Genetics and Molecular Research

Selection index based on the relative importance of traits and possibilities in breeding popcorn

R.A. Vieira[1], R. Rocha[1], C.A. Scapim[1], A.T. Amaral Júnior[2] and M. Vivas[2]

[1]Departmento de Agronomia, Universidade Estadual de Maringá, Maringá, PR, Brasil
[2]Laboratório de Melhoramento Genético Vegetal, Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brasil

Corresponding author: A.T. Amaral Júnior
E-mail: amaraljr@pq.cnpq.br

Genet. Mol. Res. 15 (2): gmr.15027719
Received September 23, 2015
Accepted November 6, 2015
Published April 26, 2016
DOI http://dx.doi.org/10.4238/gmr.15027719

ABSTRACT. One of the major difficulties faced by popcorn breeders is the negative correlation between popping expansion (PE) and grain yield (GY). It is necessary to overcome this difficulty to obtain promising genotypes. One helpful tool in this process is a selection index because it allows multiple features of interest to be selected. Thus, the present study proposes a new and comprehensive selection index applied in 169 half-sib families in *UEM-Co1* and *UEM-Co2* composites during two cycles of recurrent selection. An experiment was conducted in a 13 x 13 lattice square in the 2004/2005 and 2006/2007 crop years in Maringá, Paraná State, and PE and GY were evaluated. To calculate F_i statistics, the following relative importance (RI) assignments were used: 0.5 for both PE and GY, and 0.70 and 0.30 for PE and GY, respectively. Families were classified according to F_i values such that $F_i = 0$ indicated that genotypes met the average of those selected by direct selection, $F_i < 0$ indicated that genotypes fell below the average of those selected, and $Fi > 0$ indicated that genotypes exceeded the average of those selected. Thus, desirable values of F_i were positive, indicating that the selected families were higher than those families that would be selected by direct selection for both traits. Therefore, we concluded that the novel F_i statistic was satisfactory for family selection because simultaneous and higher gains for both traits in both composites were obtained.

Key words: *Zea mays*; Multi-trait selection; Popping expansion; Grain yield

INTRODUCTION

Popcorn breeding remains in beginning phases. However, as popcorn is grown in many diverse environments, research with the goal of developing varieties and hybrids adapted to different cultivation conditions is required to guarantee high productivity and grain quality (Vilarinho et al., 2003; Faria et al., 2008). Among common crop breeding methods, recurrent selection is often highlighted as it aims to increase the frequency of favorable alleles (Hallauer and Miranda Filho, 1988; Amaral Júnior et al., 2013). However, success in obtaining superior popcorn genotypes depends on previous knowledge of the negative correlation that exists between the two main traits of interest, popping expansion (PE) and grain yield (GY) (Zinsly and Machado, 1978; Dofing et al., 1991; Sawazaki, 1995; Pacheco et al., 1998; Coimbra et al., 2001; Vilarinho et al., 2003; Daros et al., 2004; Faria et al., 2008).

Selection indices have frequently been used for family selection in recurrent selection programs for various crops (Subandi et al., 1973; Rosielle and Frey, 1975; Sharma and Duveiller, 2003; Silva and Vieira, 2008; Sezegen and Carena, 2009; Silva et al., 2009; Heinz et al., 2012; Vivas et al., 2012; Vivas et al., 2013). Although selection indices (Smith, 1936; Hazel, 1943; Williams, 1962; Pešek and Baker, 1969; Mulamba and Mock, 1978) have been used successfully (Santos et al., 2007; Freitas Júnior et al., 2009; Amaral Júnior et al., 2010; Rangel et al., 2011; Ribeiro et al., 2012; Amaral Júnior et al., 2013), these indices contain some limitations. For this reason, novel indices have been suggested to overcome those limitations.

The selection index proposed by Smith (1936) is recognized as the most efficient for attaining maximum aggregate genetic gain especially in terms of economic return (St Martin et al., 1982; Baker, 1986; Wells and Kofoid, 1986). However, this index contains limitations, especially in the attribution of economic weight to each trait (Subandi et al., 1973; Suwantaradon et al., 1975; St Martin et al., 1982; Baker, 1986; Wells and Kofoid, 1986; Cerón-Rojas et al., 2006). This selection index was adapted to animal improvement by Hazel (1943). The application of these selection indices requires information regarding the economic value of each trait in addition to the genotypic and phenotypic covariances relating each pair of traits.

