Vol. 14(17), pp. 787-793, 25 April, 2019
DOI: 10.5897/AJAR2015.10696
Article Number: 7B6AB8E60749
ISSN: 1991-637X
Copyright ©2019
Author(s) retain the copyright of this article
http://www.academicjournals.org/AJAR

African Journal of Agricultural Research

Full Length Research Paper

Prediction of genetic gain using selection indices in maize lines

Silviane de Santiago[1*], Claudio Lopes de Souza Junior [2], Leandro Borges Lemos [1] and Gustavo Vitti Môro[1]

[1]Departament of Vegetal Production, Paulista State University, UNESP – Jaboticabal/SP, Brazil.
[2]Departament of Genetic, University of São Paulo" – ESALQ/USP, Piracicaba/SP, Brazil.

Received 30 November, 2015; Accepted 4 January, 2019

Maize is an important cereal crop in scientific research area and the world economy, where Brazil is one of the leading producers. High production and productivity are partly due to plant breeding programs, where the selection of superior genotypes is based on indexes. This strategy has been very efficient o obtaining superior genotypes since there are simultaneous gains for various agronomic and economic characters. The aim of the research was to measure genetic gain through inbred selection based on the selection index, as well to compare the efficiency of the different index in order to verify which one is more recommended to a phenotypic selection of maize inbreeds. To achieve this, 256 inbreeds were experimentally evaluated in 12 environments. The characters evaluated were grain yield, fecundity, lodging and breaking plant, plant height, ear height, relative position of the ear, male and female flowering and the flowering interval. Selection intensities of 10 and 20% were applied in the direct selection in seven study indexes. The analysis showed that the direct selection of the characters was not effective for the selection of superior maize genotypes. and the Smith and Hazel's index and Williams's index got higher gains yield for the genotypes evaluated.

Key words: direct selection, obtaining hybrids, pure lines, *Zea may* L.

INTRODUCTION

Maize is an important food crop in the world economy and in scientific research. It is grown worldwide and serves as a food source for human beings and animals as well as a raw material for industry (Embrapa, 2015).

According to Conab (2018), the grain production of the Brazilian 2017-2018 crop is estimated at around 87 million of tons, ranking the country in third place for world maize production, ranked only behind the USA and China. The current mean Brazilian productivity is higher than 5,000 kg ha^{-1}, compared to around 3,500 kg ha^{-1} for 10 years ago. This increase has been driven by research in various areas, principally with hybrids. Plant genetic improvement is the most valuable strategy for a sustainable and ecologically balanced increase in production and productivity, combined with the best cultural practices, involving suitable management, fertilizer application and irrigation (Borém and Miranda, 2005). Among the main objectives of research institutions working with genetic improvement in maize is the development and recommendation of lines which are

---

*Corresponding author. E-mail: silvianesantiago@hotmail.com.

good parentes with specific characteristics between male or female in a certain environment and which result in lower costs for hybrid seed production. The selection of superior genotypes in breeding programs are based on index selections and not for each character separately. This strategy has been very efficient since that there are simultaneous gains for various important agronomic and economic characters. Selection indices function like an additional characters which is a result of the combination of various characteristics from which selection responses are desired (Santos et al., 2007), which allows the improvement of various characters simultaneously, independently of the existence or not of a correlation between them (Smith, 1936; Hazel, 1943; Williams, 1962; Cruz and Regazzi, 2001; Vilarinho et al., 2003).

The best selection index depends on the relative importance of the characters that have been considered, the type of material which is being selected and the objectives of the breeding program and, therefore, there can be changes over time. Thus, the most suitable index may be changed, and it is not possible to define the best general index. However, independently of the index under consideration, it is an objective method, which can determine the relative merit of a series of genotypes and thereby provide a basis for differentiating them (Carena, 2009). Therefore, the selection of inbred lines is based on an index can increase the efficiency of the selection process, permitting the selection of genotypes with agronomic standards closer to ideal genotypes (ideotypes) within a shorter space of time (Lande and Thompson, 1990). The aim of the present research was to compare the gains from selection in maize inbred lines considering different selection strategies and observing which one is the most efficient.

