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Selection of top cross hybrids for green maize yield via REML/Blup method

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Abstract

The purpose of this study was to select top cross hybrids of green maize for yield, derived from partially inbred S₁ lines based on genetic values using the REML/Blup method, and to estimate important genetic parameters for green maize breeding programs. The experiment was conducted in an experimental area located between 17°53′ S and 52°43′ W, 680 m altitude. The evaluation of 75 top cross hybrids was performed in a randomized block design with four replicates. A sample of five plants/ears was used in each plot to evaluate grain mass trait (MASS). For commercial ear yield trait (CEYIELD), evaluations were carried out for the total number of plants per plot. Hybrids were selected via BLUP procedures using the Selegen-REML/Blup program. Based on the Restricted Maximum Likelihood (REML), we estimated the coefficients of genetic and residual variation and components of variance, by which a genetic variability between the top cross hybrids was observed. This shows the possibility of successful selection for the traits under evaluation. The estimated accuracy for the selection of top cross hybrids was 0.81 for commercial ear yield and 0.64 for grain mass, pointing to high and moderate precision levels for CEYIELD and MASS traits, respectively, corroborating the possibility of success in selecting top cross hybrids based on the CEYIELD trait. The predicted genetic gain from the selection was 20.12%, for CEYIELD, and 6.10%, for MASS. Therefore, the REML/Blup statistical tool was efficient in selecting top cross hybrids of green maize, providing significant genetic gains for the traits under evaluation. There was evidence that hybrids 19 and 48 were distinguished from others because of the high genetic effects obtained for the commercial ear yield and grain mass weight.

Keywords: maize breeding; mixed models; genetic values; Zea mays.

Abbreviations: REML/Blup_ Restricted Maximum Likelihood/ Best linear unbiased prediction; CEYIELD_commercial ear yield; MASS_ mean grain mass weight; σ_{g}^2 genotypic variance; σ_{e}^2 environmental variance; σ_{f}^2 phenotypic variance; h_a^2 broad individual sense heritability; h_{mh}^2 progeny mean heritability; A_{cline} progeny selection accuracy; $CV_g(\%)$ genetic coefficient of variation; $CV_e(\%)$ environmental coefficient of variation; CV_r relative coefficient of variation.

Introduction

Cultivated worldwide, maize (*Zea mays*) is a cereal with agricultural and economic characteristics and social impact, being used for human and domestic animal consumption, also providing the raw material for processing food products (Wen et al., 2016; Szareski et al., 2018). Its increasing demands have been a constant challenge for breeders, which requires them to develop ways to achieve a higher yield, together with quality genotypes (Ufaz and Galili, 2008). Breeding is crucial to increase maize yield. Conventional breeding techniques make use of available germplasms, and hybridization and selection strategies are used to develop agronomic ideotypes expected by breeders (Carvalho et al., 2018).

Maize crop for green maize yield is one of the most important agricultural activities in Brazil. It is a product appreciated throughout the country and can be consumed *in natura* or in several ways in cooking. It can also be industrialized and sold as canned green maize (DoVale et al., 2011), thereby increasing the economic value of the final product and motivating farmers to increase their incomes. In maize breeding programs, genetic progress is achieved by means of the search for populations with a higher frequency of heterozygous loci for traits of interest, increasing the likelihood of achieving promising lines (Lima et al., 2000). Researches have evidenced the potential of landraces and open-pollinated varieties as germplasm for maize breeding pointing at cycle (Nardino et al., 2016b), grain yield components (Baretta et al., 2016), bioactive compounds, and micronutrients in maize seeds (Carvalho et al., 2018). Maize breeding programs have constantly researched for cultivars with superior performance for the various traits of interest, in order to meet the demand of producers and consumers. Regarding green maize, commercial ear yield and grain mass weight are important traits to be selected from the cultivars to be used in this niche market. Nevertheless, this is not an easy task to do, given that these traits are highly influenced by environmental conditions. Moreover, it is essential to adopt increasingly powerful statistical tools, which enable the breeder to select genotypes more efficiently, on the basis of genetic values, resulting in progressive gains in selection.

