conducted based on recommendations for the culture.

The traits assessed were: number of days for female flowering (FF), measured when 50% of the plants in the plot presented emerged style-stigma; mean plant height (MPH), measured from the soil level to the tassel insertion knot (in m); mean insertion height of the first spike (MIHFS), measured from the soil level to the basis of the upper spike in the culm (in m); mean stem diameter (MSD), measured in the first internode above plant stem (in m); spike yield with straw at silage stage (SYWSS) (in kg·ha^{-1}); spike yield without

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straw at silage stage (SYNSS) (in kg·ha^{-1}); grain yield at silage point (GY) (in kg·ha^{-1}); proportion of grains in the green mass (GGM) (in %); and green mass yield (GMY) (in kg·ha^{-1}).

The MPH, MIHFS and MSD were randomly measured in 6 plants from the plots after flowering feminine whereas the SYWSS, SYNSS, GY and GMY were measured in 15 plants per plot, thus totaling 3.0 m of each row in the plot. Harvest was performed by cutting the plant 20 cm from the soil when the grains were at the farenaceous point (3/4 from the milk line) (Restle et al. 2002). SYWSS and SYNSS were measured by weighing the spikes with and without straw at silage stage. GY was obtained by weighing the threshed grain at silage stage. GMY was found by weighing the plants (leaf + stalk + cob + spike straw + grain) from each plot at harvest. GGM was obtained by the ratio between GY and GMY.

The bromatological analyses were performed in the Zootechny Laboratory (LZNA) of UENF, in Campos dos Goytacazes County, Rio de Janeiro State. The following analyses were carried out: dry matter content (DM), gross protein content (GP), fiber in neutral detergent (FND), gross fat (GF), Lignin (LIG); and mineral matter (MM).

The beam with the 15 plants was weighed after harvest, spikes were removed, thrashed and the weight of the grains was recorded. The straw (leaf + stalk + cob + straw) was processed in forage chopper and homogenized; a subsample of it was collected. The grain and straw samples were dried in ventilated oven at 55 °C for 72 h right after harvest. The dried sample (grains + straw) was ground (1 mm) in Wilye (Logen Scientific – model WLS-3004) mill for bromatological analysis.

The forage samples were tested for gross fat (Method 2003,06) (Thiex et al. 2003), mineral matter (Method 942,05; AOAC, 1990), gross protein (Method AOAC 984,13; Method AOAC 2001,11; AOAC, 1990) (Thiex et al. 2002), fibrous organic matter (aFNDmo) (AOAC 2002,04) (Mertens 2002) and lignin (AOAC 973,18; AOAC, 1990) (Möller 2009). All bromatological variables (DM, GF, FND, GP, LIG and MM) were expressed in kg·ha^{-1}.

A joint analysis of variance was carried out by taking into account the following statistical model (Eq. 1):

$$Y_{ijk} = \mu + G_i + B/A_j + A_j + GA_{ij} + e_{ijk} \tag{1}$$

where Y_{ijk} is the observation in the k^th^ block, which is assessed in the i^th^ genotype and in the j^th^ environment; μ is the general constant of the assay; G_i is the random effect of the genotype i; B/A_{jk} is the effect of block K on environment j; A_j is the fixed effect of environment j; is the interaction effect between genotype i and environment j; and e_{ijk} is the random error associated with observation Y_{ijk}, e_{ijk} ~NID $(0,\sigma^2)$.

Variance components were estimated based on expected mean square values, considering:

Genotypic variance: $\sigma^2_g = (QSG - MSR)/rl$;

Phenotypic variance: $\sigma^2_f = QSG/rl$;

Residual variance: $\sigma^2_e = MSR/rl$;

Mean heritability of the genotypes: $h^2_{\bar{x}} = \sigma^2_g / \sigma^2_f$;

Coefficient of experimental variation: $CV_e(\%) = 100(\sqrt{\sigma^2_e/\bar{x}})$;

Coefficient of genetic variation: $CV_g(\%) = 100(\sqrt{\sigma^2_g/\bar{x}})$;

Variation index: $I_V(\%) = 100\ (CV_g/CV_e)$;

Accuracy: $\hat{r}gg = \sqrt{(1-1/F)}$;

Standard deviation: $DP = \sqrt{\sigma}$.

where MSR = mean square of residue; MSG = mean square of genotype; r = number of repetitions; l = number of environments; and F = MSR/MSG ratio.

Phenotypic correlation coefficients (r_f):

$$r_f = (COV_{f(x,y)}/\sqrt{(\sigma^2{}_{fx} \cdot \sigma^2{}_{fy})})$$

where $COV_{f(x,y)}$ = phenotypic covariance estimates between traits x and y, respectively; $\sigma^2{}_{fx}$ = phenotypic variance estimates of trait x; and $\sigma^2{}_{fy}$ = phenotypic variance estimates of trait y.

