

Genetic gain estimates and selection of S₁ progenies based on selection indices and REML/BLUP in super sweet corn

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Abstract

This study aimed to compare estimates of genetic gains using four indices of selection, based on the least squares method and the additive index through the multi-trait REML/BLUP (Best linear unbiased prediction/restricted maximum likelihood) to perform a selection early in S₁ families. Eighty S₁ testcross hybrids were proportionally separated into two groups: the CIMMYT-SH (CSH) and CIMMYT-8HS (C8HS) populations and assessed for main trait required by the market. The selection indices Smith & Hazel, Williams, Pesek & Baker, Mulamba & Mock and the additive multi-trait REML/BLUP were tested. The estimated gains from selection were assessed for each group (CSH and C8HS) separately, so as to maintain the identity of each population. Among the four selection indices based on the ANOVA (analysis of variance), the Mulamba & Mock was the most suitable for the selection of half-sib families in super sweet corn. The additive multi-trait REML/BLUP index showed even better predicted genetic gains than Mulamba & Mock, and was efficient to select half-sib families in super sweet corn. Based on the REML/BLUP were selected from each population, the 20 most promising progenies to continue the super sweet corn breeding program. The high level of coincidence between the multi-trait REML/BLUP and Mulamba & Mock indices indicates similar efficiency for selection purposes. However, REML/BLUP method showed better genetics gains, may be recommend the use of for future selection activities.

Keywords: Mixed models; specialty corn; shrunken; *Zea mays*.

Abbreviations: REML/BLUP_Best linear unbiased prediction/restricted maximum likelihood; CSH_CIMMYT-SH population; C8HS_CIMMYT-8HS population.

Introduction

Corn is one of the most important and dynamic agricultural crops in the world. This dynamism is related to its multiple applications. The different applications allow the use of corn grain for so-called special purposes, according to the specific characteristics of the grain, and with this utility, corn is called specialty grain (Texeira et al. 2014). The sugary taste of sweet corn grain is due to variations in the starch and sugar levels in the endosperm. The mature corn grain contains only 3% sugar, compared to sweet corn grain with 9 to 14%. There are also cultivars known as super sweet, with a grain content of 15 to 25% sugar. These variations are genetically controlled and the alleles that determine the sweet phenotype are recessive (Silva e Karan, 1994, Schultheis, 1998). Among the different alleles that confer the phenotype known as sweet corn, those with the genes shrunken-2 (*sh₂*) (Yousef and Juvik, 2002) and brittle-2(*bt₂*), both super sweet, have the greatest commercial potential (Brewbaker and Banafunzi 1975, Brewbaker, 1977).

Several studies involving the development and releasing of common corn cultivars have received much attention from the scientific community. However, the same has not been observed for green corn cultivars, either derived from super sweet corn or common corn (Albuquerque et al. 2008). By 2001, there were about 300 varieties of open-pollinated sweet corn in the world, of which only three cultivars formed the genetic basis for the development of all sweet corn breeding

programs (Tracy, 2001). According to the Ministry of Agriculture, Livestock and Supply, only 45 sweet corn cultivars were recorded by six different companies including two genetically modified cultivars. However, only three are being traded (Brazil, 2014). The number of varieties of this vegetable available in the elite collections and germplasm banks is small as compared to common corn (Texeira et al. 2013). Super sweet corn can be exploited throughout the year with the use of irrigation systems and scheduled production, which allows more consistent production to supply the market (Texeira et al. 2001). Super sweet corn cultivation can be a cost effective alternative that will soon become relevant for Brazilian economy. It must be emphasized that, in order to meet the interests of the potting industry and consumers of fresh products, a super sweet corn cultivar must have ear length exceeding 15 cm and a diameter longer than 3 cm, so as to improve the efficiency of industrial machinery. Besides, ears with at least 14 grain rows and field ear yield superior to 12 tonnes per hectare are also desirable (Barbieri et al. 2005; Souza et al. 2013). Overall, sweet corn breeding programs has goals realized superior cultivars that meet market requirements. In plant breeding, the selection of new genotypes, are made with the help selection indices. These are multivariate techniques that match the information about various traits under selection with the genetic properties of the population under study. The selection indices allow the