Williams (1962) proposed a base index which does not require estimates of phenotypic and genotypic variances and covariances. This index is established by the linear combination of average phenotypic values of traits weighted by their respective economic weights. This index was proposed as a method for avoiding interference of phenotypic and genotypic covariance matrix errors in the estimation of index coefficients (Cruz et al., 2014).

Pešek and Baker (1969) proposed the desired genetic gains index in which the economic weights of traits could be substituted by the genetic gains desired by the plant breeder for each trait, which are easily determined. The authors proposed this index to overcome the difficulties of accurately assigning economic weights to different traits (Cruz et al., 2014). Use of this index requires information on genotype averages along with phenotypic and genotypic variance and covariance matrices. The calculation of coefficients for use by this index is therefore possible without defining economic weights. This results in maximum genetic gain for each trait according to the relative importance (RI) assigned by the plant breeder in the specification of each desired gain, subject to restrictions resulting from the phenotypic and genotypic composition of the population. One criticism of constructing an index on desired gains is that secondary traits (for which breeding is less important) cannot be included to assist the genetic improvement of primary traits (Cruz et al., 2014).

The rank-summation index proposed by Mulamba and Mock (1978) is based on the sum of ranks and requires ranking genotypic materials for each trait in an order that favors breeding. Following ranking, a selection index is obtained by summing the ranks of the genetic materials associated with each trait (Cruz et al., 2014).

Other selection indices described in the literature may assist plant breeders in identifying superior progeny. Each index displays certain particularities in its calculations and, as such, application is generally laborious due to the need to assign adequate economic weights to each trait. This effort is required because certain traits may not be measurable or product prices may not be consistent with their markets. In addition, the majority of indices are statistically weighed, and single entries are ignored by plant breeders in their calculations.

Therefore, the development of more comprehensive methods that may be quickly applied quickly is suggested. These methods would allow determination of RI values for selected traits according to plant breeder preferences and would augment research studies. As such, the goal of the present study was to select popcorn half-sib families of *UEM-Co1* and *UEM-Co2* composites in two recurrent selection cycles using a novel and comprehensive multiple trait selection index.

MATERIAL AND METHODS

Two composite popcorn (*Zea mays* L.) populations (*UEM-Co1* and *UEM-Co2*) were evaluated during two selection cycles (C_0 and C_1). *UEM-Co1* displayed yellow grains and originated from eleven genotypes, whereas *UEM-Co2* exhibited white grains and originated from nine genotypes. Treatment evaluations were performed during the 2004/2005 and 2006/2007 harvests at the Experimental Farm of the State University of Maringá (Universidade Estadual de Maringá; UEM) located in the Iguatemi district of Maringá municipality in the northwest of the state of Paraná, Brazil.

A total of 169 half-sib families were tested in both selection cycles. Experiments were conducted in a 13 x 13 lattice square where each experimental unit consisted of a single 5-m row with row spacing of 0.9 m and 25 plants per unit after thinning. Fertilization was performed according to requirements previously established by soil analysis. The remaining crop management was performed according to technical recommendations for the cultivation of corn in southern Brazil.

Popping expansion (PE) and grain yield (GY) were measured. For measurement of PE, 30 g popcorn (containing 13% moisture) was removed from the central portion of the cobs and the grains were then popped using an electrical popcorn maker at 270°C for 2.5 min. The volume of expanded popcorn was measured in a 2 L graduated cylinder. PE was expressed in grams of popcorn per volume of popped popcorn (g/mL). For GY, values were corrected for 13% moisture and expressed as kg/ha.

Data for each selection cycle was analyzed using the program GENES (Cruz, 2013). Intra-block analyses were performed using the following statistical model:

$$Y_{ijk} = m + g_i + b/r_{kj} + r_j + E_{ijk} \qquad \text{Equation 1}$$

where i^{th} = half-sib family located at the k^{th} block from the j^{th} replicate; Y_{ijk} = observation of each half-sib family; m = experimental average; g_i = effect of each half-sib family; b/r_{kj} = effect of the k^{th} block from the j^{th} replicate; r_j = effect of r^{th} replicate of the experiment; and E_{ijk} = experimental error associated to Y_{ijk}. g_i and b/r_{kj} were adjusted for the analysis of variance. The effect of half-sib families (g_i) was considered a random effect. Heritability and variability (CVg) were estimated using the expected mean square in the analysis of variance. After obtaining average values for each selection cycle, the F_i statistic was calculated:

$$F_i = \sum_{j=1}^{J} 1000 \times \left(\frac{\frac{(Y_{ij} - Y_{selj})^2 \times \left(\frac{(Y_{ij} - Y_{selj})}{|Y_{ij} - Y_{selj}| + 1/1000000} \times \mathrm{DirSel} \right)}{2}}{Y_{\cdot j}^{\,2}} \right) \times \mathrm{RelImpj} \qquad \text{Equation 2}$$

where Yij = average value of the i^{th} family for trait j^{th}; Y_{selj} = average value of families, which would be selected by direct selection for j^{th} traits for the specific selection rate; $Y_{\cdot j}$ = overall average for trait j^{th}; *DirSel* = direction of selection (1 for desirable traits, e.g., GY, and -1 for undesirable traits, e.g., plant height); and *RelImp* = RI of the j^{th} trait varying between 0.01 and 0.99, where the sum should always equal 1. In the present study, two sets of RI values were tested: 0.5 for both PE and GY in the first set and 0.70 for PE and 0.30 for GY in the second set.

Large values are desired when using F_i as a selection index. Positive genetic values for a given trait indicate that families are superior to the average of the remaining families that would be selected by direct selection, whereas families with highly negative F_i values have low genetic value. For the proposed selection index, average genetic values of the families that would be selected by direct selection for each trait represent possibilities for population breeding. Therefore, increased breeding possibilities for each trait result in greater restrictions imposed on the families that cannot reach that genetic value. In addition, the proposed index considers trait RI by entering a specific value for each trait included in the calculation. This value varies between 0.01 and 0.99 and is defined for each trait according to its importance as determined by the researcher. As previously mentioned, the sum of the weights selected for each trait should equal 1, as in the following examples: i) 0.50 for PE and GY, or ii) 0.65, 0.25, and 0.10 for GY, plant height, and oil content traits, respectively.

For the classification of half-sib families based on F_i values, the following was considered: $F_i = 0$ indicates that genotypes are within the average of genotypes selected by direct selection; $F_i < 0$ indicates that genotypes are genetically inferior to the average of selected genotypes, and $F_i > 0$ indicates that genotypes are genetically superior to the average of selected genotypes.

RESULTS AND DISCUSSION

Phenotypic values for PE and GY of the two popcorn composites in two recurrent selection cycles (C_0 and C_1) are shown in Table 1. Both traits increased upon selection. Similar observations were reported by Rangel et al. (2011), who found genetic variability in future cycles at the fifth cycle of intrapopulation recurrent selection in a population of full-sib popcorn families that included the traits studied in the present study.

Table 1. Average, maximum, and minimum values of popping expansion (PE) and grain yield (GY) for popcorn composites *UEM-Co1* and *UEM-Co2* in two recurrent selection cycles.

Family	PE (mL/g)		GY (kg/ha)	
	C_0*	C_1	C_0	C_1
UEM-Co1				
Maximum	38	39	2.913	3.274
Minimum	18	20	1.088	1.286
Average	30	31	1.967	2.167
UEM-Co2				
Maximum	31	38	3.093	3.763
Minimum	11	17	1.349	1.739
Average	23	29	2.176	2.631

*C0 and C1 represent the 0 and 1 cycles of recurrent selection, respectively.

Significant differences were observed ($P < 0.05$) among the 169 families tested for both composites and selection cycles (C_0 and C_1) (Table 2). High percentages of heritability for the studied traits were also observed, and gains could be obtained over the two selection cycles. For *UEM-Co1*, the highest percentages of heritability were observed in cycle C_0 (64% for PE and 63% for GY) whereas lower percentages were found in cycle C_1 for both traits (54% for PE and 42% for GY). For *UEM-Co2*, high values of heritability in cycle C_0 were observed for both traits (75% for PE and 70% for GY). The highest heritability for PE (76%) was observed in cycle C_1, which compares favorably to observations of the *UEM-Co1* composite. GY heritability in cycle C_1 was 42%. Arnhold et al. (2009) observed higher values for PE than GY which was partly in agreement with the present study as GY heritability decreased from cycle C_0 to C_1 for both composites.