MATERIALS AND METHODS

The S1 maize lines were obtained from a crossing between the L14-04B and L08-05F lines, both of which were developed by the Department of Genetics of ESALQ (Escola Superior Luiz de Queiroz) of the University of São Paulo (USP). A random sample of 256 plants was taken from the F2 generation, sown in rows. The manual crossing by the SIB scheme (*Self in Brothers*) were made in each row to increase the quantity of available seeds. This resulted in obtaining 256 S1 progeny, which were evaluated at up to four sites per year between 2002/2003 and 2006/2007 in Piracicaba county in São Paulo state, creating 12 environments.

The experimental design was a simple 16 x 16 lattice, with the plots composed of 4 m of rows with 0.80 m between rows and 0.20 m between plants. Fifty seeds were distributed per plot and plants thinned out approximately 30 days after sowing, leaving approximately 20 plants per each plot. This sowing density corresponds to a mean population of 62,500 plants per hectare. The following data were collected for all plot plants evaluating male and female flowering, on days when 50% of the plants had produced the male and female inflorescences respectively; the stand, considering the number of plants per plot at harvest; lodging, considering the number of plants per plot with an angle of inclination greater than 30° compared to the vertical; breakage, considering the number of plants per plot broken off below the main ear; number of ears per plot; grain weight per plot and percentage grain humidity. Data on plant height and ear height, was measured at distance in centimeters from the soil to the flag leaf and up to the insertion of the first ear respectively, were collected for five plants per plot (Moro, 2011).

The statistical-genetic analyses were made on the following characters: grain production (PG) in t ha^{-1}, lodging and breakage (ACQ) in percentage of lodged plants, fecundity (PROL) in number of ears per plant, interval between flowering (IF) in days, male flowering (FM) in days, female flowering (FF) in days, relative position of the ear (PRE), plant height (AP) in cm and ear height (AE) in cm. The statistical-genetic analyses were carried out using the "PROC GLM" procedure of the SAS software (SAS Institute, 2012). First of all, an individual analysis of variance was made for each environment, according to the mathematical model for lattice experiments:

$$Yijk = m + Li + Rj + bk(j) + eijk,$$

were $Yijk$ is the observed value of lineage i in block k, within the repeat j; m is the overall mean of the experiment; L_i is the effect of strain i, with i ranging from 1 to 256; R_j is the effect of repetition j, with j being 1 or 2; $b_{k(j}$ is the effect of block k, hierarchical within the repetition j and e_{ijk} is the experimental error. After, the adjusted means obtained from the individual analysis, joint analysis of variance of the experiments were made and based on the mean squares of the joint analysis of variance the following the model $Yijk = m + Li + Rj + (LR)ij + eijk$ were Y_{ijk} is the observed value of lineage i in block k, within the environment j; m is the overall mean; L_i is the effect of the lineage i with i ranging from 1 to 256; R_j is the effect of the environment j; $(LR)_{ij}$ is the effect of the interaction of the lineage i with the environment j and e_{ijk} is the average effective error (Cochram and Cox, 1976).

The variance components for each character were estimated by the phenotypic variance for mean values ($\hat{\sigma}_F^2 = QM_L/A*R$), genotypic variance ($\hat{\sigma}_g^2 = (QM_L - QM_{GxE}/A*R$), variance of the genotype × environment interaction ($\hat{\sigma}^2_{GxE} = QM_{GxE}/A*R$), environmental variance ($\hat{\sigma}_E^2 = QM_e$) and coefficient of the herdability in the broad sense for mean values ($h^2 = \hat{\sigma}_g^2/ \hat{\sigma}_F^2$) were QM_L is the middle square of the lineages; A is the number of environments; R is the number of repetitions; QM_{GxA} is the middle square of the genotype x environment interaction and the QM_e is the middle square of the residue.

The correlation and covariance analyses were made to be used in calculating some selection indices. After obtaining the means, different selection indices for the lines were constructed using all the characters considered. The selection indices proposed by Cruz (2006); Elston (1963); Smith (1936); Hazel, (1943); Williams (1962); Pesek and Baker (1969); Mulamba and Mock (1978) and Subandi et al. (1973), were calculated. The selection indices and gains were calculated using the Genes Program (Cruz, 2006) and when the weighting coefficients and population parameters were not obtained directly, the values in Table 1 were used. Different selection indices were obtained for each line and after ranking, selection indices of 10 and 20% were applied, selecting the 26 and the 52 best lines respectively. The direct and indirect selection for each character was simulated by estimating the gains with different types of selection (Cruz and Regazzi, 1994).