The REML/BLUP method is an efficient statistical tool for data analysis, both balanced and unbalanced. In this methodology, treatment effects are considered as random ones, and the other main effects as fixed (Resende, 2007). Moreover, this technique involves estimating components of variance and prediction of genetic values simultaneously, making it a very accurate tool to be used in plant breeding selection and variety tests (Piepho et al., 2008).

Therefore, information on genetic progress is of utmost importance, since it enables breeding programs to be regularly analyzed to estimate their success. Furthermore, they facilitate the study of new methodologies that enhance their efficiency and lead to future research. As such, the estimate of genetic progress is a significant option for assessing breeding programs (Cruz et al., 2018).

Hence, the goal of the current study is to select top cross hybrids of green maize for yield from partially inbred S_1 lines, based on genetic values by means of the REML/Blup method, and to estimate important genetic parameters for green maize breeding programs.

Results and Discussion

Estimates the genetic parameters

Table 1 shows the genetic parameters for CEYIELD and MASS traits. Results indicated the genetic variability between the evaluated hybrids is embedded, having presented genetic variance of 996,609.75 and 77.91, for CEYIELD and MASS traits, respectively, promising for obtaining genetic gains by selection. Sousa et al. (2017) stated, the estimate of genetic variance (σ_g^2) that displays positive and different values of zero shows variability due to the genotype and, consequently, the possibility of successful selection for the evaluated trait. As such, the top cross hybrids from partially inbred S₁ lines presented significant genetic variability for commercial ear yield in kg per hectare and mean grain mass in grams, pointing out to be promising materials for commercialization of fresh consumption or processing in pamonharias (factory of pamonha, which is a traditional Brazilian food).

The estimates of individual heritability in the broad sense (h_b^2) for CEYIELD and MASS traits were 0.328 and 0.146, respectively. For mean heritability of hybrids (h_{mh}^2) , the estimates were 0.66 for CEYIELD and 0.41, for MASS traits. In general, these estimates are moderate to low, respectively, for the traits given that they are very much influenced by environmental effects. These values can be explained by the complex genetic nature of the trait, resulting from the action of several genes with little effect on the phenotype (Allard, 1971). Arnhold et al. (2009); Nardino et al. (2016a); Faria et al. (2017); Oliveira et al. (2017); and Olivoto et al. (2017), also found moderate to low heritability values for maize yield, which confirmed the results of this study.

For the estimates of selective accuracy (A_{Cline}) , values in the order of 0.81 and 0.64 were observed for CEYIELD and MASS traits, respectively, indicating the possibility of selecting

hybrids on the basis of CEYIELD trait, as it had a higher accuracy value. Resende and Duarte (2007) reported that the selective accuracy can vary from 0 to 1, which can be classified as very high (Acline≥0.90), high (0.70≤ Acline≤0.90), moderate (0.50 \leq Ac_{line}<0.70), and low (Ac_{line}<0.50). In this way, the authors noted high and moderate precision levels for CEYIELD and MASS traits, respectively, corroborating the possibility of success in the selection of top cross hybrids based on CEYIELD trait. High magnitude estimates for selective accuracy were also found by Baretta et al. (2017) for yield trait in maize populations. Another parameter that provides information regarding the genetic contribution to the variation of the trait is the coefficient of genetic variation (CV_g(%)), which in this work, were 18.83 and 6.78%, for CEYIELD and MASS traits, respectively. This denotes genetic variability between the traits under study. Equally important, the relative coefficient of variation (CV_r), is the best breeding strategy for defining each trait, which is expressed as the ratio between CV_g and CV_e . Vencovsky (1987) explained, when this ratio is close to or higher than 1, there is a favorable selection situation for a particular trait. The values of 0.70 and 0.41 for CEYIELD and MASS traits, suggest a more suitable selection situation for CEYIELD trait.