Table 2. Analysis of variance (ANOVA) for popping expansion (PE) and grain yield (GY) for two popcorn populations under two recurrent selection cycles and for two popcorn composites.

Source of variation	GL	Mean squares			
		PE (mL/g)		GY (kg/ha)	
		C_0	C_1	C_0	C_1
UEM-Co1					
Family	168	27.3*	22.3*	1.90^{E+5}*	1.67^{E+5}*
Block / Replications	24	9.50	10.8	0.89^{E+5}	1.26^{E+5}
Replications	1	18.9	10.0	2.52^{E+5}	7.34^{E+6}
Error	144	9.9	10.3	7.00^{E+4}	9.70^{E+4}
CVg		9.96	8.02	12.48	8.58
Heritability		0.638	0.540	0.634	0.415
UEM-Co2					
Family	168	31.2*	26.0*	1.98^{E+5}*	1.70^{E+5}*
Block / Replications	24	11.3	5.5	0.96^{E+5}	1.22^{E+5}
Replications	1	0.1	1.1	0.73^{E+5}	1.70^{E+5}
Error	144	7.7	6.2	6.00^{E+4}	9.84^{E+4}
CVg		15.04	11.10	12.06	7.20
Heritability		0.750	0.762	0.697	0.422

*Significant at 5% probability. +C0 and C1 correspond to the 0 and 1 cycles of recurrent selection, respectively.

PE values obtained in the present study were comparable to those reported by Pacheco et al. (1998) (60%) and Coimbra et al. (2001) (61%). Faria et al. (2008) observed 60 and 46% PE heritability for S_0 x S_0 hybrids using a hot air popcorn maker and a metric weight volume tester, respectively, along with a value of 20% for S_1 x S_1 hybrids using a hot air popcorn maker. Arnhold et al. (2009) observed higher heritability for PE than GY at three sites with values of 74, 85 and 67% for PE and 62, 53, and 48% for GY. The distinct behavior observed in the two main popcorn traits indicates that PE is less influenced by environmental and dominance deviation than GY, which may result in higher association between performance *per se* and in crossing (Arnhold et al., 2009).

Average values of the 169 popcorn half-sib families and the average of families selected by truncation selection with 20% selection intensity (34 families) are shown in Table 3. Although obtained values were high for both traits, the direct selection strategy is not efficient for breeding when the goal is to obtain simultaneous satisfactory genetic gains for various traits, as is the case with PE and GY, which are negatively correlated (Pacheco et al., 1998; Daros et al., 2004; Faria et al., 2008). This situation is undesirable in popcorn breeding because these traits are fundamental for the acceptance of new materials by both farmers and end consumers. This is in accordance with Scapim et al. (2002), who stated that the farmer is interested in high productivity and the remaining attributes of a good population of normal corn, whereas the consumer is interested in high PE, which results in better texture and softness of popcorn.

Table 3. Averages of the 169 popcorn half-sib families and averages of the families selected using direct selection for PE and GY.

Population	PE^{+}	GY^{+}	PE^{++}	GY^{++}
UEM-Co1/ Cycle C_0	30	1.967	34	2.406
UEM-Co1/ Cycle C_1	30	2.166	35	2.577
UEM-Co2/ Cycle C_0	23	2.176	28	2.614
UEM-Co2/ Cycle C_1	28	2.631	33	3.050

$^{+}$Overall average of half-sib families; $^{++}$average selected by direct selection for a selection intensity of 20% families. RG and EC were expressed in ml/g and kg/ha, respectively.

F_i values for the 169 families of the *UEM-Co1* composite for cycle C_0 and the two sets of RI values tested (0.5 for both traits; and 0.7 and 0.3 for PE and GY, respectively) are shown in Table 4. Seven families of the 169 tested for the population *UEM-Co1* in cycle C_0 with 0.5 RI for both traits exhibited positive F_i, indicating that these families were generally superior to the average of families selected by direct selection (Table 3) for both traits (Table 4).

Table 4. *Fi* statistic for the best half-sib families of the *UEM-Co1* population for cycle C_0 using two different sets of relative importance (RI) values.

Family	Trait		RI	
	PE (mL/g)	GY (kg/ha)	0.5 - 0.5	0.7-0.3
36	32	2.913	14.25	6.63
162	32	2.791	7.97	3.47
72	38	2.318	3.19	4.88
39	37	2.416	1.94	2.70
30	37	2.376	1.87	2.67
13	34	2.580	1.72	0.85
67	34	2.503	0.38	0.04

RI = values assigned to PE and GY, respectively, were obtained from these values for the *Fi* statistic.