RESULTS AND DISCUSSION

Significant differences ($p < 0.01$) were observed in the analysis of variance between lines and lines × environments for all the characters analyzed (Table 2). These differences demonstrate the genetic variability,

Table 1. Weighting and ki values to calculate the b coefficient, established for each selection index.

Selection Index	PG	ACQ	PROL	IF	FM	FF	PRE	AP	AE
Cruz (2006)	10%	-10%	8%	-7%	-7%	-7%	-7%	-8%	-7%
Elston (1963)	4.0	3.0	0.95	1.3	71	72	0.8	240	145
Mulamba and Mock (1978)	1	1	1	1	1	1	1	1	1
Pesek and Backer (1969)	10%	-10%	8%	-7%	-7%	-7%	-7%	-8%	-7%
Smith (1936) and Hazel (1943)	1.0	-1.0	0.8	-0.7	-0.7	-0.7	-0.7	-0.8	-0.7
Subandi et al (1973)	1.0	-1.0	0.8	-0.7	-0.7	-0.7	-0.7	-0.8	-0.7
Williams (1962)	1.0	-1.0	0.8	-0.7	-0.7	-0.7	-0.7	-0.8	-0.7

Table 2. Summary of analysis of variance

F V	GL	PG	ACQ	PROL	IF	FM	FF	PRE	AP	AE
A	11	1115.265 **	505.691 **	15.807 **	195.674 **	1590.314 **	1322.312 **	0.410 **	124183.478 **	68906.016 **
P	255	25.256 **	12.695 **	0.350 **	14.530 **	90.954 **	124.47 **	0.010 **	1928.633 **	959.429 **
QM P x A	2805	1.392 **	2.472 **	0.032 **	1.683 **	3.202 **	3.971 **	0.001 **	132.305 **	75.687 **
Effective error	2700	0.590	1.986	0.024	1.379	2.163	2.620	0.001	96.089	56.528
CV (%)	-	19.377	43.479	17.097	116.038	2.055	2.220	4.910	5.202	7.494
Mean	-	4.630	2.516	0.935	1.210	67.694	68.585	0.527	190.899	105.317

PG = production in tons per ha; ACQ = lodging and breakage in percentage of plants; PROL = fecundity in number of ears per plant; IF = interval between flowering in days; FM = male flowering in days; FF = female flowering in days; PRE = relative position of the ear; AP = plant height in cm; AE = ear height in cm; FV = Sources of Variation; GL = degrees of freedom; QM = mean square; A = Environment; P = Progeny; CV = Coefficient of Variation; ** Significant at the 1% level of probability by the F test, respectively.

essential for selection and difference in the development of lines in the experimental environments, indicating that the relative behavior of the lines was inconsistent between the different years. This same variability was observed by Garbuglio et al. (2007) when they evaluated 7 populations of maize lines in the S1 generation. The coefficients of variation for each character considered are within the ideal limits for this type of genotypes and characters (Hallauer and Miranda, 1988), making the data very reliable.

The principal function of heritability is its predictive role, which expresses the reliability of the phenotypic value in relation to the estimate of the genotypic value (Falconer, 1978). Thus, we can see that the values of the coefficient of heritability are satisfactory and above 80%, also including PG and ACQ which are the two main characters for plant breeders and farmers (Table 3). Values for genetic gain in percentage and unit of the characters for direct and indirect selection are shown in Table 4. Despite the high gains in direct selection, it should be remembered that these values were only obtained for the character in question and when the indirect response to the selection of each characteristic is analyzed, values which adversely affect the selection are apparent. An example is the direct selection for PG which shows a high gain for the character, but the ACQ also increases which is undesirable for breeding programs. These data show that the gains obtained from direct and indirect selections did not produce satisfactory combined results for the 9 characters evaluated. Similar findings obtained by Martins et al. (2006), concluded that direct and indirect selections were not efficient in distributing expected gains when the aim was to do a selection for a group of characters with

Table 3. Estimates of the components of variance.

