

Recurrent selection of popcorn composites *UEM-CO1* and *UEM-CO2* based on selection indices

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Abstract: Selection indices were applied to data sets of 169 half-sib families of the popcorn composites *UEM-Co1* and *UEM-Co2* in four cycles of recurrent selection. From 2005 to 2008, the experiments were arranged in a 13 by 13 lattice square design, with two replications per cycle and composite. Genetic gains for popping expansion (PE) and grain yield (GY) were estimated based on several selection indices and truncation selection. The magnitude and balance of gains estimated for each trait by the indices were compared by an auxiliary statistical value (C_i). This value C_i consists of an arbitrary value, resulting from differences between the gains estimated for n traits by truncation selection and by index i . The indices of Subandi and Mulamba and Mock were the most promising to estimate high and balanced genetic gains for PE and GY in recurrent selection of half-sib popcorn families.

Key words: *Zea mays L.*, multiple-trait selection, popping expansion, grain yield.

INTRODUCTION

Popcorn is highly appreciated by the Brazilian population and the crop acreage in the country is on the rise. However, factors such as the limited availability of hybrid seeds and high-quality varieties are pressing towards higher popcorn imports (Sawazaki et al. 2003). On the other hand, researchers are dedicated to developing superior and adapted genotypes, especially with regard to popping expansion (PE) and grain yield (GY) (Amaral Júnior et al. 2013, Ribeiro et al. 2016). In some situations, the obstacle of negative correlation between PE and GY has to be overcome, so that the developed product satisfies both producers and consumers (Zinsly and Machado 1987, Carpentieri-Pípolo et al. 2002, Broccoli and Burak 2004, Faria et al. 2008, Freitas et al. 2013).

With a view to increase the accuracy of choice of the genotypes that contain a combination of both agronomic and quality traits in a single line, selection indices are very useful breeding tools for crops such as popcorn, for allowing the choice of the target traits for improvement. In this context, Granate et al. (2002) evaluated half-sib families of the popcorn composite CMS-43, and found that the Smith and Hazel index predicted higher gains for a greater number of traits, and that the percentage gain for the combination of the two most important traits was 9.14%. In a study of the performance of S_1 and S_2 progenies obtained from the popcorn population Beija-Flor, Vilarinho et al. (2003) selected superior families with the Mulamba and Mock index recommended by the authors. To select progenies in a third cycle population of intrapopulation recurrent selection

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(UNB-2U/UENF-14) by the method of half-sib families, Santos et al. (2007) found that the Mulamba and Mock index using arbitrary weights, resulted in higher gains for most traits, including PE and GY (7.6% and 10%). In the fourth recurrent selection cycle of the same population, Freitas Júnior et al. (2009) selected 30 superior families by the Mulamba and Mock selection index with arbitrary weights, (10.55% for PE and 8.50% for GY). In an evaluation of the fifth selection cycle of population UNB-2U, Rangel et al. (2011) found that the selection of superior families should be based on the Mulamba and Mock index, for estimating highest gains (6.01% for PE and 8.53% for GY). Analyzing the sixth recurrent selection cycle in population UENF-14, Ribeiro et al. (2012) observed, as in the previous publications, that the Mulamba and Mock index predicted the best gains (PE 10.97% and GY 15.30%), based on random economic weights.

Although the above studies demonstrate the efficiency of the tested indices, to date only part of the methodologies have been applied. Among the indices used in popcorn breeding, those of Smith (1936) and Hazel (1943), Williams (1962), Pesek and Baker (1969) and Mulamba and Mock (1978) are noteworthy. However, the indices of Tallis (1962), Cunningham et al. (1970) and Subandi et al. (1973) have not been applied in segregating popcorn populations so far. Moreover, previous studies failed to indicate a measurable form of comparing the selection indices in terms of the genetic gain estimates. In this context, this paper proposes and describes the statistical value C_p , which is promising for indicating which index estimates high and balanced genetic gains for traits. In this sense, the different selection indices for popcorn were compared, based on data collected in four recurrent selection cycles of half-sib families of the composites *UEM-Co1* and *UEM-Co2*.

