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Genetic improvement of silage maize: predicting genetic gain using selection indexes and best linear unbiased prediction[1]

Melhoramento de milho para silagem: predição de ganhos via índices de seleção e via BLUP

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ABSTRACT - The objective of this study was to evaluate four selection indexes and best linear unbiased prediction (BLUP) for predicting genetic gain in maize hybrids used for silage. The genetic gain was compared between four selection indexes and BLUP. Nineteen topcross hybrids and five controls were evaluated using a completely randomized block design with four replicates in two areas located in Campos dos Goytacazes and Itaocara, Rio de Janeiro, Brazil, in the growing season 2013-2014. Plant height, first ear height, average stem diameter, grain yield at the silage stage, and green mass yield were evaluated. The genetic gain was predicted using the selection indexes proposed by Pesek and Baker, Smith and Hazel, Mulamba and Mock, Willians, and BLUP. The index of Mulamba and Mock provided higher gain estimates for selecting hybrids. BLUP was efficient and selected hybrids with higher performance than hybrids obtained using the four selection indexes. Hybrids UENF-2205, UENF-2208, UENF-2209, and UENF-2210 presented better performance, indicating the high potential of these dent hybrids for silage production in the north and northwest regions of Rio de Janeiro.

Key words: Topcrosses. Tester. Hybrids. Yield.

RESUMO - O objetivo deste trabalho foi avaliar quatro índices de seleção e o método BLUP na predição de ganhos genéticos em híbridos de milho para silagem. Foram comparados quatro índices de seleção e o método BLUP na predição de ganhos genéticos. Foram avaliados 19 híbridos topcrosses, e cinco testemunhas em delineamento experimental de blocos casualizados com quatro repetições em dois ambientes, nos municípios de Campos dos Goytacazes e Itaocara - RJ, no ano agrícola 2013/2014. Avaliaram-se as características altura de plantas, altura de inserção da primeira espiga, diâmetro do colmo, produtividade de grãos no ponto de silagem e produtividade de massa verde. Para predição de ganhos foram empregados os índices de seleção de Pesek & Baker, Smith & Hazel, Mulamba & Mock e Willians, além do método BLUP. Dentre os índices de seleção avaliados, o de Mulamba & Mock proporcionou maiores magnitudes na estimativa de ganhos para a seleção dos híbridos. O método BLUP mostrou-se eficiente, selecionando híbridos com desempenho elevado e superiores aos obtidos pelos índices de seleção testados. Os híbridos UENF-2205, UENF-2208, UENF-2209 e UENF-2210, foram os que apresentaram melhor desempenho indicando elevado potencial dos híbridos dentado para produção de silagem na região Norte e Noroeste Fluminense.

Palavras-chave: Topcrosses. Testador. Híbridos. Produtividade.

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INTRODUCTION

Maize is the most important crop for silage production in Brazil because of its favorable agronomic and bromatological characteristics. In addition, the use of maize for silage increases farm productivity by increasing milk production and animal weight gain (DEMINICIS *et al*., 2009).

In this context, silage maize continues to be one of the best supplementation options in the dry season because of the high dry matter production capacity per unit area, high green mass yield per hectare, good silage quality, high fermentability during storage, and good acceptance by the animals (RESTLE *et al*., 2006).

The best maize hybrids intended for grain production are usually recommended for silage production because genetic improvement programs in Brazil give greater emphasis to developing hybrids for grain production (GOMES *et al*., 2004).

The lack of data on the agronomic, productive, and nutritional characteristics has become an obstacle to choosing maize hybrids for silage production. Therefore, the agronomic characterization of genetic material is essential for obtaining high-quality silage (ROSA *et al*., 2004).

Maize breeding programs in Brazil have used the dent and flint heterotic groups. Most hybrids originate from the cross between heterotic groups (BORÉM; MIRANDA, 2005). Recent evidence indicates that rumen digestibility of cornstarch is variable because of genetic differences between hybrids. Phillippeau, Le Deschault de Moredon and Michalet-Doreau (1999) have shown that there are differences in kernel vitreousness between the flint and dent maize varieties.

Genetic selection involves choosing phenotypes with improved agronomic characteristics. Selection indexes are useful tools in plant breeding by allowing the efficient selection of superior genotypes. The most used indexes are those proposed by Smith (1936) and Hazel (1943), Willians (1962), Pesek and Baker (1969), Mulamba and Mock (1978) (CRUZ; REGAZZI; CARNEIRO, 2004).