Parameter	PG	ACQ	PROL	IF	FM	FF	PRE1	AP	AE
σ2G	0.994	0.426	0.013	0.535	3.656	5.021	0.36	74.847	36.823
σ2GxE	0.401	0.243	0.004	0.152	0.519	0.675	0.1	18.108	9.58
σ2F	1.052	0.529	0.015	0.605	3.79	5.186	0.397	80.36	39.976
σ2E	0.59	1.986	0.024	1.379	2.163	2.62	0.706	96.089	56.528
h2	0.945	0.805	0.909	0.884	0.965	0.968	0.905	0.931	0.921

PG = production in tons per ha; ACQ = lodging and breakage in percentage of plants; PROL = fecundity in number of ears per plant; IF = interval between flowering in days; FM = male flowering in days; FF = female flowering in days; PRE = relative position of the ear; AP = plant height in cm; AE = ear height in cm; G = genotypic variance; σ^2G_{xA} = variance of genotype x environment interaction; σ^2F = phenotypic variance; σ^2E = environmental variance; h = heritability coefficient; 1 The parameters: σ^2G σ^2G_{xA}, σ^2Fe σ^2E were multiplied by 1000 due to the low values.

negative and positive gains. Costa et al. (2004) also observed lower gains with direct and indirect selection in soybean lines when compared to other selection methods. Coimbra et al. (1999) achieved satisfactory gains with this type of selection in dry beans and Oliveira et al. (2008) with passion fruit since all the characters under study showed a favorable correlation. According to Falconer and Mackay (1996), indirect selection requires a very favorable correlation between the variable and the study variables as well as high heritability for the character to be selected.

The estimated genetic gains calculated using the index selection method with a selection intensity of 10 and 20% are shown in Table 5. Arnhold and Silva (2009) were positive results for the simultaneous selection of 3 characteristics in sweet corn genotypes were see using the index of Cruz (2006) and gains by Vasconcelos et al. (2010) were higher compared to other selection indices. According to Oliveira et al. (2008), even with high gains using direct selection, the distance genotype-ideotype index was more promising for the selection of superior genotypes. Rocha et al. (2012) oberved that simultaneous selection of 4 characters in *Jatropha curcas,* showed that this index produced a higher total gain and resulted in a more balanced change in the character means. However, despite positive results, the index used by Cruz (2006) did not show the best gains for the characters analyzed.

The index used by Elston gave the best gain for the IF character when compared to other indices. This character shows a high percentage gain due to its low absolute value and to the fact that this index apportions the same weight to all the characters, which may result in an undesirable distribution for line selection. However, Elston's selection index was unable to distribute gains in accordance with the aims established the selection of a single progeny of passion fruit. Martins et al. (2006) observed that the construction structure of the index, which establishes minimum values for selection, showed a tendency to increase characters associated with production in Eucalyptus. Oliveira et al. (2008) observed desired gains using the same index for the primary characters directly correlated with production in passion fruit.

Cruz et al. (1993) and Costa et al. (2004) achieved positive results superior gains with the index proposed by Mulamba and Mock (1978), using the indices of Mulamba and Mock in soybeans and maize respectively. Vilarinho et al. (2003) found that this index gave the best estimates of gains in sweet corn S1 and S2 progenies. Santos et al. (2007) also obtained satisfactory gains in maize with the selection index for families of half-siblings. The use of Mulamba and Mock's index allowed Rangel et al. (2011) to forecast simultaneous gains for the two main characteristics (production and expansion) associated with improvement in sweet corn. The index of Pesek and Backer (1969) showed the highest gain for the 10% selection intensity for the ACQ character compared to other indices. Bárbaro et al. (2007) did not obtain satisfactory results using this index for selecting a soybean genotype. Gonçalves et al., (2007) also observed similar results to Mulamba and Mock's index when selecting superior genotypes of yellow passion fruit. Smith and Hazel's index showed a satisfactory gain for the primary characters PG and ACQ and a superior gain for PG compared to other characters. The results were also satisfactory for the other characters, except for AP and AE, where the gain was positive. This result disagreed with that observed by Gonçalves et al., (2007), who found that Mulamba and Mock's index showed a superior gain, compared to the index of Smith (1936) and Hazel (1943). Paula et al. (2002) showed that Smith and Hazel's index is promising for the improvement of multiple characteristics and better than other selection criteria. Working with 166 families of half-siblings of sweet corn, Granate et al. (2002) obtained higher predicted gains with this same selection index. According to Ferreira et al. (2005), when this index was used for simultaneous selection with weightings obtained after various attempts and it allowed more suitable predicted gains to be estimated for the improvement of *C. canephora*.