Prediction of genetic effects and genetic gain

Table 2 depicts the prediction of genetic effects, predicted genetic gain, and a new inbred mean of the population for CEYIELD and MASS traits. About 50% of the total hybrids evaluated showed positive genetic effects for both traits, suggesting the possibility of high genetic gains during the selection stages of the breeding program. This is congruent with the high predicted genetic gain for hybrids, the superiority obtained for hybrid 19, highest predicted gain for CEYIELD trait and hybrid 8 for MASS trait, when compared with the commercial hybrid AG 1051 (control), and with the population that was used as a tester. Regarding the classification of top cross hybrids selected for CEYIELD and MASS traits, 24 hybrids (19, 48, 42, 25, 5, 40, 14, 2, 17, 60, 9, 10, 23, 11, 74, 43, 73, 69, 18, 26, 29, 31, 8, and 27) presented positive and superior predicted genetic effects for the two evaluated traits (Figure 1). This made the mean and predicted gains increase as possible (Table 3).

Predicted genetic values (μ + g)

Table 3 displays the mean predicted genetic values (μ + g) of the chosen hybrids for CEYIELD and MASS traits (in accordance with Figure 1). We was noted that the mean of the selected hybrids was superior to the overall mean of the hybrids, with values 5918.58 kg ha⁻¹ and 135.17 g for CEYIELD and MASS traits, respectively, providing predicted genetic gains of around 20.12% and 6.10% for the traits. Thus, the REML/Blup methodology is an important statistical tool, which can help breeders to conduct breeding programs during selection processes. Similar results demonstrating the potential for the REML/Blup technique were seen in studies on beans, by Sousa et al. (2017), Gomes et al. (2018), and Cruz et al. (2018); and maize, by Arnhold et al. (2009), Oliveira et al. (2016), Entringer et al. (2016), and Mendonça et al. (2016), all confirming the results of this study.

Table 1. Genetic parameters for commercial ear yield (CEYIELD) (kg ha⁻¹), mean grain mass weight (MASS) (g) and overall mean of hybrids of 75 top cross hybrids of green maize from partially inbred S_1 lines, commercial hybrid AG 1051, and broad genetic base tester (F_2 of the AG 1051), via REML/Blup mixed model analysis, municipality of Jataí, Goiás State, Brazil, UFG, 2018.

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ESTIMATE	CEYIELD	MASS
σ_{g}^{2}	996609.75	77.91
σ_{e}^{2}	2041313.38	454.83
$\sigma_{\rm f}^2$	3037923.13	532.75
h_a^2	0.328056 +- 0.0923	0.14625 +- 0.0616
h ² _{mh}	0.66	0.41
Acline	0.81	0.64
CV _g (%)	18.83	6.78
CV _e (%)	26.94	16.38
CV _r	0.70	0.41
Mean	5302.96	130.22

 σ_g^2 =genotypic variance; σ_e^2 = environmental variance; σ_f^2 = phenotypic variance; h_a^2 = broad individual sense heritability; h_{mh}^2 = progeny mean heritability; A_{cline} = progeny selection accuracy; $CV_g(\%)$ = genetic coefficient of variation; $CV_e(\%)$ = environmental coefficient of variation; CV_r = relative coefficient of variation; $(CV_r = CV_g/CV_e)$.



Fig 1. Diagram of dispersion of the predicted genetic effects of 75 top cross hybrids of green maize from partially inbred S_1 lines, the commercial hybrid AG 1051, and the broad genetic base tester (F_2 of the AG 1051) for commercial yield (kg ha⁻¹) and mean grain mass, municipality of Jataí, Goiás State, Brazil, UFG, 2018.

Table 2. Prediction of genetic effects, predicted genetic gains, and new inbred mean of population for commercial ear yield trait (CEYIELD), in kg ha⁻¹, and mean grain mass weight trait (MASS), in grams, in 75 topcross hybrids of green maize from partially inbred S_1 lines, commercial hybrid AG 1051, and broad genetic base tester (F_2 of the AG 1051), via REML/Blup mixed model methodology, municipality of Jataí, Goiás State, Brazil, UFG, 2018.