Cruz, Regazzi and Carneiro (2004) have shown that selection indexes use multivariate techniques that combine data on the agronomic and genetic characteristics of the evaluated population. These indexes allow creating a numerical value, which functions as an additional theoretical characteristic, by combining specific traits selected by breeders and for which simultaneous selection is desired.

In the initial or final phase of a breeding program, inferences about genotypes under selection should be based on true genotypic values, i.e., genotypic and not phenotypic data (BORGES *et al*., 2010).

In this respect, animal and plant breeding programs have used the restricted maximum likelihood (REML) method and best linear unbiased prediction (BLUP) to predict genotypic values and select better genotypes accurately (RODRIGUES *et al*., 2013).

Therefore, the objective of this study was to evaluate four selection indexes and BLUP for predicting genetic gain in maize hybrids for silage.

MATERIALS AND METHODS

Topcross hybrids were obtained from an area belonging to Barra do Pomba Island Experimental Station located in Itaocara in the northwest region of Rio de Janeiro, Brazil.

The evaluated genotypes were obtained from the maize collection of the Darcy Ribeiro State University of Northern Rio de Janeiro (Universidade Estadual do Norte Fluminense Darcy Ribeiro). Nineteen genotypes were selected from the dent heterotic group. Each genotype was crossed with the tester Piranão 12. This broad genetic tester belonged to the same dent heterotic group and was used to generate topcross dent hybrids (Table 1).

Each genotype was grown in 10.0-m rows, with an inter-row spacing of 1.0 m and five rows per linear meter, totaling 50 plants per row spaced 0.20 m apart.

During flowering, the females were detasseled before the ears released the stigma-styles to avoid contamination. Therefore, the stigma-styles received pollen only from the tester. Harvesting was performed 120 days after sowing (DAS).

The evaluation of topcross hybrids was performed simultaneously in the municipalities of Campos dos Goytacazes and Itaocara in the growing season of 2013-2014.

The experimental design was completely randomized with four replicates, each with 24 treatments, including 19 topcross hybrids and five controls (BR106, AG 1051, UENF 506-11, UENF-2196, and UENF-2197).

Each plot consisted of 25 plants with a height of 5.0 m, inter-row spacing of 1.0 m, and inter-plant spacing of 0.20 m. The seeding density was three seeds per pit. Thinning was performed at 21 DAS, leaving only one plant per pit.

Sowing was performed using a conventional planting system. Fertilization consisted of applying 400 kg ha^{-1} of NPK formulation 8-28-16. After that,

Table 1 - Description of 19 topcross hybrids, five controls, and one genetic tester according to grain type, genetic cross, and origin. Campos dos Goytacazes and Itaocara, Rio de Janeiro state, Brazil, in the growing season of 2013-2014

Identification	Hybrids	Grain type	Genetic cross	Origin
1	UENF-2194*	Dent	S7	UENF
2	UENF-2195*	Dent	S7	UENF
3	UENF-2199*	Dent	S6	UENF
4	UENF-2205*	Dent	S0	UENF
5	UENF-2198*	Dent	S7	UENF
6	UENF-2203*	Dent	S0	UENF
7	UENF-2192*	Dent	S7	UENF
8	UENF-2206*	Dent	S0	UENF
9	UENF-2207*	Dent	S0	UENF
10	UENF-2208*	Dent	S4	UENF
11	UENF-2209*	Dent	S0	UENF
12	UENF-2210*	Dent	S0	UENF
13	UENF- 2200*	Dent	S0	UENF
14	UENF-2202*	Dent	S0	UENF
15	UENF-2201*	Dent	S0	UENF
16	UENF-2204*	Dent	S0	UENF
17	UENF-2193*	Dent	S7	UENF
18	UENF-2191*	Dent	S7	UENF
19	Piranão 13*	Dent	S0	UENF
20	‘AG 1051**’	Dent	DH	Commercial
21	‘UENF-2197**’	Flint	S5	UENF
22	‘UENF-2196**’	Flint	S5	UENF
23	‘Br 106**’	Semi-dent	-	Commercial
24	‘UENF 506-11**’	Semi-dent	IPH	UENF
	Piranão 12***	Dent	S0	UENF

*Topcross hybrids; **Controls; ***Tester; DH, double hybrid; IPH, interpopulation hybrid. Genotypes 1 to 19, 21, and 22 were crossed with Piranão 12

two maintenance fertilizations were performed: one at 30 DAS using 300 kg ha^{-1} of NPK formulation 20-00-20 and the other at 45 DAS using 200 kg ha^{-1} of urea. Weed control was carried out by applying the herbicide Roundup before sowing and manual weeding. Irrigation was used when necessary.