Multicollinearity diagnosis covered each group of traits (morphoagronomic and bromatological) after the phenotypic correlation matrices were found. Multicollinearity magnitude within each group of traits was checked through number of conditions (NC) and classified based on the criterion by Montgomery and Peck (1982). This process was followed in order to avoid phenotypic and canonical correlation coefficients overestimates (Cruz et al. 2012).

Canonical correlations were estimated between pairs of the groups of morphoagronomic and bromatological traits. The maximum correlation among the linear combinations

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of traits distributed in the group pairs were estimated, as well as the weighing coefficients of the traits in each linear combination.

After finding severe multicollinearity between groups of morphoagronomic and bromatological traits, there were eliminated the traits grain yield at silage point (GY), proportion of grains in the green mass (GGM) and dry matter content (DM) in the groups of morphoagronomic and bromatological traits, respectively. The canonical correlation analysis was applied to traits that remained within each group: morphoagronomic (FF, MPH, MIHFS, MSD, SYWSS, SYNSS and GMY) and bromatological (GP, FND, LIG, CF and MM).

The canonical correlations between group pairs of traits were expressed in coefficient of canonical pairs and in canonical coefficients. The significance of canonical correlations was tested through chi-square test at ($p > 0.05$) significance level. The statistical analyses were conducted in the Genes software (Cruz 2013) and *software* SAS (SAS Institute Inc. 2013).

RESULTS AND DISCUSSION

Significant effects were observed in all studied features, indicating genetic variability between genotypes. The effects of the genotype vs. environment interaction were significant in MPH, MSD, GGM, GMY and FND, only. The significant interaction highlights that the response from the genotypes was not coincident in different environments (Table 2).

The assessed hybrids general mean has shown satisfactory outcomes, i.e., it has shown high yield potential in the Northern and Northwestern region of Rio de Janeiro State (Table 2).

Based on genetic parameter estimates, total phenotypic variance recorded genetic variation, fact that indicated genetic variability between genotypes and allowed inferring the possibility of successfully selecting superior hybrids (Maia et al. 2009).

Values estimated for the genotypic variance of morphoagronomic traits ranged from 0.01552 to 11591194.85, whereas the ones estimated for bromatological traits ranged from 450.82 to 1975900.32 (Table 3). The highest estimates concerned variables GMY and DM (11591194.85 and 1975900.32, respectively).

However, it is worth highlighting the proportion of these estimates in residual and phenotypic variances, rather than their magnitude. The proportions of all morphoagronomic variables ranged from 48.30% to 94.17% in comparison to the total phenotypic variance. This outcome indicated that the evaluated genotypes presented high genetic variability in the analyzed traits. On the other hand, with respect to bromatological traits, the proportions of genotypic variances in comparison to the phenotypic ones ranged from 54.85% to 73.23% (Table 3).

The coefficient of experimental variations (CVe) ranged from 2.33% to 23.12% in the morphoagronomic traits and from 23.02% to 27.49% in the bromatological variables (Table 3). Based on the classification by Fritsche-Neto et al. (2012), the morphoagronomic traits presented great experimental precision. However, the other variables related to yield and to the quality of the forage values were high. This outcome was expected, since these traits are strongly influenced by environmental conditions.

It was observed that the heritability based on the mean has ranged from 48.30% (SYWSS) to 94.17% (MPH) in the morphoagronomic traits and from 54.85% (LIG) to 73.23% (MM) in the bromatological variables (Table 3).

Therefore, it is possible predicting the possibility of success by selecting the breeding program according to the heritability estimate.

According to Ramalho et al. (2012), the higher the magnitude of the accuracy (closer to 100%), the better the quality of the experiment and the greater the reliability of the experimental information. The selective accuracy in our study was high (0.69) and indicated the possibility of successfully selecting topcross hybrids. The selective accuracy for the morphoagronomic and bromatological traits ranged from high to very high (Ac > 0.78) in the present study, except for SYWSS, SYNSS, GY, LIG and GF, which were moderate: 0.69, 0.69, 0.71, 0.74 and 0.77, respectively (Table 3).

Knowing the relationship between the traits of interest is an important aspect for the genotypic selection. Highly correlated traits allow making a selection based on the easily measured traits, leading to similar gain in the other ones (Cruz et al. 2012). Correlation estimates can be used to set the guidelines and to manage corn genetic improvement programs. These results allow achieving gains through indirect selection, which makes the improvement process faster and more effective (Alves et al. 2016).