MATERIAL AND METHODS

Four recurrent selection cycles (C_0 , C_1 , C_2 , and C_3) of the popcorn composites *UEM-Co1* and *UEM-Co2* were evaluated in this study. Composite *UEM-Co1* has yellow grain, resulting from open pollination among 17 popcorn genotypes. Composite *UEM-Co2* has white grain, derived from 12 popcorn genotypes. The selection cycles of the composites *UEM-Co1* and *UEM-Co2* were performed and evaluated in the municipality of Iguatemi, Maringá, in the north of Paraná, Brazil. One hundred and sixty-nine half-sib families were tested in a 13 by 13 lattice square design, with two replications for each selection cycle of the composites. The experimental units consisted of a single 5-m row, spaced 0.90 m apart, with a total of 25 plants per plot. The experiments were carried out between 2005 and 2008. Basal and topdressing fertilization were applied according to the crop requirements, as indicated by soil analysis. Other cultural practices were applied as recommended for maize cultivation in southern Brazil.

The half-sib families were evaluated for the traits grain yield (GY) and popping expansion (PE) in each selection cycle of the two composites. Grain yield was measured by weighing the amount of grain produced per plot, adjusted to kg ha⁻¹, at 13% moisture. The PE was determined based on a grain sample of 30 g taken from the intermediate portion of the cobs, at 13% moisture (mL g⁻¹). The grain samples were popped for 2.5 minutes at 270 °C in an electric popcorn popper. The best families were selected and recombined, according to the method between and within half-sib families (Paterniani 1967).

For data analyses, analysis of variance (ANOVA) was performed for each selection cycle and composite. The intra-block analysis followed the lattice model: $Y_{ijk} = m + g_i + b_{k/j} + r^j + E_{ijk}$, where: Y_{ijk} = observation of each half-sib family i^{th} , located in the k^{th} block in the j^{th} replication; m = overall mean; g_i = effect of each half-sib family; $b_{k/j}$ = effect of the k^{th} block, in the j^{th} replication; r_j = effect of the r^{th} replication of the experiment; E_{ijk} = experimental error associated with Y_{ijk} ; and g_i and $b_{k/j}$ were adjusted by analysis of variance.

The effect of half-sib families (g_i) was considered random. Heritability and variability (CVg) were estimated from the expected mean squares of the analysis of variance. For all selection and cycles and composites, the genetic gains for GY and PE were estimated by selection indices and truncation selection (direct selection). The following indices were used: i) Smith (1936) and Hazel (1943) (classical index); ii) Williams (1962); iii) Mulamba and Mock (1978); iv) Cunningham et al. (1970); v) Tallis (1962); vi) Pesek and Baker (1969) and vii) Subandi et al. (1973). The methodologies proposed by Tallis (1962) and Cunningham et al. (1970) consist of restricted indices, unlike the others used in this study. For the indices i, ii, iii, iv and v, three sets of economic weights were used, namely: a) CVg for both traits, b) 350 for PE and 1 for GY, and c) 1 for both evaluated traits. The selection intensity of this study was 20%, selecting, consequently, a total of 34 families per cycle and composite. The statistical analyses were performed with software Genes (Cruz 2013).

The statistical value C_i was designed to compare the selection indices with regard to maximization and balance of genetic gains for GY and PE. This value is based on the difference between the genetic gain for each trait of a set, estimated by an index, and the maximum possible gain of this trait in the study population. We suggest the measurement of the maximum genetic gain by truncation selection. The C_i value should be calculated for each selection index under study. The most appropriate selection index is the one represented by the lowest C_i value, indicating effectiveness and the possibility of considerable genetic gain for several traits under the specific conditions of the study population. The reason is that in every trait, the genetic gains of an index are subtracted from the maximum possible genetic gains in the study population. It is expected that good selection indices will estimate high gains for the traits with highest chances for improvement in the population, as estimated by truncation selection. In the opposite case, the higher C_i value indicates the situation. This procedure is performed at the beginning of the calculation. The basis of the maximum possible gain is a key point of using C_i . Nevertheless, it is also expected that good selection indices will achieve relevant gains for the other target traits, a condition measured by the sum of all effects of n characters, incorporated in the general expression of C_i . Furthermore, when the genetic gain of truncation selection is reduced to one trait, the difference between the maximum gain and the gain estimated by an index is not as important in terms of increase in the C_i value. In this sense, the statistical value C_i allows an identification of the selection index that fits best in view of the possibilities of breeding and limitations of each population, i.e., this index can provide high and balanced genetic gains for the studied traits and makes better use of the opportunities for breeding intrinsic to the study population.

$$\text{The general expression to calculate } C_i \text{ is: } C_i = \sum_{j=1}^J \frac{(GG_{ij} - GGts_j)^2}{2 |GGts_j|}$$

Where: GG_{ij} is the genetic gain estimated by the i^{th} selection index for the j^{th} trait; $GGts_j$ = maximum possible genetic gain for the j^{th} trait, estimated by truncation selection. If the truncation selection cannot be estimated, $GGts_j$ can be represented by the maximum genetic gain for the j^{th} trait, for the i^{th} selection index. In this study, the genetic gains for each index were estimated over four selection cycles of the two composites at a selection intensity of 20%. Then the statistical value C_i was applied, using Microsoft Office Excel spreadsheets.