Sequence	Hybrid	CEYIELD			Hybrid	MASS		
		Genetic Effect	Gain	New Mean		Genetic Effect	Gain	New Mean
1	19	2200.92	2200.92	7503.88	8	14.02	14.02	144.24
2	77	1769.48	1985.20	7288.16	42	10.77	12.39	142.61
3	48	1689.13	1886.51	7189.48	61	10.71	11.83	142.05
4	6	1295.56	1738.77	7041.74	25	9.55	11.26	141.48
5	28	1211.96	1633.41	6936.37	48	9.55	10.92	141.14
6	42	1067.03	1539.01	6841.98	10	8.84	10.57	140.79
7	25	902.73	1448.12	6751.08	5	8.63	10.29	140.51
8	5	880.53	1377.17	6680.13	27	8.53	10.07	140.29
9	40	877.77	1321.68	6624.64	43	6.86	9.72	139.93
10	14	813.78	1270.89	6573.85	3	6.56	9.40	139.62
11	2	786.24	1226.83	6529.79	23	6.11	9.10	139.32
12	59	776.94	1189.34	6492.30	11	6.04	8.85	139.07
13	38	738.91	1154.69	6457.66	18	5.42	8.58	138.80
14	24	728.55	1124.25	6427.22	26	5.38	8.35	138.57

continue

15	70	726.50	1097.74	6400.70	55	4.40	8.09	138.31
16	17	690.40	1072.28	6375.24	53	4.04	7.84	138.06
17	34	671.71	1048.71	6351.68	9	3.55	7.59	137.80
18	60	619.09	1024.85	6327.81	58	3.53	7.36	137.58
19	9	523.36	998.45	6301.42	51	3.45	7.15	137.37
20	10	484.06	972.73	6275.70	32	3.37	6.97	137.18
21	23	479.75	949.26	6252.22	19	3.35	6.79	137.01
22	66	400 31	924 31	6227.27	40	3 23	6.63	136.85
22	15	374 72	900 / 1	6203 37	56	3.02	6.05	136.69
23	11	357 37	877 78	6180 75	12	2 59	6 31	136 53
24	74	220 52	856.25	6150.75	65	2.33	6.15	126.27
25	/4	335.JZ	030.23	6120.10	60	2.27	6.00	130.37
20	45	222.01	030.25	6139.19	26	2.17	0.00 F 9F	130.22
27	75	333.37	817.60	6120.57	30	2.15	5.85	130.07
28	73	320.81	800.08	6103.04	14	1.80	5.71	135.93
29	35	316.27	783.39	6086.36	7	1.70	5.57	135.79
30	69	297.95	/6/.21	6070.17	/3	1.42	5.44	135.65
31	21	263.15	750.95	6053.91	22	1.21	5.30	135.52
32	18	219.40	734.34	6037.30	29	1.15	5.17	135.39
33	26	213.72	718.56	6021.53	17	1.09	5.05	135.26
34	29	189.33	703.00	6005.96	2	0.50	4.91	135.13
35	31	171.49	687.81	5990.78	54	0.48	4.79	135.00
36	8	171.31	673.47	5976.43	39	0.38	4.66	134.88
37	27	137.45	658.98	5961.94	69	0.34	4.55	134.76
38	63	94.29	644.12	5947.08	31	0.32	4.44	134.65
39	57	-46.26	626.42	5929.38	74	0.16	4.33	134.54
40	4	-91.44	608.47	5911.43	68	-0.03	4.22	134.43
41	12	-107.21	591.01	5893.98	37	-0.19	4.11	134.33
42	3	-121.28	574.05	5877.02	71	-0.25	4.01	134.22
43	22	-140.72	557.43	5860.40	64	-0.35	3.90	134.12
44	68	-149.42	541.37	5844.33	6	-0.50	3.80	134.02
45	55	-180.30	525.33	5828.29	50	-0.56	3.71	133.93
46	61	-185.43	509.88	5812.84	70	-0.84	3.61	133.83
47	51	-197.18	494.84	5797.80	38	-0.88	3.51	133.73
48	65	-256.60	479 18	5782 14	33	-0.94	3 42	133.64
49	7	-261 52	464.06	5767.03	21	-1 13	3 33	133 55
50	20	-299 45	448 79	5751 76	28	-1 78	3 22	133.44
50	71	-403.85	432.08	5735.04	75	-2.39	3.22	133.44
52	11	-405.05	452.00	5718 93	11	-2.00	3 01	133.33
52	30	-405.55	410.37	5703 /3	16	_2.45	2 90	133.23
55	53	420.00	285.00	5703.45	15	2.71	2.50	122.01
54	33	-429.90	270.19	5088.00	13	-2.65	2.79	133.01
55	40	-433.27	370.18	5073.14	13	-3.12	2.09	132.90
50	30	-445.90	241 20	5056.00	54 20	-5.42	2.50	132.60
57	30	-450.82	341.38	5044.35	30	-3.50	2.47	132.09
58	32	-407.37	327.44	5030.40	02	-3.03	2.30	132.58
59	62	-513.00	313.18	5010.15	1	-3.93	2.20	132.48
60	58	-514.48	299.39	5602.35	41	-3.93	2.15	132.37
61	3/	-551.02	285.45	5588.41	59	-4.40	2.05	132.27
62	16	-5/1.83	271.62	5574.59	57	-4.46	1.94	132.16
63	56	-5/8./1	258.12	5561.09	46	-4.50	1.84	132.06
64	33	-613.74	244.50	5547.47	66	-527	1.73	131.95
65	54	-680.79	230.27	5533.23	//	-5.72	1.61	131.83
66	41	-708.98	216.04	5519.00	24	-6.35	1.49	131./1
67	13	-822.10	200.54	5503.50	49	-6.39	1.38	131.59
68	50	-884.26	184.59	5487.55	20	-7.21	1.25	131.47
69	64	-998.45	167.44	5470.41	63	-7.53	1.12	131.34
70	49	-1016.99	150.52	5453.49	47	-7.65	1.00	131.22
71	1	-1081.59	133.17	5436.13	4	-7.81	0.87	131.09
72	67	-1081.74	116.29	5419.26	45	-8.71	0.74	130.96
73	72	-1097.05	99.67	5402.64	72	-8.89	0.61	130.83
74	47	-1168.29	82.54	5385.50	52	-9.11	0.48	130.69
75	52	-1852.14	56.74	5359.71	67	-10.40	0.33	130.55
76	45	-1891.45	31.11	5334,07	76	-11.05	0.18	130.40
77	76	-2364.28	0.00	5302.96	35	-13.83	0.00	130.22