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Table 2. Summary of the joint analysis of variance applied to eight traits assessed in corn hybrids for silage production. Campos dos Goytacazes and Itaocara, Rio de Janeiro State, growing seasons 2013/2014.

Variation sources	DF	Mean squares								
		FF	MPH	MIHFS	MSD	SYWSS	SYNSS	GY	GGM	GMY
		Morphoagronomic								
Block/Environment	6	6.38021	0.15058	0.10512	7.2901	7703347.81	3156771.42	2326959.02	7.24918	30492784.42
Genotype (G)	23	28.28782**	0.21463**	0.13513**	13.3324**	11610599.83*	6454681.93*	4328791.36**	31.08513**	134884400.48**
Environment (A)	1	84.00521**	0.3048^{ns}	0.06901^{ns}	730.4700**	250189404.08^{ns}	89257438.02^{ns}	51268834.50^{ns}	33.17519^{ns}	746457228.0^{ns}
GXA	23	1.65738^{ns}	0.07743*	0.01416^{ns}	4.7725*	7177267.64^{ns}	3349994.97^{ns}	1829489.16^{ns}	12.12635**	70140897.07*
Error	138	2.21716	0.0125	0.01099	2.8877	6002445.40	3315059.51	2121672.55	4.39022	42154841.64
General Average		63.66	2.01	1.26	22.49	11,758	8,729	6,298	19.94	31,774
Average hybrids topcross		63.65	2.06	1.27	22.56	11,939	8,888	6,445	20.01	32,400
Average Checks		63.70	1.84	1.22	22.22	11,067	8,125	5,742	19.68	29,396

Variation sources	DF	Mean squares					
		DM	GP	FND	LIG	GF	MM
		Bromatological					
Block/Environment	6	7311382.53	25421.55	2073165.86	19269.66	4634.52	24138.41
Genotype (G)	23	24044017.30**	126728.80**	6317563.94**	23075.28**	6075.27**	64491.05**
Environment (A)	1	155997365.75^{ns}	499290.00^{ns}	47096294.08^{ns}	18703.25^{ns}	74655.18^{ns}	87210.75^{ns}
GXA	23	11896023.36^{ns}	57321.37^{ns}	3934291.94*	16123.23^{ns}	3329.26^{ns}	21208.54^{ns}
Error	138	8236814.69	39222.88	2204457.08	10404.42	2468.68	17253.42
General Average		12,343	860	6,379	370	196	510
Average hybrids topcross		12,569	871	6,504	376	200	519
Average Checks		11,458	815	5,904	350	183	478

FF = number of days for flowering; MPH = mean plant height (m); MIHFS = mean insertion height of the first spike (m); MSD = mean stem diameter (m); SYWSS = spike yield with straw at silage stage (kg·ha^{-1}); SYNSS = spike yield without straw at silage stage (kg·ha^{-1}); GY = grain yield at silage point (kg·ha^{-1}); GGM = proportion of grains in the green mass (kg·ha^{-1}); GMY = green mass yield (kg.ha^{-1}); DM = dry matter content (kg.ha^{-1}); GP = gross protein (kg·ha^{-1}); FND = fiber in neutral detergent (kg·ha^{-1}); LIG = Lignin (kg·ha^{-1}); GF = gross fat (kg·ha^{-1}); MM = and mineral matter (kg·ha^{-1}). ^{ns} Not Significant by the F test; ** Significant ($p < 0.01$) by the F test; * Significant ($p < 0.05$) by the F test.

Phenotypic correlations were used in the analyses canonical correlations since phenotypes are often used as basis for selection purposes. Phenotypically-correlated variables present practical selection value since they have strong genetic components in their phenotypic expressions, which results in gains through visual selection (Andrade et al. 2010; Ferreira et al. 2007).

Pearson's phenotypic correlation estimates for maize genotypes ranged from $r = -0.59$ to $r = 0.98$ (Table 4). The morphoagronomic traits presented significant positive and high-magnitude correlation to most bromatological traits – such outcome showed that the morphoagronomic traits influenced the bromatological ones, since they increased simultaneously.

GMY recorded the highest phenotypic correlation coefficients with DM, GP, NDF, LIG, CF and MM – 0.96 **; 0.94 **; 0.96 **; 0.93 **; 0.85 ** and 0.92 **, respectively (Table 4). These high correlation values showed high linear relationships between green mass yield and traits such as dry matter content, crude protein content, neutral detergent fiber, lignin, crude fat and mineral matter.