When an equal RI was considered for both traits, the highest F_i value (14.25) was observed for family 36. This family also stood out when RI values of 0.7 for PE and 0.3 for GY were considered, with $F_i = 6.63$. F_i decreased when more importance was attributed to PE (Table 4) because it had a lower value than the average of the families selected by direct selection (Table 3) (family average of 32 g/mL and direct selection average of 34 g/mL). However, F_i was not negative because this trait was anchored by GY (2913 kg/ha), which exhibited values higher than the average of the genotypes selected by direct selection in this family (2406 kg/ha) (Table 3). Conversely, an increase in F_i was observed for family 72 (Table 4) when RI values of 0.7 and 0.3 were considered for PE and GY, respectively, because this family exhibited high PE values (38 mL/mL) and GY values close to the average of the genotypes selected by truncation selection (2318 kg/ha GY for the family and 2,406 kg/ha for direct selection) (Table 3).

Use of F_i allowed the identification of promising families for both traits of interest simultaneously which differed from truncation selection where only one trait is considered at a time. This conclusion can be generalized to the two composites and selection cycles (Tables 4, 5, 6, and 7). The information obtained from F_i is valuable for the plant breeder because it indicates the families with the best trait values to be used in popcorn breeding programs.

Table 5. *Fi* statistics for the best half-sib families of the *UEM-Co1* population for cycle C_1 using two different sets of relative importance (RI) values.

Family	Trait		RI	
	PE (mL/g)	GY (kg/ha)	0.5-0.5	0.7-0.3
8	32	3.274	23.38	11.99
162	34	3.054	11.47	6.36
72	39	2.616	4.17	5.78
30	38	2.501	2.65	3.96
13	36	2.719	1.29	0.95
136	35	2.709	0.92	0.55

RI = values assigned to PE and GY, respectively, were obtained from these values for the *Fi* statistic.

Table 6. *Fi* statistics for the best half-sib families of the *UEM-Co2* population for cycle C_0 using two different sets of relative importance (RI) values.

Family	Trait		RI	
	PE (mL/g)	GY (kg/ha)	0.5-0.5	0.7-0.3
36	30	3.023	10.50	7.66
162	26	3.093	10.05	4.41
72	31	2.665	5.07	6.99
30	30	2.567	2.84	4.08
39	30	2.510	0.84	1.63

RI = assigned values for PE and GY, respectively, were obtained from these values for the *Fi* statistic.

F_i of the 169 half-sib families of the *UEM-Co1* composite for cycle C_1 and the two sets of RI values tested are shown in Table 5. The use of F_i allowed the identification of the most promising families. Family eight exhibited the best values for both sets of RI values. F_i was 23.38 using 0.5 RI for both PE and GY, and was 11.99 using 0.7 RI for PE and 0.3 RI for GY. The high F_i value in this family was due to its high GY, which was 21% higher than the average of the families selected by direct selection (Table 3). However, its PE value was not much lower than the average of families selected using truncation selection (Table 3). In contrast with what was observed for family nine, families 72 and 30 exhibited an increase in F_i (5.78 and 3.96, respectively) when using an RI of 0.7 and 0.3, which was due to PE being high as compared to direct selection. Increases of 10 and 8% were observed for families 72 and 30, respectively, as compared to the average for families selected using direct selection (Table 3). In addition, GY of these families was close to the average of the selected genotypes, which contributed to the F_i values observed (Table 5).

Table 7. *Fi* statistics for the best half-sib families of the UEM-Co2 population for cycle C_1 using two different sets of relative importance (RI) values.

Family	Trait		RI	
	PE (mL/g)	GY (kg/ha)	0.5-0.5	0.7-0.3
8	30	3.763	13.86	4.68
162	31	3.544	6.35	1.84
30	38	2.997	5.45	7.70
72	37	3.070	3.23	4.52
20	37	2.967	2.97	4.36
13	34	3.208	0.92	0.56
36	35	2.971	0.69	1.14
17	35	3.024	0.43	0.62
67	33	3.120	0.15	0.07

RI = assigned values for PE and GY, respectively, were obtained from these values for the *Fi* statistic.