RESULTS AND DISCUSSION

The results of the analysis of variance (ANOVA) for all cycles and composites are shown in Table 1. Significant differences were observed for the source of variation ($p < 0.05$) for all cycles and composites for both traits (PE and GY). It is well-documented that the presence of genetic variability is imperative for good results with selection (Silva et al. 2001). In this context, the genetic variability for the composite *UEM-Co2* was generally greater, a factor that can explain the relatively higher gains of this composite than of *UEM-Co1* in the different selection cycles (Table 1).

Different conditions of variability (CVg) and heritability based on the family means were observed for the study traits of the composites throughout the selection cycles. The CVg values varied from 3.86 to 15.04% for PE and from 7.20 to 12.54% for GY. High heritability estimates were also found, indicating the possibility of selecting half-sib families with good accuracy. In fact, the heritability of composite *UEM-Co1* in C_0 was 0.638 for PE and 0.634 for GY. The heritability estimated for composite *UEM-Co2* was 0.754 and 0.606 for PE and 0.697 and 0.757 for GY, in the cycles C_0 and C_2 , respectively (Table 1). High heritability values for PE and GY were also reported by other authors (Pacheco et al. 1998, Coimbra et al. 2002, Santos et al. 2008).

The results of truncation selection at a selection intensity of 20%, for the composites *UEM-Co1* and *UEM-Co2*, are shown in Tables 2 and 3. For both composites, positive genetic gains were estimated in most selection cycles on the basis of truncation selection. For composite *UEM-Co1*, the most significant gains for GY were estimated in cycles C_0 and C_3 (14.2% and 11.3% respectively), while for PE, in the cycles C_0 and C_1 (11.1% and 8.0%, respectively). The highest gains for PE and GY were estimated in the first selection cycle C_0 (Table 2). For composite *UEM-Co2*, based on truncation selection, the genetic gains estimates were highest in the cycles C_2 (16.5%) and C_0 (14.1%) for GY, while higher PE estimates were found in the cycles C_0 and C_1 (18.2 and 13.6%, respectively) (Table 3). These results indicate that, for both populations and traits, truncation selection would maximize the efficiency in the initial breeding cycle (C_0), which may be related to the greater genetic variability and heritability commonly found in this cycle (Table 1). Although the estimated values were

Table 1. Analysis of variance (ANOVA) for popping expansion (PE) and grain yield (GY) in two popcorn populations in four selection cycles of two popcorn composites *UEM-Co1* and *UEM-Co2*

Source of variation	df	Mean squares							
		PE				GY			
		C ₀	C ₁	C ₂	C ₃	C ₀	C ₁	C ₂	C ₃
UEM-Co1									
Families	168	27.3*	22.3*	19.2*	17.6*	1.90 ^{E+5*}	1.67 ^{E+5*}	1.70 ^{E+5*}	1.98 ^{E+5*}
Block/Replications	24	9.5	10.8	30.4	58.8	0.89 ^{E+5}	1.26 ^{E+5}	4.29 ^{E+5}	4.12 ^{E+5}
Replications	1	18.9	10.0	4.5	84.5	2.52 ^{E+5}	7.34 ^{E+6}	5.62 ^{E+6}	1.22 ^{E+6}
Erro	144	9.9	10.3	11.9	14.2	7.00 ^{E+4}	9.70 ^{E+4}	1.09 ^{E+5}	8.40 ^{E+4}
Mean		29.6	30.6	31.3	32.3	1.97 ^{E+3}	2.17 ^{E+3}	2.15 ^{E+3}	2.35 ^{E+3}
CVe		10.63	10.49	11.02	11.67	13.45	14.38	15.38	12.36
CVg		9.96	8.02	6.11	4.04	12.48	8.58	8.16	10.17
Heritability		0.638	0.540	0.379	0.193	0.634	0.415	0.361	0.576
UEM-Co2									
Families	168	31.2*	26.0*	22.7*	17.6*	1.98 ^{E+5*}	1.70 ^{E+5*}	1.42 ^{E+6*}	1.97 ^{E+5*}
Blocks/Replications	24	11.3	5.5	15.7	52.5	0.96 ^{E+5}	1.22 ^{E+5}	4.83 ^{E+5}	4.22 ^{E+5}
Replications	1	0.1	1.1	4.3	3.6	0.73 ^{E+5}	1.70 ^{E+5}	3.42 ^{E+4}	1.96 ^{E+5}
Error	144	7.7	6.2	9.0	14.2	6.00 ^{E+4}	9.84 ^{E+4}	8.31 ^{E+4}	8.78 ^{E+4}
Mean		22.8	28.2	33.3	33.9	2.18 ^{E+3}	2.63 ^{E+3}	2.87 ^{E+3}	3.10 ^{E+3}
CVe		12.17	8.83	9.01	11.12	11.26	11.92	10.04	9.56
CVg		15.04	11.10	7.87	3.86	12.06	7.20	12.54	7.53
Heritability		0.750	0.762	0.606	0.194	0.697	0.422	0.757	0.554