The evaluated characteristics were average plant height (PH), measured in meters from the soil level to the tassel peduncle; average first ear height (FEH), measured in meters from the soil level to the base of the upper ear on the stalk; average stem diameter (ASD), measured in meters at the first internode above the root collar; grain yield at the silage stage (GY) in kg ha^{-1}, and green mass yield (GMY) in kg ha^{-1}.

PH, FEH, and ASD were randomly measured in six plots at 80 DAS. GY was obtained by weighing the grains threshed at the silage stage, and GMY was obtained by weighing the plants (leaves, stalks, cobs, ear husk, and kernel) of each plot at the time of harvest.

The GY and GMY were measured in 15 plants per plot (corresponding to 3.0 m of each row in each plot) at 90 DAS. Harvest was done by cutting the plants at 20 cm from the soil when three of the four replications were at the dough stage.

Combined analysis of variance was performed considering the following statistical model:

$$Y_{ijk} = \mu + G_i + B/A_{jk} + A_j + AF_{ij} + e_{ijk} \quad (1)$$

where: Y_{ijk} is the observation in the kth block evaluated in the ith genotype and jth environment; μ is the general test constant; G_i is the random effect of genotype i, B/A_{jk} is the effect of block k in environment j; A_j is the fixed effect of environment j; AF_{ij} is the effect of the interaction between genotype i and environment j; and e_{ijk} is the random error associated with the observation $Y_{ijk,}$ $e_{ijk} \sim NID(0,\sigma^2)$.

The selection gain estimated using the selection indexes was based on the average values of the joint analysis of the two environments.

The chosen selection indexes were those proposed by Smith (1936) and Hazel (1943), Pesek and Baker (1969), Willians (1962), Mulamba and Mock (1978). Selection intensity was defined at 25%. The economic weights assigned arbitrarily were 1, 1, 50, 100, and 100 for each analyzed characteristic (PH, FEH, ASD, GY, and GMY), respectively. Statistical analyses were performed using software Genes (CRUZ, 2013).

The genotypic evaluations were also performed using software Selegen-BLUP. The statistical model used to perform the analyses was progenies of half-siblings in complete randomized blocks (RESENDE, 2002).

$$Y = Xr + Za + Wi + e \qquad (2)$$

where: *y* is the data vector; *r* is the vector of the fixed repetition effects summed to the general mean; *a* is the vector of the individual additive genetic effects considered random; *i* is the vector of the effects of the interaction genotype × environment (random), and *e* is the vector of errors or residuals (random). The incidence matrices for these effects are represented by uppercase letters. The vector *r* represents all replicates of all plots. In this study, vector *r* represents the effects of plots and replicates within the plots.

The mean value of the improved population was obtained by summing the overall mean value and genetic gain. The relative performance of each family was obtained by determining the relation between the mean values of the improved population of each family and the mean values of the family with the highest genetic value.

The coincidence index between the families was estimated by determining the relation between the double of the number of coincident families and the sum of the total number of progenies selected from selection indexes A and B (PEDROZO *et al*., 2009). The coefficients of coincidence (CC) were calculated for GY and GMY.

RESULTS AND DISCUSSION

There were significant differences between the genotypes ($p<0.01$) for all evaluated variables, evidencing the existence of variability, which allows effectively selecting suitable genotypes (Table 2). The effects of the genotype × environment interaction were significant for most of the studied variables, except for FEH and GY. The significant interaction indicates that the response of the genotypes was not coincident in the different environments.

Similarly, Oliveira *et al*. (2007) found an interaction between the hybrids and the evaluation sites, evidencing the need for the regionalized recommendation of hybrids.