establishment of numeric values, which work as an additional, theoretical trait, resulting from the combination of certain traits selected by the breeder, on which simultaneous selection should be maintained. Different indices - Mulamba and Mock (1978), Pesek and Baker (1969), Smith (1936) and Hazel (1943) and Williams (1962) are alternatives for selection in breeding programs Cruz et al. (2004). Inferences about genotypes under selection, either at initial or final stages of a breeding program, can be consider the true genotypic values, i.e., should be based on genotypic rather than phenotypic data (Borges et al. 2010). An alternative very much employed nowadays, which is highly accurate in the selection process in animal and perennial species breeding program is the use of variance components estimated by restricted maximum likelihood (REML) and by genotypic values predicted by the best linear unbiased predictor (BLUP) (Henderson, 1974; Rodrigues et al., 2013). This method is also used in some annual plants. In recent years, this approach has been incorporated into allogamous and autogamous plant breeding programs. (Piepho et al. 2008; Baldissera et al. 2012; Freitas et al. 2013)

Thus, the present study aimed to (1) compare four selection indices based on the least squares method and the additive index through the multi-trait REML/BLUP method in the assessment of predicted genetic gain and (2) practice an early soft selection (disposal of progenies with the poorest performance) with 50% selection intensity on the S_1 progenies from two groups of super sweet corn CIMMYT-SH (CSH) and CIMMYT-8HS (C8HS), assessed according to the main traits required by the market.

Results and Discussion

The analysis of joint variance indicates the existence of genetic variability for all variables under selection (Table 1). Heritability estimates showed a high value that ranged from 61.53 to 76.19%. Based on heritability estimates, it is possible to foresee a likely successful selection in breeding programs targeting to obtain superior cultivars (Cruz et al., 2004).

Estimates of genetic gains by selection indices

A super sweet cultivar must meet mainly the following requirements, among others, in order to be accepted in the market: about 20 cm-long ears, cylindrical shape with minimum of 14 rows and a diameter greater than 30 mm; and minimum EY of 12 t.ha⁻¹ (Pereira Filho et al. 2009). Aiming to meet all the needs of the consumer market, more attention has been given to the trait number of grain rows, since this is the only one that still does not comply with the commercial standard in the studied populations.

Estimates of predicted genetic gains revealed that the Mulamba & Mock index provided better genetic gains for both populations as compared with the other three indices used. It allowed the prediction of gains that are best suited to the objectives of the program, i.e., a higher genetic gain for the NGR, which is considered the most important trait for the populations under analysis, and significant genetic gains for the other traits (Tables 2 and 3). A comparison between the Mulamba & Mock and Williams indices, for example, for the CSH population corroborates this. The Mulamba & Mock index was 88.42% higher for the NGR, and 63.07% higher for EY, compared with the Williams index (Table 2). Similar results are observed when the Mulamba & Mock and Smith & Hazel indices are compared. For the traits NGR and EY,

genetic gain prediction values by Mulamba & Mock were 77.23% and 26.36% higher, respectively (Table 2).

For C8HS, the comparison of the estimates of predicted gains between the Pesek & Baker and Mulamba & Mock indices shows that the first exceeds the second, on average, in 94.4% only for the trait EY. However, Mulamba and Mock index shows, for example, superiority of 700 and 100% for NGR and HEL, respectively (Table 3). Comparison between the Mulamba & Mock and Smith & Hazel indices shows conclusions similar to those of the first group (CSH). In other words, Mulamba & Mock provided the best predictions of genetic gains desired by the UENF super sweet corn breeding program (Table 3). These results are in agreement with other investigations. Vilarinho et al. (2003) evaluated the efficiency of the truncated selection of the indices Smith & Hazel; Willians; Pesek & Baker; Mulamba & Mock and Elston, in the identification of S_1 and S_2 popcorn progenies, and concluded that, the Mulamba & Mock index provided the most desirable results for satisfactory genetic gains in grain yield and expansion ability. Santos et al. (2007) tested four selection indices in a popcorn half-sib family recurrent selection program and concluded that the selection based on Mulamba & Mock index produced predicted gains most suitable for the objectives. Berilli et al. (2013) worked with full-sib reciprocal recurrent selection between and showed that, among the tested indices, the Mulamba & Mock index was the most suitable to the objectives of the program, i.e., the gains predicted by the Mulamba & Mock selection index were higher than those predicted by the other indices.