*Significant at 5% probability; C₀, C₁, C₂, and C₃, indicating the recurrent selection cycles, 0, 1, 2, and 3, respectively

Table 2. Genetic gains estimated by selection indices and truncation selection for grain yield (GY) and popping expansion (PE) in four cycles of the composite *UEM-Co1* with yellow popcorn grain

Selection indices and truncation selection [†]	Estimated genetic gains									
	C ₀		C ₁		C ₂		C ₃			
	GY	PE	GY	PE	GY	PE	GY	PE	GY	PE
Truncated for GY	14.2	1.9	7.9	2.1	7.1	0.4	11.3	0.1		
Truncated for PE	-0.1	11.1	0.9	8.0	-0.8	5.3	-0.9	2.4		
SH _{CVg}	14.1	1.0	7.9	2.2	6.9	-1.3	11.1	-0.3		
SH _{350.1}	4.2	10.8	3.0	7.7	1.7	5.1	8.2	2.0		
SH _{1.1}	14.1	1.0	7.9	2.2	6.9	-1.3	11.1	-0.3		
W _{CVg}	14.2	1.9	7.9	2.1	7.1	0.4	11.3	0.1		
W _{350.1}	5.7	9.8	3.6	7.8	2.6	5.0	5.4	2.3		
W _{1.1}	14.2	1.9	7.9	2.1	7.1	0.4	11.3	0.1		
MM _{CVg}	11.5	6.9	6.1	5.5	5.2	3.8	10.0	1.4		
MM _{350.1}	2.0	10.3	0.9	8.0	0.2	5.2	0.1	2.4		
MM _{1.1}	9.9	7.9	6.0	5.5	5.0	3.9	8.2	1.8		
Cunn _{CVg}	13.4	4.9	7.4	4.2	1.7	5.1	11.2	0.5		
Cunn _{350.1}	10.3	2.0	-0.4	7.8	6.9	2.0	1.9	2.4		
Cunn _{1.1}	13.0	5.6	7.4	4.2	6.9	2.0	10.8	1.1		
Tallis _{CVg}	10.9	7.7	6.5	5.7	5.3	3.9	7.2	2.1		
Tallis _{350.1}	10.9	7.7	6.5	5.7	5.3	3.9	7.2	2.1		
Tallis _{1.1}	10.9	7.7	6.5	5.7	5.3	3.9	7.2	2.1		
PB _{1-DPG}	10.9	7.3	5.5	5.7	5.3	3.9	7.2	2.1		
Sub	11.7	6.9	6.7	5.5	5.6	3.7	9.6	1.6		

[†]SH_{CVg}, SH_{350.1}, SH_{1.1}: indices based on Smith (1936) and Hazel (1943); W_{CVg}, W_{350.1}, W_{1.1}: indices of Williams (1962); MM_{CVg}, MM_{350.1}, MM_{1.1}: indices based on the sum of "ranks" of Mulamba and Mock (1978); Cunn_{CVg}, Cunn_{350.1}, Cunn_{1.1}: restricted index of Cunningham et al. (1970); Tallis_{CVg}, Tallis_{350.1}, Tallis_{1.1}: restricted selection index of Tallis (1962); PB_{1-DPG}: index proposed by Pesek and Baker (1969) based on a genetic standard deviation as desired genetic gain; Sub: multiplicative index of Subandi et al. (1973); the following economic weights were tested: CVg 350 for PE; 1 for GY; and 1 for both (GY and PE).

higher for both traits, this direct selection strategy - also called truncated - is inadequate for satisfactory simultaneous genetic gains for two or more traits, as in the case of PE and GY, which are occasionally negatively correlated as well (Pacheco et al. 1998, Carpentieri-Pipolo et al. 2002, Daros et al. 2004b, Faria et al. 2008).