The mean GY at the silage stage and the GMY were 6,298.90 and 31,774.84 kg ha^{-1}, respectively

Table 2 - Summary of the combined analysis of variance of five characteristics evaluated in maize hybrids for silage. Campos dos Goytacazes and Itaocara, Rio de Janeiro, Brazil, growing season of 2013-2014

Variation Sources	DF	Mean Squares				
		PH	FEH	ASD	GY	GMY
Block/environment	6	0.1505	0.1052	7.2901	2326959.02	30492784.42
Genotype (G)	23	0.2146**	0.1351**	13.3324**	4328791.36**	134884400.48**
Environment (A)	1	0.3048^{ns}	0.0690^{ns}	730.4700**	51268834.50^{ns}	746457228.0^{ns}
GXA	23	0.0774**	0.0141^{ns}	4.7725*	1829489.16^{ns}	70140897.07*
Error	138	0.0125	0.0109	2.8877	2121672.55	42154841.64
Mean		2.01	1.26	22.49	6,298.90	31,774.84
h^2		94.17	91.86	78.34	50.98	68.74
ECV (%)		5.54	8.29	7.55	23.12	20.43
VI		1.42	1.18	0.67	0.36	0.52
GCV (%)		7.88	9.85	5.07	8.33	10.71

PH, plant height (m); FEH, first ear height (m); ASD, average stem diameter (mm); GY, grain yield at the silage stage (kg ha^{-1}); and GMY, green mass yield (kg ha^{-1}); ns: Not significant using the F-test; ** Significant ($p<0.01$) using the F-test; * Significant ($p<0.05$) using the F-test; h^2, average heritability of genotypes; ECV, experimental coefficient of variation; GCV: genetic coefficient of variation; VI: variation index

(Table 2). Paziani *et al*. (2009) evaluated agronomic characteristics in maize hybrids for silage and found that the mean GY at the silage stage and GMY were 6,916.00 and 50,470.00 kg ha^{-1}, respectively. Mendes *et al*. (2008) reported that the mean GY and GMY were 6,140.00 and 31,370.00 kg ha^{-1}, respectively. Similar results were obtained in the present study.

Moreover, all evaluated characteristics achieved heritability higher than 50.98% on the basis of the average values of the families. The heritability rate for the most relevant characteristics, GY and GMY, was 50.98% and 68.74%, respectively (Table 2). Faria *et al.* (2008) evaluated the efficiency of reciprocal recurrent selection in popcorn hybrids and found that the heritability rate for productivity and expansion capacity was 50.37% and 60.48%, respectively.

Cruz, Regazzi and Carneiro (2004) analyzed heritability rates and reported that it was possible to foresee the possibility of success in genetic selection for producing superior genotypes. Therefore, selection can be successfully performed for all characteristics of interest using high heritability rates.

According to the classification of Scapim, Carvalho and Cruz (1995), most of the characteristics evaluated in the present study had low to high ECV. The coefficients of variation ranged from 5.54% for PH to 23.12% for GY (Table 2). These values evidence acceptable experimental precision for all evaluated characteristics, contributing to the increase in the reliability of the estimates and the obtained results.

It is essential to know the genetic coefficient of variation (GCV) to experimental coefficient of variation (ECV) ratio of the evaluated characteristics for genetic improvement. PH, CH, ASD, and GMY presented a variation index (VI) higher than 0.5, whereas GY presented an IV of 0.36 (Table 2). VI values higher than 0.5 indicate satisfactory genetic gain.

The GCV expresses the existing level of genetic variation and allows breeders to assess the relative magnitude of the changes potentially obtained during genetic selection.

The analyzed characteristics presented relatively high GCV values, especially GMY, whose GCV value was 10.71% (Table 2).

The evaluation of the economic weights assigned arbitrarily indicated that PH and FEH had negative gains of –3.6 and –8.2%, respectively, using the index of Pesek and Baker (Table 3).

The present study attempted to improve all the evaluated variables simultaneously. Negative gains are undesirable in silage production; therefore, the index of Pesek and Baker is not recommended for selection under the conditions used in this study.

Deminicis *et al.* (2009) have shown that the percentage of biomass and grains is fundamental for silage quality, which, in turn, directly affects the efficiency of animal nutrition. The quality of the grains and fibrous fraction (stalks, leaves, cobs, and ear husks) determines the nutritional quality of the silage (DEMARQUILLY, 1994).