Table 4. Estimates of genetic gains in units of the character and percentage using the direct (values diagonally in bold type) and indirect selection methods.

I S		PG	ACQ	PROL	IF	FM	FF	PRE1	AP	AE
	PG	**55.84**	11.71	19.24	-37.66	-4.81	-3.91	1.01	3.65	4.63
		-2.59	-0.29	-0.18	(-0.46)	(-3.25)	(-2.68)	-0.06	-6.98	-4.88
	ACQ	-7.09	**-65.76**	-4.48	-5.14	0.09	0	-2.1	-0.43	-2.6
		(-0.33)	**(-1.66)**	(-0.04)	(-0.06)	-0.06	0	(-0.12)	(-0.82)	(-2.74)
	PROL	39.92	3.59	**33.23**	-28.9	-3.67	-2.9	0.8	2.82	3.69
		-1.85	-0.09	**-0.31**	(-0.35)	(-2.48)	(-1.99)	-0.04	-5.38	-3.88
	IF	11.28	10.03	7.03	**-80.93**	-1.63	-1.88	-0.18	0.56	0.63
		-0.52	-0.25	-0.07	**(-0.98)**	(-1.11)	(-1.29)	(-0.01)	-1.07	-0.67
	FM	39.41	1.03	11.36	-35.32	**-6.47**	-4.86	-1.51	2.17	0.67
		-1.83	-0.03	-0.11	(-0.43)	**(-4.38)**	(-3.33)	(-0.08)	-4.14	-0.71
	FF	46.68	12.43	16.78	-56.33	-6.27	**-5.07**	-0.55	3.64	3.05
		-2.16	-0.31	-0.16	(-0.68)	(-4.25)	**(-3.48)**	(-0.03)	-6.94	-3.21
	PRE	-6.37	-25.43	-8.25	-12.88	-0.87	-0.8	**-9.37**	0.04	-9.41
	(-0.29)		(-0.64)	(-0.08)	(-0.16)	(-0.59)	(-0.55)	**(-0.05)**	-0.07	(-9.92)
	AP	-20.07	-8.66	-11.77	8.87	1.06	0.75	-0.48	**-9.4**	-9.67
	(-0.93)		(-0.22)	(-0.11)	-0.11	-0.72	-0.51	(-0.03)	**(-17.94)**	(-10.19)
	AE	-22.45	-23.31	-13.1	-1.23	0.26	0.2	-6.31	-6.97	**-12.89**
	(-1.04)		(-0.59)	(-0.12)	(-0.02)	-0.18	-0.14	(-0.04)	(-13.31)	**(-13.58)**
	PG	41.63	7.95	16.46	-36.62	-3.7	-3.02	1.11	2.9	**4**
		(-1.93)	(-0.2)	-0.15	(-0.45)	(-2.50)	(-2.07)	(-0.06)	(-5.54)	**(-4.22)**
	ACQ	-4.06	-55.2	-2.27	11.05	-0.01	0.08	-2.23	-0.16	**-2.39**
		(-0.19)	(-1.39)	(-0.02)	-0.13	(-0.01)	-0.05	(-0.12)	(-0.30)	**(-2.52)**
	PROL	29.96	5.34	25.37	-25.59	-2.57	-2.04	0.75	1.35	**2.14**
		-1.39	-0.13	-0.24	(-0.31)	(-1.74)	(-1.40)	-0.04	-2.57	**-2.25**
	IF	14.99	5.09	7.61	-75.44	-1.96	-2.08	-0.08	0.46	**0.43**
		-0.69	-0.13	-0.07	(-0.92)	(-1.33)	(-1.42)	0	-0.88	**-0.45**
20%	FM	31.6	2.2	10.6	-27.09	-5.18	-3.74	-0.54	1.64	**1.18**
		-1.46	-0.06	-0.1	(-0.33)	(-3.51)	(-2.59)	(-0.03)	-3.13	**-1.25**
	FF	31.65	1.31	13.05	-51.97	-4.74	-4.02	-0.47	1.96	**1.54**
		-1.47	-0.03	-0.12	(-0.63)	(-3.21)	(-2.76)	(-0.03)	-3.75	**-1.62**
	PRE	-7.92	-16.79	-5.83	-2.3	-0.32	-0.14	-7.37	-0.16	**-7.54**
		(-0.37)	(-0.42)	(-0.06)	(-0.03)	(-0.22)	(-0.10)	(-0.04)	(-0.30)	**(-7.94)**
	AP	-16.64	-4.53	-8.72	18.01	0.74	0.71	-0.63	-7.63	**-8.11**
		(-0.77)	(-0.11)	(-0.08)	-0.22	-0.5	-0.49	(-0.03)	(-14.56)	**(-8.54)**
	AE	-12.21	-10.35	-7.52	-4.84	-0.33	-0.23	-5.45	-5.35	**-10.52**
		(-0.57)	(-0.26)	(-0.07)	(-0.06)	(-0.23)	(-0.16)	(-0.03)	(-10.22)	**(-11.07)**