With regard to the applied selection indices, in a first analysis, the classical index of Smith and Hazel (1936, 1943) and that of Williams (1962) did not estimate balanced gains for both traits of the study populations (Table 2 and Table 3), suggesting limited applicability. Our results for the index of Williams (1962) confirmed those of Granate et al. (2002), who could find no advantage of using it. Other authors, however, reported different results. For example Daros et al. (2004a), when selecting families by the Smith and Hazel index, predicted relatively high genetic gains (17.8% for PE and 26.95% for GY). Similarly, Granate et al. (2002) found that this index allowed the prediction of higher gains for a larger number of characters, with joint gains of 9.14% for GY and PE. The results of the above authors differ from those in this study, since the Smith and Hazel index proved unsatisfactory for the prediction of genetic gains of the two main target traits in popcorn breeding (Tables 2 and 3). For both composites, the index of Tallis (1962), for all studied possibilities of economic weights, and that of Pesek and Baker (1969) using a genetic standard deviation as desired gain, estimated balanced genetic gains for GY and PE, except in cycle C₃ of composite UEM-Co1, with gains of 7.2% for GY and 2.1 for PE (Table 2). For composite UEM-Co2 in cycle C₃, however, genetic gains of 12.8% and 6.9% for GY and PE, respectively, were estimated by the Pesek and Baker method (Table 3). Good simultaneous gains were predicted by the index of Pesek and Baker (7.99% for GY, and 10.75% for PE), according to Freitas Junior et al. (2009), in an evaluation of 200 full-sib families in cycle C₄ of the popcorn population UENF-14. Other selection indices, as that of Mulamba and Mock, also estimated balanced gains for the selection cycles of both composites. For this the economic weights were determined as CVg and 1 for PE and 1 for GY, in cycle C₁ of composite UEM- Co1- (Table 2) and in C₀ of UEM-Co2 (Table 3). The use of this index was also effective in popcorn breeding of the germplasm studied by Vilarinho et al. (2003), Santos et al. (2007), Freitas Júnior et al. (2009), Amaral Júnior et al. (2010), Rangel et al. (2011), Ribeiro et al. (2012) and Freitas et al. (2014).

For the index of Subandi et al. (1973), the genetic gains estimated for composite UEM-Co1 in cycles C₀ to C₃ for GY ranged from 5.6% to 11.7%, and from 1.6% to 6.9% for PE. For UEM-Co2, genetic gains between 5.2% and 14.7% were estimated for GY and from 1.6% to 12.7% for PE (Tables 2 and 3).

Table 3. Genetic gains estimated by selection indices and truncation selection for grain yield (GY) and popping expansion (PE) in four cycles of the composite UEM-Co2 with yellow popcorn grain

Selection indices and truncation selection [†]	Estimated genetic gains							
	C ₀		C ₁		C ₂		C ₃	
	GY	PE	GY	PE	GY	PE	GY	PE
Truncada para GY	14.1	2.7	6.7	4.2	16.5	2.4	8.0	-0.1
Truncada para PE	0.2	18.2	0.2	13.6	1.4	8.6	-0.1	2.3
SH _{CVg}	14.1	2.4	6.7	4.6	16.5	2.4	7.8	-0.5
SH _{350.1}	4.0	16.3	0.9	13.5	11.5	7.3	4.2	2.1
SH _{1.1}	14.1	2.4	6.7	4.6	16.5	2.4	7.8	-0.5
W _{CVg}	14.1	3.0	6.7	4.2	16.5	2.4	8.0	0.2
W _{350.1}	4.0	16.3	2.4	13.0	10.3	7.6	3.7	2.2
W _{1.1}	14.1	3.0	6.7	4.2	16.5	2.4	8.0	0.2
MM _{CVg}	10.0	12.4	4.6	10.9	14.2	6.0	7.1	1.4
MM _{350.1}	0.9	16.4	0.2	13.6	8.2	4.1	-0.1	2.3
MM _{1.1}	10.7	11.9	5.1	9.7	12.9	6.5	5.5	1.8
Cunn _{CVg}	11.8	10.6	5.7	9.3	15.8	4.3	8.0	0.6
Cunn _{350.1}	0.6	16.4	-0.4	13.4	4.1	8.2	2.3	2.3
Cunn _{1.1}	12.8	9.1	6.1	7.9	14.7	5.8	7.8	1.0
Tallis _{CVg}	11.3	11.4	5.9	8.6	12.8	6.9	5.0	2.0
Tallis _{350.1}	11.3	11.4	5.9	8.6	12.8	6.9	5.0	2.0
Tallis _{1.1}	11.3	11.4	5.9	8.6	12.8	6.9	5.0	2.0
PB _{1-DPG}	11.3	11.4	5.9	8.6	12.3	6.9	5.0	2.0
Sub	10.1	12.7	5.2	10.1	14.7	5.8	6.7	1.6