Bromatological analyses conducted in laboratory are expensive and laborious for plant breeding programs aimed at producing silage. Thus, it is essential identifying morphoagronomic traits with high potential to silage production in order to enable the shortest evaluation time, the lowest cost and progress in the development of new cultivars.

According to Oliveira et al. (2010), significant correlations indicate the possibility of indirectly selecting important traits based on easily measured agronomic traits. Green mass yield showed significant positive correlations to plant height (0.58), ear yield with straw

Table 3. Estimates of the genetic parameters of the morphoagronomic and bromatological traits in hybrid corn for silage production. Campos dos Goytacazes and Itaocara, Rio de Janeiro State, growing seasons 2013/2014.

Traits	σ^2_g	σ^2_f	σ^2_e	CV_e (%)	h^2_x	CV_g (%)	I_v (%)	$\hat{r}gg$	DP
					Morphoagronomic				
FF	3.25883	3.53597	0.277145	2.33	92.16	2.83	1.21	0.96	1.8
MPH	0.02527	0.02682	0.0015625	5.54	94.17	7.88	1.42	0.97	0.15
MIHFS	0.01552	0.01689	0.00137375	8.29	91.86	9.85	1.18	0.95	0.12
MSD	1.30558	1.66655	0.36097375	7.55	78.34	5.07	0.67	0.88	1.14
SYWSS	701019.30414	1451324.979	750305.6758	20.83	48.30	7.12	0.34	0.69	837.26
SYNSS	392452.80246	806835.24	414382.4393	20.85	48.64	7.17	0.34	0.69	626.46
GY	275889.85224	541098.92	265209.0689	23.12	50.98	8.33	0.36	0.71	525.25
GGM	3.33686	3.88566	0.5487775	10.50	85.87	9.15	0.87	0.92	1.82
GMY	11591194.85	16860550.06	5269355.205	20.43	68.74	10.71	0.52	0.82	3404.58
					Bromatological				
DM	1975900.32	3005502.16	1029601.836	23.24	65.74	11.38	0.48	0.81	1405.66
GP	10938.23	15841.10	4902.86	23.02	69.04	12.15	0.52	0.83	104.58
FND	514138.35	789695.49	275557.135	23.27	65.10	11.24	0.48	0.80	717.03
LIG	1583.85	2884.41	1300.5525	27.49	54.85	10.71	0.38	0.74	39.79
GF	450.82	759.40	308.585	25.28	59.34	10.79	0.42	0.77	21.23
MM	5904.70	8061.38	2156.6775	25.72	73.23	15.04	0.58	0.85	76.84

FF = number of days for flowering; MPH = mean plant height (m); MIHFS = mean insertion height of the first spike (m); MSD = mean stem diameter (m); SYWSS = spike yield with straw at silage stage ($kg \cdot ha^{-1}$); SYNSS = spike yield without straw at silage stage ($kg \cdot ha^{-1}$); GY = grain yield at silage point ($kg \cdot ha^{-1}$); GGM = proportion of grains in the green mass ($kg \cdot ha^{-1}$); GMY = green mass yield ($kg \cdot ha^{-1}$); DM = dry matter content ($kg \cdot ha^{-1}$); GP = gross protein ($kg \cdot ha^{-1}$); FND = fiber in neutral detergent ($kg \cdot ha^{-1}$); LIG = Lignin ($kg \cdot ha^{-1}$); GF = gross fat ($kg \cdot ha^{-1}$); and MM = mineral matter ($kg \cdot ha^{-1}$). σ^2_g = genotypic variance; σ^2_f = phenotypic variance; σ^2_e = residual variance; CV_e = coefficient of experimental variation; CV_g = coefficient of genetic variation; I_v = variation index; h^2_x = mean heritability of the genotypes; $\hat{r}gg$ = Accuracy in genotypes selection. DP = standard deviation.

(0.92), ear yield without straw (0.75) and to grain yield at silage point (0.70) (Table 4). These estimates showed association of inheritable nature between traits. Therefore they can be used in indirect selection processes in breeding programs.

In addition, variables presented positive correlation to each other, fact that showed the complexity of the relationship between traits capable of influencing GMY. This outcome indicates that it is possible to indirectly select plants with higher MPH, SYWSS, SYNSS and GY whenever higher GMY is desired (Table 4).

Therefore, the most regionally-adapted hybrids for green mass yield may be used for silage production when there is no specific information about maize hybrids adopted for this purpose. In addition, grain yield at silage point, ear yield with and without straw at silage point and plant height should be taken into consideration due to the high correlation between these traits and green mass yield.

Correlations between morphoagronomic and bromatological variables in corn for forage production remain poorly assessed, although these variables are essential to select strategies to improve the herein addressed culture. However, correlation magnitude and value are not enough to determine the relations between groups of variables. Canonical correlation is also a valid strategy to define weights for selection indices (Cern-Rojas et al. 2008).