Families 36 and 162 were the two best families when 0.5 RI was considered for cycle C_0 and composite *UEM-Co2* with F_i values of 10.5 and 10.05, respectively (Table 6), which was indicated by the high GY values for both families. Family 36 also displayed a higher F_i value (7.66) than the remaining families of its composite population when RI values of 0.7 and 0.3 were used. This result occurred because, in addition to displaying a high productivity (3,023 kg/ha), family 36 exhibited an average PE (30 g/mL) above the average of the families selected using truncation selection (Table 3). For family 162, 3093 kg/ha GY and 26 g/mL PE were observed with GY being 16% higher than the selected genotypes using direct selection (2614 kg/ha) (Table 3). This result showed the limitations of truncation/direct selection in popcorn breeding due to several factors, including the negative correlation between PE and GY. Selection based on only one of these traits may result in undesirable changes in the other (Vilarinho et al., 2003). Arnhold et al. (2009) found higher estimated correlations for PE than for GY because PE is less influenced by the environment and non-additive genetic factors.

Similar results to those found in the present study regarding the direct selection of traits have been previously reported (Vilarinho et al., 2003; Daros et al., 2004; Rangel et al., 2007; Santos et al., 2007; Vieira et al., 2009). To avoid direct selection, Freitas Júnior et al. (2009) suggested the use of selection indices where the statistical efficiency outweighs the negative correlation, thus allowing selection of productive progeny and those with high popping quality in recurrent selection programs, which was in accordance with the present results of selection using the novel F_i index.

F_i values of the 169 half-sib families of the *UEM-Co2* composite for cycle C_1 are shown in Table 7. Family eight was the most promising using both tested RI sets with F_i values of 13.86 and 4.68. This family exhibited elevated GY potential with an average of 3736 kg/ha, which was 19% higher than the average of families selected using direct selection (Table 3). The decrease in the F_i value when 0.7 and 0.3 RI values were used was supported as this family displayed lower PE than the average for the selected families (Table 3). However, this value was not negative due to high productivity and to the fact that the PE was not tangibly lower than the average of selected families (Table 3). Therefore, it can be concluded that this family is the best indicated of all the 169 study families for use in recurrent selection breeding programs. When greater importance was given to PE, family 72 also emerged as a family of interest due to its F_i value of 4.52. Family 72 displayed slightly higher productivity than the average of the selected families and had an 11% higher PE than the average for families chosen using direct selection (Table 3). This result showed that use of the F_i statistic is effective for the selection of half-sib families because it resulted in higher gains than truncation selection of the two main popcorn traits.

The use of the F_i index exhibited good results in terms of obtaining high values for the two traits simultaneously. The efficiency of the statistic proposed in the present study was indicated by the fact that individual trait averages for families selected using this index were higher than averages for families selected using direct selection (Table 3) for PE and for GY on both tested composites and cycles (Tables 4, 5, 6, and 7). In support of this conclusion, Cruz et al. (2014) noted that comparisons with direct selection indicate that the use of indices as selection criteria has better results. In general, the gain for a given trait decreases but that decrease is compensated for by a better distribution of favorable gains in the remaining traits.

The results of the present study indicate that the F_i statistic is useful for the identification of promising families to be used in recurrent selection programs in popcorn breeding. In addition, the F_i index can be applied to selection processes where a balance is sought between genetic gain of traits with agronomic and commercial interest, which is the case of popcorn as it exhibits a negative correlation between GY and PE. This index can be easily applied to other crops with the goal of obtaining superior families with high genetic gains for more than one trait.

Conflicts of interest

The authors declare no conflict of interest.

REFERENCES

Amaral Júnior AT, Freitas Júnior SP, Rangel RM, Pena GF, et al. (2010). Improvement of a popcorn population using selection indexes from a fourth cycle of recurrent selection program carried out in two different environments. *Genet. Mol. Res.* 9: 340-347. http://dx.doi.org/10.4238/vol9-1gmr702

Amaral Júnior AT, Azeredo Gonçalves LS, Freitas Júnior SP, Candido LS, et al. (2013). UENF 14: a new popcorn cultivar. *Crop Breed. Appl. Biotechnol.* 13: 218-220.

Arnhold E, Viana JMS and Silva RG (2009). Associação de desempenho entre famílias S3 e seus híbridos topcross de milho-pipoca. *Rev. Ciênc. Agron.* 40: 396-399.