Estimates of genetic gains by selection indices and the REML / Blup method

Since the Mulamba & Mock index was recognized as the most satisfactory among the selection indices based on the least squares methods, the estimated genetic gains were compared with the additive selection index based on the multitrait REML/BLUP procedure (Table 4). This additive selection index based on multitrait REML/BLUP methodology showed higher predicted gains for all traits than the Mulamba and Mock index.

A comparison between the values of the genetic gains of the trait NGR, for example, can demonstrate numerically the superiority of the REML/BLUP procedure. This, in turn, showed differences in predicted genetic gains of 4.66% in CSH population and 4.13% in C8HS population (Table 4). The trait PH showed high genetic gain for both groups (CHS and C8HS), by the REML/BLUP, unlike the Mulamba & Mock index (Table 4). It was reported that tall plants of common corn or popcorn are not suitable for selection, as tall plants tend to tip (Freitas et al. 2013). However, this statement is not valid for corn crops harvested green. Secondly, the presence of the br_2 allele on these super sweet corn populations can minimize the problem of tipping. When homozygous, this allele confers dwarf plant phenotypes (Galston and Davies, 1972). Thus, the gains of 2.62% and 2.24% for the groups CSH and C8HS, respectively does not compromise the final goals of the program. The difference between the estimates of the genetic gains predicted by the two procedures can be explained by the fact that the Mulamba & Mock index is based on linear combinations of measures of various traits based on estimates of genetic parameters and phenotypic averages obtained by analysis of variance. On the other hand, the REML/BLUP method uses, the components of variance estimated by restricted maximum likelihood (REML) and the genetic or genotypic values predicted by the best linear unbiased predictor (BLUP)

Table 1. Summary of the analysis of variance and estimates of heritability h_{fm}^2 and coefficient of experimental variation CV_e of the average of the experiments in both environments (Colégio Agrícola and Itaocara) - RJ in the 2012/2013 agricultural year.

Mean squares		PH	NGR	ED	HEL	HEW	EY ^{1/}
FV	GL						
Environment (E)	1	29.56**	0.002 ^{ns}	504.58**	57.34**	129804.00**	98.32**
Block/E	4	0.16**	0.99**	62.11**	6.57**	13908.97**	1.34 ^{ns}
Genotype (G)	79	0.08**	1.27**	45.35**	3.02**	2409.16**	22.89**
CSH	39	0.06**	1.23**	16.58**	4.01**	2655.13**	24.83**
C8HS	39	0.06**	1.54**	11.54**	2.10**	1544.17**	10.65**
CSH x C8HS	1	1.59**	7.42**	112.53**	0.001 ^{ns}	44709.14**	424.12**
G x E	79	0.03 ^{ns}	0.34 ^{ns}	50.50 ^{ns}	1.21 ^{ns}	781.474 ^{ns}	10.94 ^{ns}
CSH x E	39	0.04 ^{ns}	0.31 ^{ns}	5.07 ^{ns}	1.18 ^{ns}	692.408 ^{ns}	14.25 ^{ns}
C8HS x E	39	0.03 ^{ns}	0.37 ^{ns}	5.91 ^{ns}	1.23 ^{ns}	873.03 ^{ns}	7.91 ^{ns}
CSHxC8HSxE	1	0.006 ^{ns}	0.04 ^{ns}	5.94 ^{ns}	1.76 ^{ns}	684.147 ^{ns}	0.07 ^{ns}
Error	316	0.03	0.29	4.99	1.17	780.334	8.47
h_{fm}^2		61.53	76.19	67.45	62.00	67.61	65.85
CV_e (%)		7.83	12.5	4.85	5.24	12.14	19.55
\bar{X}		2.23	12.5	46.02	20.65	230.05	14.89

^{1/} PH= Plant height (meters), HEW= husked ear weight (grams), HEL= average husked ear length (cm), NGR= number of grain rows, ED=ear diameter (mm), and EY = husked ear productivity (tonnes.ha⁻¹).

Table 2. Estimates of the genetic gains (%) based on different selection indices, by simultaneous selection of six traits of half-sib progenies of super sweet corn from the CSH population.

Traits ^{1/}	Selection Indices			
	Pesek & Baker	Smith & Hazel	Mulamba & Mock	Willians
PH	0.27	0.80	0.12	0.85
HEW	3.8	4.05	3.37	4.49
HEL	2.39	2.01	1.05	1.53
NGR	0.81	1.01	1.79	0.95
ED	0.69	1.11	1.12	1.11
EY	2.53	3.11	3.93	2.41

^{1/} PH= Plant height (meters), HEW= husked ear weight (grams), HEL= average husked ear length (cm), NGR= number of grain rows, ED=ear diameter (mm), and EY = husked ear productivity (tonnes.ha⁻¹).