The study about the association between two groups of characters can be performed through canonical correlation analysis, which aims at determining a linear combination to each group of variables, since these variables are capable of minimizing the correlation between the two groups (Witten and Tibshirani 2009).

The canonical correlation analysis allowed observing that the groups of morphoagronomic and bromatological traits were linearly dependent on each other, i.e., the groups were not independent if one takes into consideration at

Table 4. Estimates of the coefficients of phenotypic Pearson's correlations between traits in hybrid corn for silage production. Campos dos Goytacazes and Itaocara, Rio de Janeiro State, growing seasons 2013/2014.

	MPH	MIHFS	MSD	SYWSS	SYNSS	GY	GGM	GMY	DM	GP	FND	LIG	GF	MM
FF	–0.30^{ns}	–0.39^{ns}	0.72**	0.03^{ns}	–0.26^{ns}	–0.17^{ns}	–0.36^{ns}	0.14^{ns}	0.19^{ns}	0.21^{ns}	0.21^{ns}	–0.03^{ns}	0.10^{ns}	0.20^{ns}
MPH		0.79**	–0.39^{ns}	0.54**	0.65**	0.57**	–0.07^{ns}	0.58**	0.54**	0.52**	0.54**	0.59**	0.48*	0.50*
MIHFS			–0.46*	0.43*	0.56**	0.47*	–0.004^{ns}	0.45*	0.45*	0.42*	0.43*	0.57**	0.47*	0.44*
MSD				0.22^{ns}	–0.04^{ns}	0.04^{ns}	–0.18^{ns}	0.19^{ns}	0.21^{ns}	0.19^{ns}	0.23^{ns}	0.03^{ns}	0.22^{ns}	0.19^{ns}
SYWSS					0.89**	0.83**	–0.19^{ns}	0.92**	0.87**	0.82**	0.85**	0.87**	0.83**	0.80**
SYNSS						0.94**	0.15^{ns}	0.75**	0.68**	0.65**	0.64**	0.80**	0.75**	0.61**
GY							0.29^{ns}	0.70**	0.63**	0.61**	0.55**	0.71**	0.75**	0.56**
GGM								–0.47*	–0.51*	–0.50*	–0.59**	–0.37^{ns}	–0.22^{ns}	0.52**
GMY									0.96**	0.94**	0.96**	0.93**	0.85**	0.92**
DM										0.97**	0.98**	0.92**	0.90**	0.96**
GP											0.94**	0.88**	0.88**	0.95**
FND												0.91**	0.84**	0.93**
LIG													0.84**	0.87**
GF														0.84**

FF = number of days for flowering; MPH = mean plant height (m); MIHFS = mean insertion height of the first spike (m); MSD = mean stem diameter (m); SYWSS = spike yield with straw at silage stage (kg·ha^{-1}); SYNSS = spike yield without straw at silage stage (kg·ha^{-1}); GY = grain yield at silage point (kg·ha^{-1}); GGM = proportion of grains in the green mass (kg·ha^{-1}); GMY = green mass yield (kg·ha^{-1}); DM = dry matter content (kg·ha^{-1}); GP = gross protein (kg·ha^{-1}); FND = fiber in neutral detergent (kg·ha^{-1}); LIG = Lignin (kg·ha^{-1}); GF = gross fat (kg.ha^{-1}); and MM = mineral matter (kg·ha^{-1}).^{ns} Not Significant by the t test; ** Significant ($p < 0.01$) by the t test; * Significant ($p < 0.05$) by the t test.

least the first canonical pair at ($p < 0.01$) probability level in the chi-square test (Tables 5).

The canonical correlation between bromatological and morphoagronomic variables indicated that associations based on the first coefficient of the canonical pair were significant, at 1% probability level, in the Chi-square test, besides presenting correlation r = 0.98. Therefore this is the only pair of interest in such associations. Associations between bromatological and morphoagronomic variables are mainly set by variables such as GP, FND, LIG, GF, MM, SYWSS, SYNSS and GMY (Table 5).

Thus, it was possible to identify promising morphoagronomic traits (SYWSS, SYNSS and GMY) for maize genetic improvement since they indicated the quality of bromatological variables.

The coefficient of the first canonical pair showed that plants recording the highest spike yield with or without straw at silage stage and green mass yield significantly increased the gross protein, fiber, lignin, gross fat and mineral matter content in neutral detergent. However, it is necessary to select plants with the highest spike yield with or without straw at silage stage and the highest green mass yield in order to have a cultivar presenting higher gross protein, fiber in neutral detergent, lignin, gross fat and mineral matter accumulation.