Hybrid	CEYIELD (µ + g)	MASS (μ + g)
19	7503.88	133.57
48	6992.10	139.77
42	6370.00	140.99
25	6205.69	139.77
5	6183.49	138.85
40	6180.74	133.44
14	6116.74	132.08
2	6089.21	130.72
17	5993.36	131.31
60	5922.05	132.39
9	5826.33	133.77
10	5787.02	139.05
23	5782.72	136.33
11	5660.33	136.26
74	5642.48	130.37
43	5638.57	137.08
73	5629.77	131.63
69	5600.91	130.56
18	5522.37	135.64
26	5516.68	135.60
29	5492.30	131.37
31	5474.46	130.54
8	5474.27	144.24
27	5440.41	138.75
Overall Mean of Hybrids	5302.96	130.22
Mean of Selected Hybrids	5918.58	135.17
Predicted Genetic Gain	1066.77	7.95
Predicted Genetic Gain (%)	20.12	6.10

Table 3. Predicted mean genetic value (μ + g) of the selected hybrids for commercial ear yield trait (CEYIELD), in kg ha⁻¹, and mean grain mass weight (MASS) trait, in grams, via REML/Blup mixed model methodology, municipality of Jataí, Goiás State, Brazil, UFG, 2018.

 Table 4. Genealogy of maize lines used to obtain top crosses. UFG – municipality of Jataí, Goiás State, Brazil, 2018.