Table 3. Estimates of the genetic gains (%) based on different selection indices, by simultaneous selection of six traits of half-sib progenies of super sweet corn from the C8HS population.

Traits ^{1/}	Selection indices			
	Pesek & Baker	Smith & Hazel	Mulamba & Mock	Willians
PH	-0.68	0.09	-0.25	0.14
HEW	1.18	3.01	2.24	3.02
HEL	0.14	0.18	0.28	0.25
NGR	0.2	1.46	1.60	1.02
ED	0.38	1.03	0.79	0.09
EY	2.93	1.04	1.51	1.04

^{1/} PH= Plant height (meters), HEW= husked ear weight (grams), HEL= average husked ear length (cm), NGR= number of grain rows, ED=ear diameter (mm), and EY = husked ear productivity (tonnes.ha⁻¹).

Table 4. Estimates of the genetic gains (%) based on two selection indices by simultaneous selection of six traits of half-sib progenies of super sweet corn from the two populations.

Traits ^{1/}	Selection Indices			
	CSH		C8HS	
	Mulamba &Mock	REML/BLUP	Mulamba &Mock	REML/BLUP
PH	0.12	2.62	-0.25	2.24
HEW	3.37	12.00	2.24	6.64
HEL	1.05	6.29	0.28	1.75
NGR	1.79	6.45	1.60	5.73
ED	1.12	4.30	0.79	2.56
EY	3.93	8.97	1.51	5.16

^{1/} PH= Plant height (meters), HEW= husked ear weight (grams), HEL= average husked ear length (cm), NGR= number of grain rows, ED=ear diameter (mm), and EY = husked ear productivity (tonnes.ha⁻¹).

Table 5. Coefficients of coincidence of 20 progenies selected by different selection indices, by simultaneous selection of six traits. Above the diagonal line are the estimates for the CSH population and below it, those related to the C8HS population of half-sib progenies of super sweet corn.

	Pesek & Baker	Smith &Hazel	Mulamba &Mock	Willians	REML/BLUP
Pesek & Baker	-	0.75	0.70	0.8	0.75
Smith &Hazel	0.65	-	0.75	0.8	0.70
Mulamba &Mock	0.75	0.85	-	0.85	0.95
Willians	0.65	0.95	0.85	-	0.70
REML/BLUP	0.75	0.85	0.95	0.85	-

Table 6. Ranking of the 20 half-sib progenies from two populations and estimate of the new predicted average (BLUP) for the six main traits of interest to sweet corn crop.

Ranking	CSH							C8HS						
	Progenies	New averages						Progenies	New averages					
		PH	HEW	HEL	NGR	ED	EY		PH	HEW	HEL	NGR	ED	EY ^{1/}
1	27	2.31	275.6	20.95	13.88	47.96	19.33	25	2.21	246.79	20.95	13.13	47.16	15.42
2	32	2.32	271.01	21.2	14.18	47.76	17.72	23	2.31	250.71	21.2	13.7	46.48	14.79
3	31	2.29	279.74	21.03	13.42	49.49	17.43	9	2.21	242.16	21.03	13.34	47.02	15.13
4	37	2.37	254.28	20.94	14.12	48.09	16.15	31	2.22	238.65	20.94	12.96	47.07	15.45
5	33	2.39	284.37	20.98	13.46	49.18	16.4	39	2.24	241.4	20.98	13.23	47.28	15.05
6	26	2.43	273.08	20.91	14.05	48.77	16.99	6	2.19	245.63	20.91	13.11	47.37	14.42
7	16	2.43	262.24	21.23	13.24	50.59	17.12	14	2.26	240.00	21.23	13.65	47.21	14.22
8	15	2.33	260.37	21.13	13.29	47.37	16.52	12	2.23	233.83	21.13	13.28	46.87	14.48
9	9	2.37	284.06	20.82	13.50	49.92	17.66	21	2.25	237.39	20.82	13.2	46.32	14.6
10	25	2.34	258.66	21.43	13.27	48.02	18.21	10	2.34	244.28	21.43	13.41	47.11	14.06
11	34	2.30	253.41	21.17	13.36	48.22	17.55	7	2.29	232.86	21.17	12.99	46.18	15.00
12	10	2.35	282.96	21.31	13.06	48.86	17.49	18	2.26	243.08	21.31	12.6	46.47	15.24
13	2	2.35	265.33	20.8	13.29	47.82	17.25	22	2.24	240.8	20.8	13.16	46.73	14.08
14	22	2.35	250.73	21.02	13.50	49.69	16.67	3	2.27	238.01	21.02	13.5	46.44	14.03
15	30	2.34	245.37	20.71	13.67	47.51	18.35	38	2.2	234.9	20.71	12.67	46.14	14.82
16	40	2.29	278.06	21.01	13.6	49.57	18.07	16	2.22	230.7	21.01	13.02	46.63	14.51
17	13	2.31	255.28	21.1	13.09	48.15	16.78	13	2.29	248.26	21.1	12.58	47.61	14.67
18	18	2.39	264.25	20.99	13.17	48.54	17.79	24	2.19	225.95	20.99	13.05	45.71	14.17
19	20	2.44	269.34	21.07	13.12	47.89	16.72	37	2.19	224.72	21.07	12.71	46.93	14.74
20	28	2.33	251.68	20.84	13.14	48.39	17.61	30	2.18	229.08	20.84	12.53	46.04	14.53
\bar{X}		2.35	265.99	21.03	13.47	48.58	17.39		2.23	238.46	21.03	13.09	46.73	14.67