Alves et al. (2017) verified that the phenological traits can be used for indirect selection as an indicative of energetic-nutritional quality in grains of maize. Souza et al. (2015) Verified that hybrids with higher plant height, insertion of ear and leaf angle and fewer branches and tassel length are associated with the increase in weight of hundred grains in maize. To increase the grain weight, there should be considered hybrids with greater insertion of the ear, leaf area and shorter length of the tassel.

Although the number of coefficients of canonical pairs is equal to the number of traits of the smallest group, overall only the first two or three canonical functions are reliable, which were used in result interpretation. The significance of at least one coefficient of the canonical pair leads to the conclusion that the groups taken into consideration are dependent, so their coefficient can be used to study the association between traits of the groups.

The aim of the present study was to help genetic improvers better understanding the linear dependence between the morpholoagronomic and bromatological traits in silage corn, since there is lack of studies in this research field.

Accordingly, it is recommended to conduct further studies in order to better understand the association between these groups of traits to get better-quality silage.

Table 6 shows the mean values of morphoagronomic and bromatological traits evaluated in maize hybrids used for silage production, based on the Tukey test.

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Topcross hybrids showed promising results, since they recorded green mass yield ranging from 23263 to 39590 kg.ha^{-1} and dry matter content ranging from 8787 to 15792 kg.ha^{-1}. Among the evaluated treatments, it was possible seeing the superiority of topcross hybrids in most of the evaluated traits in comparison to the controls, with emphasis to green mass yield and dry matter. The herein evaluated UENF-2209 and UENF-2208 topcross hybrids recorded mean GMY values 39540 kg.ha^{-1} and 38040 kg.ha^{-1}, as well as mean DM values 15404 kg.ha^{-1} and 15792 kg.ha^{-1}, respectively (Table 6).

The development of hybrids with good agronomic performance is an important strategy adopted in breeding programs. The evaluation of lines based on their response to hybrid combinations is one of the most important and costly stages of hybrid programs. Topcrosses stand out among the methods developed to facilitate this evaluation process. The use of testers to evaluate the potential of new lines is a routine practice in maize breeding programs. Thus, superior hybrids can be generated based on the identification of crossbreeding lines in order to maximize heterosis.

Heterotic intragroup hybrid combinations of the dentate type were efficient, since they allowed identifying topcross hybrids with good morphoagronomic performance and nutritional value. Thus, they can be indicated for silage production in the Northern/Northwestern regions of Rio de Janeiro State.

Table 5. Correlation and coefficients of canonical pairs estimated between bromatological and morphoagronomic traits in hybrid corn for silage production. Campos dos Goytacazes and Itaocara, Rio de Janeiro State, growing seasons 2013/2014.

Traits		Canonical pairs				
		1st	2nd	3rd	4th	5th
Bromatological	Gross protein (kg·ha^{-1})	0.9699	0.0586	–0.0034	0.2143	–0.0991
	Fiber in neutral detergent (kg·ha^{-1})	0.9807	0.1385	0.1109	–0.0687	0.0426
	Lignin (kg·ha^{-1})	0.9580	–0.2516	–0.0333	–0.1291	0.0326
	Gross fat (kg·ha^{-1})	0.8708	–0.2330	0.3548	0.2403	–0.0601
	Mineral matter (kg·ha^{-1})	0.9471	0.0874	0.0570	–0.0129	–0.3030
Morphoagronomic	Number of days for flowering	0.1397	0.6201	0.3221	0.5759	–0.3259
	Mean plant height (m)	0.5824	–0.1592	–0.1405	–0.1919	0.2696
	Mean insertion height of the first spike (m)	0.4926	–0.4246	–0.0054	–0.4471	–0.1704
	Mean stem diameter	0.1543	0.3894	0.7440	0.3775	–0.0288
	Spike yield with straw at silage stage (kg·ha^{-1})	0.8926	–0.1769	0.2013	0.0203	0.3123
	Spike yield without straw at silage stage (kg·ha^{-1})	0.7243	–0.5365	0.1121	0.0722	0.3889
	Green mass yield (kg·ha^{-1})	0.9948	0.0070	0.0373	0.0261	0.0896
Canaonical correlation (r)		0.98**	0.87^{ns}	0.53^{ns}	0.32^{ns}	0.23^{ns}
Degree of freedom (GL)		35	24	15	8	3
χ^2		118.26	43.46	11.49	3.74	1.22

Significant at ($p < 0.01$) and ($p < 0.05$) probability level in the chi-square test; ^{ns}non-significant at ($p < 0.05$) probability in the chi-square test (χ^2)

Table 6. Average test between traits in hybrid corn for silage production. Campos dos Goytacazes and Itaocara, Rio de Janeiro State, growing seasons 2013/2014.