 Hybrid Code
 Origin

 Hybrid Code
 Origin

Hybrid Code	Ungin	Hybrid Code	Origin
1	TG02R2 X AG 1051	41	TG02R2 X AG 1051
2	TG02R2 X AG 1051	42	TG02R2 X AG 1051
3	TG02R2 X AG 1051	43	TG02R2 X AG 1051
4	TG02R2 X AG 1051	44	TG02R2 X AG 1051
5	TG02R2 X AG 1051	45	TG02R2 X AG 1051
6	TG02R2 X AG 1051	46	TG02R2 X AG 1051
7	TG02R2 X AG 1051	47	TG02R2 X AG 1051
8	TG02R2 X AG 1051	48	TG02R2 X AG 1051
9	TG02R2 X AG 1051	49	TG02R2 X AG 1051
10	TG02R2 X AG 1051	50	TG02R2 X AG 1051
11	TG02R2 X AG 1051	51	TG02R2 X AG 1051
12	TG02R2 X AG 1051	52	TG02R2 X AG 1051
13	TG02R2 X AG 1051	53	TG02R2 X AG 1051
14	TG02R2 X AG 1051	54	TG02R2 X AG 1051
15	TG02R2 X AG 1051	55	TG02R2 X AG 1051
16	TG02R2 X AG 1051	56	TG02R2 X AG 1051
17	TG02R2 X AG 1051	57	TG02R2 X AG 1051
18	TG02R2 X AG 1051	58	TG02R2 X AG 1051
19	TG02R2 X AG 1051	59	TG02R2 X AG 1051
20	TG02R2 X AG 1051	60	TG02R2 X AG 1051
21	TG02R2 X AG 1051	61	TG02R2 X AG 1051
22	TG02R2 X AG 1051	62	TG02R2 X AG 1051
23	TG02R2 X AG 1051	63	TG02R2 X AG 1051
24	TG02R2 X AG 1051	64	TG02R2 X AG 1051
25	TG02R2 X AG 1051	65	TG02R2 X AG 1051
26	TG02R2 X AG 1051	66	TG02R2 X AG 1051
27	TG02R2 X AG 1051	67	TG02R2 X AG 1051
28	TG02R2 X AG 1051	68	TG02R2 X AG 1051
29	TG02R2 X AG 1051	69	TG02R2 X AG 1051
30	TG02R2 X AG 1051	70	TG02R2 X AG 1051
31	TG02R2 X AG 1051	71	TG02R2 X AG 1051
32	TG02R2 X AG 1051	72	TG02R2 X AG 1051
33	TG02R2 X AG 1051	73	TG02R2 X AG 1051
34	TG02R2 X AG 1051	74	TG02R2 X AG 1051
35	TG02R2 X AG 1051	75	TG02R2 X AG 1051
36	TG02R2 X AG 1051		
37	TG02R2 X AG 1051		
38	TG02R2 X AG 1051		
39	TG02R2 X AG 1051		
40	TG02R2 X AG 1051		

Materials and Methods

Conduction of the Study

The evaluation experiment was conducted in an experimental area of the *Universidade Federal de Goiás*, located in the municipality of Jataí, Goiás State, Brazil, in the micro-region of the Southwest of Goiás State, with 17°53' S and 52°43' W, and 680 m altitude, between February and June 2018, in the second harvest (little crop).

Plant material and treatments

Top cross hybrids of partially inbred S_1 lines from a population with potential for green maize yield were used. These lines were crossed with a broad genetic base tester (F_2 of the AG 1051 hybrid), in accordance with the Irish system, to obtain the top cross hybrids. To carry out the crosses, seeds from the selected S_1 families were sown in a five-meter line. At every three lines, a tester line was sown. Planting was performed in July 2017, in an isolated area and drip irrigation. When the male flowering was occurred, the emasculation of the S_1 lines was performed in a way that only the tester would supply pollen. Then, 75 top cross hybrids were generated. At the harvest, a visual evaluation of the ears was made, and those with undesirable agronomic performances were discarded. The best quality ears were used to compose the material for experimental evaluation.

Experimental design and traits measured

The evaluation experiment of the 75 top cross hybrids (Table 4) was carried out in a randomized block design with four replicates. Plots were made up of four-meter rows spaced 0.90 m between rows and 0.20 m between plants. A sample of five plants/ears was used in each plot for the evaluation of grain mass trait (MASS). For the commercial ear yield (CEYIELD) trait, evaluations were performed for the total of plants per plot. The stand was corrected for 20 plants per plot.