PG = production in tons per ha; ACQ = lodging and breakage in percentage of plants; PROL = fecundity in number of ears per plant; IF = interval between flowering in days; FM = male flowering in days; FF = female flowering in days; PRE = relative position of the ear; AP = plant height in cm; AE = ear height in cm; IS = Selection intensity; Values in bold type for gain in the direct selection of the character in question; Values in brackets: genetic gains in units of the character; 1 Gains in unit of the character multiplied by 10 due to low values.

The index of Williams (1962) showed superior gains for the primary characters, PG and ACQ at selection intensities of 10 and 20%. The gains for IF, FM and FF were satisfactory when compared to the other indices. As previously mentioned, the undesirable gain for AP and AE did not adversely affect the selection due to the mean of the original population. Granate et al. (2002) found that estimates of simultaneous predicted gains for 2 characters of interest could not be obtained using the selection index of Williams (1962).

Although Subandi’s index showed the greatest gain for PROL, this did not result in satisfactory gains for the group of characters under study. However, research by Bhering et al. (2011), demonstrated that this index showed higher genetic gains for selection of *Jatropha curcas.* Moraes (2006) also found suitable values for gains for simultaneous selection of six characteristics in *Pinus.*

Table 5. Estimates of genetic gains in units of the character and percentage using the index selection method.

IS	Selection Index	PG	ACQ	PROL	IF	FM	FF	PRE1	AP	AE
10%	Cruz (2006)	32.53	-10.56	17.74	-25.04	-0.49	-0.77	1.20	0.24	1.38
	Elston (1963)	22.61	-25.96	15.37	-58.25	-3.89	-3.43	-1.13	0.32	-0.94
	Mulamba and Mock (1978)	25.75	-21.12	14.91	-50.80	-4.29	-3.51	-4.52	-1.48	-5.92
	Pesek Backer (1969)	25.22	-54.88	11.12	-14.95	-2.85	-2.46	-2.40	2.00	-0.52
	Smith (1936) and Hazel (1943)	46.76	-28.65	16.84	-41.46	-4.91	-4.14	-0.50	4.01	3.45
	Subandi et al (1973)	29.34	-6.06	21.47	-18.47	-3.08	-3.45	-3.68	-3.29	-0.04
	Williams (1962)	43.65	-34.16	14.87	-39.25	-4.12	-3.67	-0.32	3.33	2.98
20%	Cruz (2006)	11.73	-8.57	10.64	-23.67	-1.89	-1.75	0.34	0.44	0.68
		(0.54)	(-0.22)	(0.10)	(-0.29)	(-1.28)	(-0.12)	(0.66)	(0.47)	(1.45)
	Elston (1963)	14.32	-19.85	18.81	-49.62	-1.86	-2.05	0.36	1.59	1.91
		(0.66)	(-0.50)	(0.18)	(-0.60)	(-1.26)	(-1.41)	(0.20)	(3.04)	(2.01)
	Mulamba and Mock (1978)	19.96	-11.79	11.76	-50.47	-3.31	-2.87	-3.64	-1.23	-4.79
		(0.92)	(-0.30)	(0.11)	(-0.61)	(-2.24)	(-1.97)	(-2.00)	(-2.34)	(-5.04)
	Pesek and Backer (1969)	15.62	-47.97	6.52	-14.45	-1.93	-1.56	-1.26	1.58	0.27
		(0.72)	(-1.21)	(0.06)	(-0.18)	(-1.31)	(-1.07)	(-0.69)	(3.02)	(0.29)
	Smith (1936) and Hazel (1943)	33.06	-28.71	13.61	-26.82	-3.45	-2.77	-0.18	3.00	2.78
		(1.53)	(-0.72)	(0.13)	(-0.33)	(-2.33)	(-1.90)	(-0.10)	(5.73)	(2.93)
	Subandi et al. (1973)	30.83	-4.69	18.19	-16.87	-2.97	-2.69	-2.69	0.57	-2.11
		(1.43)	(0.12)	(0.17)	(-0.20)	(2.01)	(2.19)	(1.21)	(-0.62)	(2.00)
	Williams (1962)	30.47	-33.37	12.66	-21.17	-3.02	-2.46	-0.36	2.38	1.99
		(1.41)	(-0.84)	(0.12)	(-0.26)	(-2.04)	(-1.69)	(-0.20)	(4.55)	(2.09)