Hybrids	Traits average morphoagronomic								
	FF	MPH	MIHFS	MSD	SYWSS	SYNSS	GY	GGM	GMY
UENF-2194	67 a	2.08 abcdefg	1.23 cdefgh	22.72 abcde	11798 a	8356 ab	5812.4 ab	16.70 e	34782 abcd
UENF-2195	63.62 bcdef	1.96 cdefghi	1.20 cdefgh	22.24 abcde	11071 a	8518.9 ab	6497.1 ab	21.00 abcde	31029 abcd
UENF-2199	64 bcdef	1.93 defghi	1.15 fgh	23.51 abcde	12972 a	8991.4 ab	6515.6 ab	18.60 bcde	35300 abcd
UENF-2205	65.875 ab	2.01 bcdefg	1.12 gh	24.49 ab	13307 a	9155.6 ab	6932.4 ab	18.62 bcde	37021 abc

...continue

Table 6. Continuation...

Hybrids	Traits average morphoagronomic								
	FF	MPH	MIHFS	MSD	SYWSS	SYNSS	GY	GGM	GMY
UENF-2198	60.75 gh	2.18 abcd	1.35 cdef	21.49 bcde	11293 a	9267.6 ab	6468.5 ab	23.08 a	28315 abcd
UENF-2203	61.5 efgh	2.05 abcdefg	1.33 cdefg	21.09 cde	11049 a	8446.3 ab	5990.8 ab	22.03 abc	27225 abcd
UENF-2192	65.5 abc	1.80 ghi	1.05 h	23.34 abcde	10072 a	7744 ab	5638.1 ab	22.05 abc	25634 bcd
UENF-2206	63.75 bcdef	1.94 defghi	1.17 efgh	23.21 abcde	11885 a	8906.9 ab	6653 ab	20.50 abcde	32416 abcd
UENF-2207	65.5 abc	1.88 efghi	1.15 fgh	24.89 a	12646a	9125.5 ab	6852.3 ab	21.05 abcd	32812 abcd
UENF-2208	65.5 abc	2.33 a	1.58 a	21.80 abcde	12906 a	9219.1 ab	6999.5 ab	18.19 de	38041 ab
UENF-2209	64.5 abcd	2.28 ab	1.45 ab	23.26 abcde	13598 a	10028.6 a	6944.3 ab	17.63 de	39590 a
UENF-2210	64.5 abcd	2.23 abc	1.39 abcd	22.20 abcde	13144 a	9975.3 a	7313.6 a	21.07 abcd	34547 abcd
UENF- 2200	61.37 fgh	2.16 abcde	1.38 abcde	21.51 bcde	10884 a	8018 ab	5557.8 ab	18 cde	30790 abcd
UENF-2202	60.62 gh	2.13 abcdef	1.4 abc	20.78 de	12505 a	9991.4 a	7494.6 a	22.95 a	32936 abcd
UENF-2201	61.37 fgh	2.14 abcdef	1.37 abcde	20.98 cde	11897 a	9083.3 ab	6298 ab	19.39 abcde	32508 abcd
UENF-2204	60.25 h	2.10 abcdef	1.34 bcdef	20.49 e	12436 a	9573 ab	6887.3 ab	20.54 abcde	33506 abcd
UENF-2193	64.75 abcd	1.88 efghi	1.07 h	22.86 abcde	9109 a	6344.4 b	4489.9 b	17.98 cde	24583 cd
UENF-2191	64.25 abcde	1.95 cdefghi	1.18 defgh	23.57 abcde	11139 a	8732.5 ab	6612.1 ab	21.48 abcd	30503 abcd
Piranão 13	64.75 abcd	2.00 bcdefg	1.21 cdefgh	24.26 abc	13147 a	9405.9 ab	6501.8 ab	19.33 abcde	34078 abcd
AG 1051	62.5 defgh	1.99 cdefgh	1.25 bcdefgh	21.27 bcde	11197 a	8692 ab	6473.8 ab	22.87 ab	27951 abcd
UENF-2197	63.25 bcdefg	1.86 fghi	1.33 bcdefg	23.91 abcd	12290 a	8779.8 ab	6204 ab	18.48 cde	33665 abcd
UENF-2196	64.5 abcd	1.72 hi	1.20 cdefgh	22.96 abcde	11250 a	7993.6 ab	5668.6 ab	18.95 abcde	30009 abcd
Br 106	62.75 cdefgh	1.93 defghi	1.15 fgh	20.55 e	11252 a	8238.8 ab	5442.1 ab	16.71 e	32096 abcd
UENF 506-11	65.5 abc	1.70 i	1.20 cdefgh	22.49 abcde	9350 a	6927.6 ab	4926.3 ab	21.39 abcd	23263 d