The index of Smith and Hazel provided higher gains for GY and GMY, corresponding to 3.66% and 9.88%, respectively (Table 3). Differences between genetic gains predicted for GY were also found by Tardin *et al.* (2007) using this index in the eighth and ninth cycles of reciprocal recurrent selection in a maize population. Berilli *et al*. (2013) used this index and obtained a gain of 14.26% for GY in a recurrent selection program in common maize.

Genetic gain for GY and GMY was relatively high (5.08% and 9.61%, respectively) using the index of Mulamba and Mock (Table 3). The positive gain for GY and GMY using the Willians index was 3.68% and 10.32%, respectively. These gains were considered satisfactory in the present study.

Table 3 - Estimation of percentage gains based on the selection differential of five traits in maize genotypes for silage. Campos dos Goytacazes and Itaocara, Rio de Janeiro, Brazil, growing season of 2013–2014

Characteristics	Selection Indexes				BLUP
	Pesek and Baker	Smith and Hazel	Mulamba and Mock	Willians	
PH	-3.6	6.72	4.59	6.12	18.08
FEH	-8.2	5.00	3.46	4.34	30.93
ASD	5.10	2.18	3.01	1.75	10.95
GY	1.88	3.66	5.08	3.68	12.53
GMY	0.65	9.88	9.61	10.32	16.16

PH, plant height (m); FEH, first ear height (m); ASD, average stem diameter (mm); GY, grain yield at the silage stage (kg ha^{-1}); and GMY, green mass yield (kg ha^{-1})

Crevelari *et al*. (2017) found that the index of Mulamba and Mock resulted in higher predicted gains for GY at the silage stage and GMY with values of 6.13% and 4.46%, respectively, using economic weights assigned arbitrarily. Rangel *et al*. (2011) reported that the earnings estimated with the selection index proposed by Mulamba and Mock resulted in appropriate proportional gains for GY using arbitrary economic weights in selecting superior progenies of popcorn.

BLUP provided higher genetic gain estimates. The gain for PH, FEH, ASD, GY, and GMY was comparatively higher, corresponding to 18.08%, 30.93%, 10.95%, 12.53%, and 16.16%, respectively (Table 3).

The index proposed by Mulamba and Mock provided the highest selection gain for GY and GMY and, therefore, was the most adequate for selecting hybrids in the present study.

Other studies found differences between the predicted genetic gain for expansion and production capacity of popcorn using the index of Mulamba and Mock (ARNHOLD; SILVA, 2009; CANDIDO *et al*., 2011; FREITAS JÚNIOR *et al*., 2009; SANTOS *et al*., 2007).

PH, FEH, ASD, GY, and GMY were simultaneously improved using BLUP. Gains for GY and GMY were relatively high, corresponding to 12.53% and 16.16%, respectively, and BLUP was better than all evaluated selection indexes (Table 3). The comparison of BLUP with the index of Mulamba and Mock indicated that the former was better than the latter, with a gain of 7.45% for GY and 6.55% for GMY, respectively (Table 3).

This difference is because BLUP uses the predicted genotypic effects as a solution vector; therefore, the selection gain is assigned to each family, which corrects the values for the environmental effects, predicts the genotypic values precisely and unbiased, and allows maximizing gain using selection (RODRIGUES *et al*., 2013). In contrast, the index of Mulamba and Mock classifies the genotypic materials for each trait in an order favorable to genetic improvement. After the classification, the orders of each genetic material for each trait are summed, resulting in an additional measurement considered a selection index (CRUZ; REGAZZI; CARNEIRO, 2004). The obtained results indicated that BLUP was ideal for selecting hybrids.

Entringer *et al*. (2016) found that REML/BLUP provided the highest estimates of genetic gain when compared to the index of Mulamba and Mock and was efficient in selecting half-sibling families in super sweet corn.

The six hybrids selected using BLUP and the selection indexes had a high CC. The CC was similar and relatively higher between the indexes of Smith and Hazel and Willians and between the indexes of Mulamba and Mock and Willians, corresponding to 83% for GY and GMY. Of the six selected hybrids, five presented the two characteristics evaluated (Table 4).

The comparison of BLUP with the selection indexes indicated that the highest CC was obtained using BLUP together with the Willians index, corresponding to 83% for GMY. In contrast, the CC for GY was 66% using BLUP together with the indexes of Smith and Hazel, Mulamba and Mock, and Willians (Table 4).