Commercial ear yield (CEYIELD) was derived from the sum of the weighing of ears with no straw larger than 15 cm with a diameter greater than 3 cm, free of pests and diseases. All data collected were transformed into kilograms per hectare. Grain mass trait (MASS) was obtained using an electric maize grater, which removed all grain mass of five representative ears of the plot, then the cutting of grains from the base of the cob performed, and subsequent weighing, with the implementation of value mean.

Statistical analysis

The SELEGEN-REML/Blup software was adopted for statistical analysis of mixed models (Resende, 2016). The statistical model 21 (complete blocks) was used as follows: y = Xr + Zg + e,

in which, y is the data vector, r is the repetition effect vector (assumed as fixed) plus the overall mean, g is the genotypic effect vector (assumed as random), and e is the vector errors or residues (random). Capital letters represent the incidence matrices for these effects.

Genetic values of each top cross hybrid were calculated by summing up each genotypic effect (g) to the overall mean of the experiment (u). The genetic gain is equivalent to the mean of the vectors of the predicted genetic effects for the selected hybrids (Freitas et al., 2013). The overall mean added to the genetic gain resulted in the inbred population mean.

Conclusions

The study concluded that the REML/Blup statistical tool was efficient to select top cross hybrids of green maize from partially inbred lines, providing important genetic gains for the traits under evaluation. There was evidence that hybrids 19 and 48 distinguished themselves from the others due to the high genetic effects obtained for commercial ear yield and grain mass weight traits. It proved possible to select 24 top cross hybrids with positive and superior genetic effects for both CEYIELD and MASS traits, having been predicted genetic gains of 20.12% and 6.10%, respectively.

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References

- Allard RW (1971) Princípios do melhoramento genético de plantas. São Paulo: Edgard Lucher.
- Arnhold E, Mora F, Silva RG, Good-God PI, Rodovalho MA (2009) Evaluation of top-cross popcorn hybrids using mixed linear model methodology. Chil J Agr Res. 69:46-53.
- Baretta D, Nardino M, Carvalho I R, Danielowski R, De Souza H, Luche VFDO, De Souza VQ, De Oliveira AC, Da Maia LC (2016) Characterization of dissimilarity amongv arieties in Brazilian maize germplasm. Aust J Crop Sci. 1:1601-1607.
- Baretta D, Nardino M, Carvalho LR, Pelegrin AJde, Ferrari M, Szareski VJ, Barros WS, Souza VQde, Oliveira ACde, Maia LCda (2017) Estimates of genetic parameters and genotypic values prediction in maize landrace populations by REML/BLUP procedure. Genet Mol Res. 16:gmr16029715.
- Carvalho IR, Pelegrin AJ, Ferrari M, Szareski VJ, Rosa TC, Oliveira VF, Hoffmann JF, Nardino M, Chaves FC, Souza VQ, Oliveira, AC, Maia LC (2018) Heterosis and genetics parameters for yield and nutritional components in halfsibling maize progenies. Genet Mol Res. 17:1-12.
- Cruz DP, Gravina GA, Oliveira TRA, Gomes ABS, Silva CQ, Vivas M, Araújo KC, Daher RF, Gravina LM, Moraes R, Silva VB (2018) Selection of progenies of snap beans using mixed models (REML/BLUP). Genet Mol Res. 17:gmr16039914.
- DoVale JC, Fritsche-Neto R, Silva PSL (2011) Selection index of maize cultivars with twice fitness: baby corn and green corn. Bragantia. 70:781-787.
- Entringer GC, Vittorazzi JCF, Santos EA, Pereira MG, Viana AP (2016) Genetic gain estimates and selection of S₁ progenies based on selection indices and REML/ BLUP in super sweet corn. Aust J Crop Sci. 10:411-417.

Faria SV, Luz LS, Rodrigues MC, Carneiro JEdeS, Carneiro PCS,

DeLima RO (2017) Adaptability and stability in commercial maize hybrids in the southeast of the State of Minas Gerais, Brazil. Rev Cienc Agron. 48:347-357.