Hybrids	Traits average bromatological					
	DM	GP	FND	LIG	GF	MM
UENF-2194	13279 abcd	969.4 abc	7242.3 ab	387.75 ab	205.25 ab	519.63 abcd
UENF-2195	12199 abcd	850.8 abc	5987.4 ab	379.5 ab	205.88 ab	518.5 abcd
UENF-2199	13462 abcd	940.1 abc	7102.4 ab	406.25 ab	191 ab	586.88 abcd
UENF-2205	14534 abc	1028.8 ab	7203.8 ab	385.25 ab	232.38 ab	602.88 abc
UENF-2198	10745 abcd	788.1 abc	5544.3 ab	330 ab	193.25 ab	432.25 bcd
UENF-2203	10136 bcd	704.8 bc	5143.9 ab	299.13 ab	167.38 ab	396.75 dc
UENF-2192	10374 abcd	697.9 bc	5419.5 ab	304.13 ab	161.38 ab	434.5 bcd

...continue

Table 6. Continuation...

Hybrids	Traits average bromatological					
	DM	GP	FND	LIG	GF	MM
UENF-2206	11973 abcd	789 abc	6335.4 ab	352 ab	187.63 ab	488.75 abcd
UENF-2207	13237 aabcd	929.5 abc	6737.9 ab	362.88 ab	228.25 ab	551.5 abcd
UENF-2208	15792 a	1111.9 a	7950.9 a	448.5 ab	248.63 a	730.25 a
UENF-2209	15404 ab	1095.4 a	7982.1 a	461.25 a	223.13 ab	678.13 ab
UENF-2210	13207 abcd	879.8 abc	6855.1 ab	430.5 ab	208.88 ab	513.88 abcd
UENF- 2200	11612 abcd	793.4 abc	6261 ab	362.38 ab	169 ab	490.63 abcd
UENF-2202	11936 abcd	823.8 abc	5977.4 ab	400.38 ab	200.38 ab	473.5 bcd
UENF-2201	13375 abcd	866.6 abc	6942.9 ab	400.13 ab	216 ab	552.38 abcd
UENF-2204	13245 abcd	917.4 abc	6885.8 ab	414.75 ab	212.88 ab	508.5 abcd
UENF-2193	9635 dc	647.3 c	5179.4 ab	260.63 b	140.88 b	359.38 cd
UENF-2191	11752 abcd	860.6 abc	5894.8 ab	360.75 ab	202.88 ab	476.75 bcd
Piranão 13	12933 abcd	872.8 abc	6935.1 ab	401.5 ab	202.38 ab	546 abcd
AG 1051	10727 abcd	791.4 abc	5467.9 ab	331.75 ab	173.5 ab	445.88 bcd
UENF-2197	13628 abcd	929.9 abc	7060 ab	429 ab	228.63 ab	567.5 abcd
UENF-2196	11738 abcd	831.5 abc	6051 ab	355.63 ab	192.25 ab	469.75 bcd
Br 106	12547 abcd	918.6 abc	6406.4 ab	381.38 ab	182.5 ab	565 bcd
UENF 506-11	8787 d	606.3 c	4539.3 b	257.25 b	143 b	347.13 d

FF = number of days for flowering; MPH = mean plant height (m); MIHFS = mean insertion height of the first spike (m); MSD = mean stem diameter (m); SYWSS = spike yield with straw at silage stage (kg·ha^{-1}); SYNSS = spike yield without straw at silage stage (kg·ha^{-1}); GY = grain yield at silage point (kg·ha^{-1}); GGM = proportion of grains in the green mass (kg·ha^{-1}); GMY = green mass yield (kg·ha^{-1}); DM = dry matter content (kg·ha^{-1}); GP = gross protein (kg·ha^{-1}); FND = fiber in neutral detergent (kg.ha^{-1}); LIG = Lignin (kg·ha^{-1}); GF = gross fat (kg·ha^{-1}); and MM = mineral matter (kg·ha^{-1}). Average followed by the same letter in the same column did not differ statistically from each other by the Tukey test $p \leq 0.05$.

CONCLUSION

The results indicate that the topcross hybrids under study presented wide genetic variability.

There is also evidence that green mass yield can be adopted in indirect selection to improve bromatological quality in silage corn.

Topcross hybrids UENF-2208 and UENF-2209 presented high potential for silage yield in the North and Northwest Regions.

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