Pedrozo *et al*. (2009) observed that the CC among the indexes varied according to the genetic composition of the populations when using the REML/BLUP method in a sugarcane crop. Freitas *et al*. (2013) reported that the CC for GY was 97% using the Willians index together with the REML/BLUP method in popcorn.

In the selection process, genotypic values should be preferred by breeders because these values are predicted, and selection should be based on genotypic means. Therefore, it was decided to rank the most promising hybrids on the basis of the predicted genetic values obtained using BLUP (Table 5).

Table 4 - Percentage estimation of the coefficients of coincidence of six maize hybrids for silage selected using selection indexes and best linear unbiased prediction for the variables grain yield at the silage stage (GY) (values above the diagonal) and green mass yield (GMY) (values below the diagonal). Campos dos Goytacazes and Itaocara, Rio de Janeiro, Brazil, in the growing season of 2013-2014

Pesek and Baker	Pesek and Baker	Smith and Hazel	Mulamba and Mock	Willians	BLUP
	-	33	33	16	16
Smith and Hazel	33	-	66	83	66
Mulamba and Mock	33	66	-	83	66
Willians	16	83	83	-	66
BLUP	16	66	66	83	-

Table 5 - Ranking and estimation of six maize hybrids for silage, genetic gain, new estimated means, and relative performance (RD) for grain yield at the silage stage (GY) and green mass yield (GMY). Campos dos Goytacazes and Itaocara, Rio de Janeiro, Brazil, in the growing season of 2013-2014

Grain yield at the silage stage (Kg ha^{-1})				
Ranking	Hybrids	Gain	New Means	RD (%)
1	UENF-2202	1034.94	7840.14	100.00
2	UENF-2210	945.69	7390.89	98.80
3	UENF-2208	812.67	7257.88	97.02
4	UENF-2209	732.54	7177.75	95.95
5	UENF-2205	682.12	7127.33	95.28
6	UENF-2204	641.09	7086.30	94.73
Green mass yield (Kg ha^{-1})				
Ranking	Hybrids	Gain	New Means	RD (%)
1	UENF-2209	6807.27	39207.93	100.00
2	UENF-2208	6073.90	38474.56	98.12
3	UENF-2205	5507.62	37908.29	96.68
4	UENF-2199	4816.93	37217.60	94.92
5	UENF-2194	4304.47	36705.14	93.61
6	UENF-2210	3925.72	36326.39	92,65

From a total of 19 hybrids evaluated, the best six were selected for the variables GY and GMY using BLUP (Table 5).

The predicted genetic gain, the new estimated means, and the relative performance of the six best hybrids for GY and GMY are shown in Table 5. The hybrids UENF-2205, UENF-2208, UENF-2209, and UENF-2210 were the most promising, with significant values, and constituted the four best hybrids for GY and GMY. Furthermore, the relative deviation of the six selected hybrids was higher than 90% for the two analyzed variables, evidencing the selective accuracy BLUP (Table 5).

The predicted genetic gain and the new estimated means were higher than the overall mean for all analyzed variables (Table 5).

UENF-2202 was ranked first for GY. The predicted gain of this hybrid was 1034.94 kg ha^{-1}, with an average of approximately 7480.14 kg ha^{-1} of GY, and hybrid 16 was ranked last, with a gain of 641.09 kg ha^{-1} (Table 5). For GMY, hybrid UENF-2209 exceeded the others, with expected gains of 6807.27 kg ha^{-1} relative to the overall mean. Hybrid UENF-2210 was ranked last, with an estimated gain of 3925.72 kg ha^{-1}.

Therefore, BLUP proved to be more efficient than the selection indexes, allowing selecting hybrids with high relative performance and high predicted genetic gain for the evaluated characteristics.

CONCLUSIONS

1. The index proposed by Mulamba and Mock was better than the others indexes and was efficient in selecting maize hybrids for silage;
2. Best linear unbiased prediction was more efficient in genetic selection than the selection indexes, allowing higher predicted genetic gains;
3. Among the six hybrids selected using BLUP, four were similar for the variables GY and GMY. Hybrids UENF-2205, UENF-2208, UENF-2209, and UENF-2210 had better performance in genetic crosses with Piranão 12;
4. These results indicate the high potential of dent hybrids for silage production in the north and northwest regions of Rio de Janeiro.

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