[†]SH_{CVg}, SH_{350.1}, SH_{1.1}: indices based on Smith (1936) and Hazel (1943); W_{CVg}, W_{350.1}, W_{1.1}: indices of Williams (1962); MM_{CVg}, MM_{350.1}, MM_{1.1}: indices based on the sum of "ranks" of Mulamba and Mock (1978); Cunn_{CVg}, Cunn_{350.1}, Cunn_{1.1}: restricted index of Cunningham et al. (1970); Tallis_{CVg}, Tallis_{350.1}, Tallis_{1.1}: restricted selection index of Tallis (1962); PB_{1-DPG}: index proposed by Pesek and Baker (1969) based on a genetic standard deviation as desired genetic gain; Sub: multiplicative index of Subandi et al. (1973); the following economic weights were tested: CVg 350 for PE; 1 for GY; and 1 for both (GY and PE).

Table 4. Statistical value C_i calculated to compare the genetic gains estimated by selection indices in two popcorn populations

Indices	C_i^+		Mean
	<i>UEM-Co1</i>	<i>UEM-Co2</i>	
	GY-PE	GY-PE	
SH _{CVg}	12.33	13.78	13.05
SH _{350.1}	7.57	7.99	7.78
SH _{1.1}	12.33	13.78	13.05
W _{CVg}	9.36	12.79	11.07
W _{350.1}	6.77	7.49	7.13
W _{1.1}	9.36	12.79	11.07
MM _{CVg}	2.40	2.90	2.65
MM _{350.1}	17.28	16.79	17.03
MM _{1.1}	2.73	3.34	3.03
Cunn _{CVg}	5.48	4.25	4.86
Cunn _{350.1}	13.57	17.01	15.29
Cunn _{1.1}	3.72	4.48	4.10
Tallis _{CVg}	2.53	3.68	3.10
Tallis _{350.1}	2.53	3.68	3.10
Tallis _{1.1}	2.53	3.68	3.10
PB _{1-DPG}	2.66	3.80	3.23
Sub	2.16	2.78	2.47

[†] Low C_i values indicate that the selection indices estimate high and consistent genetic gains for traits GY and PE.

In an analysis of the results of all selection cycles (Table 1), different conditions of genetic variability and heritability were noted, which allowed an estimation of genetic gains by selection indices and thereafter the application of the new statistical value C_i . The C_i values for the different indices are listed in Table 4. For both composites, the lowest C_i values were observed for the methodology proposed by Subandi (*UEM-Co1* 2.16 and *UEM-Co2* 2.78). The second highest index was that of Mulamba and Mock, when using CVg as economic weight, with C_i values of 2.40 and 2.90 for *UEM-Co1* and *UEM-Co2*, respectively. These C_i values, derived from the mean of composites and cycles, suggest good results in the estimation of high and balanced genetic gains for both PE and GY by the indices of Subandi and of Mulamba and Mock (Table 4), suggesting that these would improve the selection responses, in magnitude as well as in the balance between the two traits, and are therefore recommended for popcorn breeding. Among the multiplicative and restrictive indices, the indices of Subandi (multiplicative) and Tallis (restricted) achieved good results and allowed favorable genetic gain estimates for GY and PE in popcorn.

The use of the statistical value C_i eliminates the subjectivity of choice of the best indices, because this statistical value, genetic gain estimated by an index for many traits, are easily summarized in a single C_i value, based on the improvement possibilities of the study population. This study is a non-exhaustive comparison of efficiency of selection indices in popcorn. In this context, other complementary studies are suggested, to address other crops and traits, testing the C_i value as a tool in new combinations of economic weights and selection indices that allow greater genetic progress.

CONCLUSIONS

The selection indices were effective to estimate the genetic gains of half-sib families, indicating that their application can lead to high and balanced genetic gains.

According to the statistical value C_i , the index of Subandi, followed by that of Mulamba and Mock, estimated high and better balanced genetic gains for grain yield and popping expansion.

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