Baker R (1986). Selection indices in plant breeding. CRC Press, Boca Raton.

Cerón-Rojas JJ, Crossa J, Sahagún-Castellanos J, Castillo-González F, et al. (2006). A selection index method based on eigenanalysis. *Crop Sci.* 46: 1711-1721. http://dx.doi.org/10.2135/cropsci2005.11-0420

Coimbra RR, Miranda GV, Viana JMS and Cruz CD (2001). Correlações entre caracteres na população de milho-pipoca DFT 1-Ribeirão. *Rev. Ceres* 48: 427-435.

Cruz CD (2013). GENES - a software package for analysis in experimental statistics and quantitative genetics. *Acta Sci. Agron.* 35: 271-276. http://dx.doi.org/10.4025/actasciagron.v35i3.21251

Cruz CD, Carneiro PCS and Regazzi AJ (2014). Modelos biométricos aplicados ao melhoramento genético. Viçosa, MG: Editora UFV.

Daros M, Amaral Júnior AT, Pereira MG, Santos FS, et al. (2004). Correlações entre caracteres agronômicos em dois ciclos de seleção recorrente em milho-pipoca. *Cienc. Rural* 34: 1389-1394. http://dx.doi.org/10.1590/S0103-84782004000500010

Dofing SM, ĎCroz-Mason N and Thomas-Compton MA (1991). Inheritance of expansion volume and yield in two popcorn ✖ dent corn crosses. *Crop Sci.* 31: 715-718. http://dx.doi.org/10.2135/cropsci1991.0011183X003100030035x

Faria VR, Viana JMS, Sobreira FM and Silva AC (2008). Seleção recorrente recíproca na obtenção de híbridos interpopulacionais de milho-pipoca. *Pesquisa Agropecu. Bras.* 43: 1749-1755. http://dx.doi.org/10.1590/S0100-204X2008001200015

Freitas Júnior SP, Amaral Júnior AT, Rangel RM and Viana AP (2009). Predição de ganhos genéticos na população de milho pipoca UNB-2U sob seleção recorrente utilizando-se diferentes índices de seleção. *Semin.: Ciênc. Agrár.* 30: 803-814.

Hallauer AR and Miranda Filho JB (1988). Quantitative genetics in maize breeding. 2edn. Iowa State University Press, Ames.

Hazel LN (1943). The genetic basis for constructing selection indexes. *Genetics* 28: 476-490.

Heinz R, Mota LHS, Gonçalves MC, Viegas Neto AL, et al. (2012). Seleção de progênies de meio-irmãos de milho para eficiência no uso de nitrogênio. *Rev. Ciênc. Agron.* 43: 731-739.

St Martin SK, Loesch PJ, Demopulos-Rodriguez JT and Wiser WJ (1982). Selection indices for the improvement of opaque-2 maize. *Crop Sci.* 22: 478-485. http://dx.doi.org/10.2135/cropsci1982.0011183X002200030010x

Mulamba NN and Mock JJ (1978). Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. *Egypt. J. Genet. Cytol.* 7: 40-51.

Pacheco CAP, Gama EEG, Guimarães PEO, Santos MX, et al. (1998). Estimativas de parâmetros genéticos nas populações CMS-42 e CMS-43 de milho pipoca. *Pesquisa Agropecu. Bras.* 33: 1995-2001.

Pešek J and Baker RJ (1969). Desired improvement in relation to selection indices. *Can. J. Plant Sci.* 49: 803-804. http://dx.doi.org/10.4141/cjps69-137

Rangel RM, Amaral Júnior AT, Viana AP, Freitas Júnior SP, et al. (2007). Prediction of popcorn hybrid and composite means. *Crop Breed. Appl. Biotechnol.* 7: 287-295. http://dx.doi.org/10.12702/1984-7033.v07n03a08

Rangel RM, Amaral Júnior AT, Gonçalves LSA, Freitas Júnior SP, et al. (2011). Análise biométrica de ganhos por seleção em população de milho pipoca de quinto ciclo de seleção recorrente. *Rev. Ciênc. Agron.* 42: 473-481.