^{1/} PH= Plant height (meters), HEW= husked ear weight (grams), HEL= average husked ear length (cm), NGR= number of grain rows, ED=ear diameter (mm), and EY = husked ear productivity (tonnes.ha⁻¹).

(Resende, 2002). Therefore, a more accurate selection process is obtained, since the predicted genotypic effects and the selection gains of each family are the vector of the solutions used. This corrects the values for the environmental effects, predicts accurately and without bias the genotypic values and leads to the maximization of genetic gain with selection (Resende and Sturion, 2001; Rodrigues et al. 2013). The predicted genetic gain values (Table 4) demonstrate that the multitrait REML/BLUP method was more efficient in predicting the genetic gains. Therefore, it is the most appropriate procedure to classify the most promising genotypes to be candidates for future commercial hybrids. However, Pedrozo et al. (2009) states that the efficiency of selection indices can be compared with the estimation of the coefficient of coincidence between two indices. The closer is the value to the unity, the greater the agreement between the selection results. The coefficients of coincidence of the 20 half-sib progenies selected by the indices Pesek & Baker, Smith & Hazel, Mulamba & Mock and Williams, and by multi-trait REML/BLUP method ranged from 0.65 to 0.95, (Table 5) and can be considered average to high. Among the coefficients, the coincidence of 95% between Mulamba & Mock and the REML/BLUP indices stands out, in both groups. The high coincidence between the multi-trait REML/BLUP index and Mulamba & Mock indicates that, they are equally efficient to select super sweet corn genotypes, under balanced data conditions. This was expected in this study as we had a balanced data set. As stated by Resende (2002), the REML/BLUP methodology has more accurate models than the least squares method when data to be analyzed has some degree of imbalance.

Ranking of the half-sib progenies by REML / Blup method

In the selection process, breeders prefer genotype values. In other words, selection should be based on the average of genotypes. Therefore, the most promising genotypes were ranked according to the values predicted by the additive index obtained by multi-trait REML/BLUP (Table 6). The REML/BLUP methodology in fact estimates and/or predicts these values. A study conducted by Borges et al. (2010), shows that the genotypic values are very close to the new average, which indicates that this method is efficient to select progenies with high relative performance and that the performance of the next crop cycle may be very close to the predicted. In this investigation, the selected progenies presented an average of NGR of 13.47 and 13.09 for the CSH and C8HS populations, respectively which were close to the market requirements. In terms of EY the respective averages were 17.39 and 14.67 tonnes.ha⁻¹ respectively. Thus, in terms of husked ear yield, these selected progenies were expressively superior to the market requirements (Pereira Filho et al. 2009) indicating high probability of success in terms of future cultivar releasing.