- Freitas ILJ, Amaral Junior AT, Viana AP, Pena GF, Cabral OS, Vittorazzi C, Silva TRC (2013) Genetic gain evaluated with selection indices and with REML/Blup in popcorn. Pesqui Agropecu Bras. 48:1464-1471.
- Gomes ABS, Oliveira TRA, Cruz DP, Gravina GA, Daher RF, Araújo LC, Araújo KC (2018) Genetic gain via REML/BLUP and selection indices in snap bean. Hortic Bras. 36:195-198.
- Lima MWP, Souza EA, Ramalho MAP (2000) Procedure to select superior maize populations for inbred line extraction. Bragantia. 59:153-158.
- Mendonça LF, Fritsche-Neto R, Granato ISC, Alves FC (2016) Accuracy and simultaneous selection gains for grain yield and earliness in tropical maize lines. Maydica. 61:01-07.
- Nardino M, Baretta D, Carvalho IR, Olivoto T, Pelegrin AJDE, Ferrari M, Szareski VJ, Konflaz VA, Caron BO, Schmidt D, Barros WS, Souza VQ (2016a) REML/ BLUP in analysis of precommercial simple maize hybrid. Intern J Cur Res. 8:37008-37013.
- Nardino M, Carvalho IR, Baretta D, Follmann DN, Leschewitz R, Olivoto T, Caron BO, Oliveira AC, Maia L, Souza VQ (2016b) Cycle segregation in crossings of landrace corn populations. Intern J Cur Res. 8: 37896-37900.
- Oliveira GHF, Amaral CB, Silva FAM, Dutra SMF, Marconato MB, Môro GV (2016) Mixed models and multivariate analysis for selection of superior maize genotypes. Chil J Agr Res. 76:427-431.
- Oliveira IJde, Atroch AL, Dias MC, Guimarães LJ, Guimarães PEdeO (2017) Selection of corn cultivars for yield, stability, and adaptability in the state of Amazonas, Brazil. Pesqui Agropecu Bras. 52:455-463.
- Olivoto T, Nardino M, Carvalho IR, Follmann DN, Ferrari M, Szareski VJ, Pelegrin AJde, Souza VQde (2017) REML/BLUP and sequential path analysis in estimating genotypic values and interrelationships among simple maize grain yieldrelated traits. Genet Mol Res. 16:gmr16019525.
- Piepho HP, Möhring J, Melchinger AE, Büchse A (2008) BLUP for phenotypic selection in plant breeding and variety testing. Euphytica. 161:209-228.
- Resende MDV (2007) Software SELEGEN REML/BLUP: sistema estatístico e seleção genética computadorizada via modelos lineares mistos. Colombo: Embrapa Florestas. 359p.
- Resende MDV (2016) Software Selegen-REML/BLUP: A useful tool for plant breeding. Crop Breed Appl Biot. 16:330-339.

Resende MDV, Duarte JB (2007) Precision and quality control in variety trials. Pesqui Agropecu Trop. 37:182-194.

Sousa CMB, Gravina GA, Viana AP, Daher RF, Souza CLM (2017) Selection of snap bean F_2 progenies for production using the REML/ BLUP methodology. Hortic Bras. 35:033-040.

- Szareski VJ, Carvalho IR, Kehl K, Pelegrin A, Nardino M, Demari G, Barbosa M, Lautenchleger F, Smaniotto D, Aumonde TZ, Pedó T, Souza VQ (2018) Interrelations of Characters and Multivariate Analysis in Corn. J Agr Sci. 10:187-194.
- Ufaz S, Galili G (2008) Improving the content of essential amino acids in crop plants: goals and opportunities. Plant Physiol. 147: 954-961.
- Venkovsky R (1987) Herança quantitativa. In: Paterniani E, Viègas GP (ed). Melhoramento e produção do milho. Campinas: Fundação Cargill. 137-214p.
- Wen W, Brotman Y, Willmitzer L, Yan J, Fernie AR (2016) Broadening Our Portfolio in the Genetic Improvement of Maize Chemical Composition. Trends Genet. 32:459-469