Ribeiro RM, do Amaral Júnior AT, Gonçalves LSA, Candido LS, et al. (2012). Genetic progress in the UNB-2U population of popcorn under recurrent selection in Rio de Janeiro, Brazil. *Genet. Mol. Res.* 11: 1417-1423. http://dx.doi.org/10.4238/2012.May.15.12

Rosielle AA and Frey KJ (1975). Application of restricted selection indices for grain yield improvement in oats. *Crop Sci.* 15: 544-547. http://dx.doi.org/10.2135/cropsci1975.0011183X001500040028x

Santos FS, Amaral Júnior AT, Freitas Júnior SP, Rangel RM, et al. (2007). Predição de ganhos genéticos por índices de seleção na população de milho pipoca UNB-2U sob seleção. *Bragantia* 66: 389-396. http://dx.doi.org/10.1590/S0006-87052007000300004

Sawazaki E (1995). Melhoramento do milho pipoca. Instituto Agronômico de Campinas, Campinas.

Scapim CA, Pacheco CAP, Tonet A, Braccini AL, et al. (2002). Análise dialélica e heterose de populações de milho-pipoca. *Bragantia* 61: 219-230. http://dx.doi.org/10.1590/S0006-87052002000300003

Sezegen B and Carena MJ (2009). Divergent recurrent selection for cold tolerance in two improved maize populations. *Euphytica* 167: 237-244. http://dx.doi.org/10.1007/s10681-008-9875-2

Sharma RC and Duveiller E (2003). Selection index for improving Helminthosporium leaf blight resistance, maturity, and kernel weight in spring wheat. *Crop Sci.* 43: 2031-2036. http://dx.doi.org/10.2135/cropsci2003.2031

Silva GO and Vieira JV (2008). Componentes genéticos e fenotípicos para caracteres de importância agronômica em população de cenoura sob seleção recorrente. *Hortic. Bras.* 26: 481-485. http://dx.doi.org/10.1590/S0102-05362008000400011

Silva MGM, Viana AP, Gonçalves GM, Amaral AT Junior., et al. (2009). Seleção recorrente intrapopulacional no maracujazeiro amarelo: alternativa de capitalização de ganhos genéticos. *Cienc. Agrotec.* 33: 170-176. http://dx.doi.org/10.1590/S1413-70542009000100024

Smith HF (1936). A discriminant function for plant selection. *Ann. Eugen.* 7: 240-250. http://dx.doi.org/10.1111/j.1469-1809.1936.tb02143.x

Subandi WA, Compton A and Empig LT (1973). Comparison of the efficiencies of selection indices for three traits in two variety crosses of corn. *Crop Sci.* 13: 184-186.

Suwantaradon K, Eberhart SA, Mock JJ, Owens JC, et al. (1975). Index selection for several agronomic traits in the BSSS2 maize population. *Crop Sci.* 15: 827-833. http://dx.doi.org/10.2135/cropsci1975.0011183X001500060025x

Vieira RA, Souza Neto IL, Bignotto LS, Cruz CD, et al. (2009). Heterotic parametrization for economically important traits in popcorn. *Acta Sci. Agron.* 31: 411-419.

Vilarinho AA, Viana JMS, dos Santos JF and Câmara TMM (2003). Eficiência da seleção de progênies S_1 e S_2 de milho-pipoca, visando à produção de linhagens. *Bragantia* 62: 9-17. http://dx.doi.org/10.1590/S0006-87052003000100002

Vivas M, da Silveira SF and Pereira MG (2012). Prediction of genetic gain from selection indices for disease resistance in papaya hybrids. *Rev. Ceres* 59: 781-786. http://dx.doi.org/10.1590/S0034-737X2012000600007

Vivas M, da Silveira SF, Vivas JMS and Pereira MG (2013). Predição de ganhos genéticos e seleção de progênies de mamoeiro para resistência à pinta-preta. *Trop. Plant Pathol.* 38: 142-148. http://dx.doi.org/10.1590/S1982-56762013000200008

Wells WC and Kofoid KD (1986). Selection indices to improve an intermating population of spring wheat. *Crop Sci.* 26: 1104-1109. http://dx.doi.org/10.2135/cropsci1986.0011183X002600060003x

Williams JS (1962). The evaluation of a selection index. *Biometrics* 18: 375-393. http://dx.doi.org/10.2307/2527479

Zinsly JR and Machado JA (1978). Milho-pipoca. In: Melhoramento e produção de milho no Brasil (Paterniani E, ed.). Fundação Cargill, Piracicaba, 339-348.