Materials and Methods

Plant materials

Three super sweet corn populations belonging to different heterotic groups; namely CSH, C8HS and Piranão 8HS (P8HS) were used in this study. The population P8HS which belongs to the heterotic group "DENT", was used as the tester (wide and unrelated base). The populations CSH and C8HS belong to the heterotic group "FLINT". Both populations CSH and C8HS have the brachytic gene (*br₂*). It is noteworthy that the populations CSH and C8HS as well as

the tester (P8HS) are broad-based populations, converted into super sweet, with the incorporation of the gene *sh₂* by backcrossing. Were obtained via top cross by the super sweet corn breeding program conducted by the Universidade Estadual do Norte Fluminense Darcy Ribeiro, 80 S₁ topcross hybrids, proportionally separated into two groups: CSH and C8HS, in order to maintain genetic identity of the respective populations to give sequence of the breeding program.

Field experiments

The field evaluation was conducted in the 2012/2013 main cropping season. The experiment was arranged in a randomized complete block design with 3 replications in two locations: Colégio Agrícola Antônio Sarlo in the city of Campos dos Goytacazes (Northern Rio de Janeiro State) and the Experimental Station of Ilha Barra do Pomba in the city of Itaocara (Northwestern Rio de Janeiro State). The sites are characterized by the following geographical coordinates: 21° 24' 48" south latitude, 41° 44' 48" W longitude and 14 m altitude and 21° 40' 09" S latitude, 42° 04' 34" W longitude, 60 m, for Campos dos Goytacazes and Itaocara, respectively. Each experimental unit (half-sib families) was cultivated in a single line of 3.6 m, spacing of 0.3 m between plants and 0.90 m between rows. Three continuous lines were used as a border around the experimental area. Five seeds per hole were used in the planting date, with subsequent thinning to one plant per hole, 30 days after sowing. N-P-K 8-28-16 was applied at the rate of 400 kg.ha⁻¹ during planting. Later, two cover fertilizations were performed: 30 days after planting, with 300 kg.ha⁻¹ of the formula N-P-K 20-00-20, and 45 days after planting, with 200 kg.ha⁻¹ of urea. Before planting, hand weeding and the herbicide Roundup were used for weed control.

Assessment of agronomic traits

The harvesting of the green ears was conducted approximately 18 to 22 days after silking. The kernels are fully developed and exude a milky liquid when punctured (Schultheis, 1998). The following traits were assessed: plant height (PH) - average height of five competitive plants, measured from soil level up to the insertion of the node of the flag leaf, in meters; average husked ear weight, in grams (HEW) - average weight of 10 husked ears, in grams; average husked ear length (HEL) - average length of 10 husked ears, in centimeters; number of grain rows (NGR); average diameter of 10 ears, in millimeters (ED) - average diameter of 10 husked ears, in millimeters; and husked ear yield (EY) - husked ears total weight of the plot in tonnes per hectare. Estimates of genetic gains were performed by selection indices based on the average of the combined data analysis carried out at the two locations (Campos and Itaocara).

Statistical analysis

Genetic gain prediction by selection indices was based on an ideal phenotype. Superior genotypes were selected based on EY, HEW and NGR. As for PH and ED, it was intended to maintain the estimated averages, since they meet market demands. The selection indices Smith (1936), Hazel (1943), Williams (1962) Pešek & Baker (1969) and Mulamba & Mock (1978) were considered. The following economic weights were assigned: 1, 20, 10, 30, 1 and 20, for the traits PH, HEW, HEL, NGR, ED and EY, respectively. The statistical analyses were performed with the use of the Genes (Cruz, 2013) software system. The phenotypic data were also

analyzed by the Selegen-REML/BLUP software system, statistical model 22: Evaluation of half-sib progenies in complete blocks and multiple locations (Resende, 2009). The genetic values of each progeny were obtained by the addition of each genotypic effect to the overall mean of the experiment. The genetic gain is equal to the average of the vectors of the predicted genetic effects for selected progenies. The coincidence ratio was obtained by the ratio between twice the number of progenies, in which both selection indices coincide, and the sum of the total number of progenies containing the selection index, A plus the total number of progenies containing the selection index B (Pedrozo et al. 2009).

Conclusions

The multi-trait REML/BLUP additive index showed better predicted gains than Mulamba & Mock and was efficient in the selection of S_1 progenies in super sweet corn.

The high coincidence between the multi-trait REML/BLUP index and Mulamba & Mock indicates that, for selection purposes, they are equally efficient to select super sweet corn genotypes, under balanced data conditions. However, REML/BLUP method showed better genetics gains, may be recommend the use of for future selection activities.

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