The selection gains were different for the different indices studied, demonstrating the need for constant evaluation of the best index in accordance with the objectives of the breeding program and of the population to be improved. Not all the indices showed appropriate gains for all the characters for this population of lines. The best gains for both selection intensities were obtained using the indices of Smith (1936), Hazel (1943) and Williams (1962).

On comparing the genotypes selected for each index at 10 and 20% intensities, it was possible to observe that some genotypes were selected in all the selection indices and, therefore, were promising to keep in breeding program. The total of 256 genotypes, 25 of them (10%) were selected in at least 5 of the 7 indices presented. This demonstrates that these genotypes have a potential to continue in the breeding program of line development for obtaining superior hybrids and therefore, merit more attention within the program.

Conclusion

The direct selection of characters was not effective in the selection of superior genotypes for the characters under study. The use of selection indices in the study population was effective within the improvement program since it allowed the simultaneous selection of characters and the indices of Smith (1936), Hazel (1943) and Williams (1962) resulted in better gains for the genotypes studied.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

Arnhold E, Silva RG (2009). Eficiência relativas de índices de seleção considerando espécies vegetais e pesos econômicos iguais entre caracteres. Bioscience Journal 25:76-82.

Bárbaro IM, Centurion MAPC, Mauro AO, Unêda-Trevisoli SH, Costa MM, Muniz FRS, Silveira GD, Sarti DGP (2007). Variabilidade e correlações entre produtividade de grãos e caracteres agronômicos de soja com aptidão para cultivo em áreas de reforma de canavial. Científica 3:136-145.

Bhering LL, Laviola BG, Salgado CC, Sánchez CFB, Alves AA (2011). Predição de ganho genético em pinhão-manso via índices de seleção. II Congresso Brasileiro de Pesquisas de Pinhão-Manso. Anais.

Borém A, Miranda GV (2005). Melhoramento de plantas (4 ed.). Editora: UFV, Viçosa 525 p.

Carena MJ (2009). Handbook of plant breeding: Cereals (ed). Editora: Springer, New York. Cochran WG, Cox GM (1976). Experimental designs. Editora: Willey, New York 661 p.

Coimbra JLM, Guidolin AF, Carvalho FIF, Coimbra SMM, Hemp S (1999). Reflexos da interação genótipo x ambiente e suas implicações nos ganhos de seleção em genótipos de feijão (*Phaseolus vulgaris* L.). Ciência Rural 29:433-439.

Conab (2018). Companhia Nacional de Abastecimento – Acompanhamento da safra brasileira de grãos V. 5 – safra 2017/18 – N. 5 – quinto levantamento – fevereiro 2018. Disponível em: https://www.conab.gov.br/info-agro/safras/graos/boletim-da-safra-de-graos/item/download/12569_5b3e0e675171f49a5b1e9215edc1064a.

Costa MM, Di Mauro, A. O., Unêda-Trevisoli SH, Arriel NHC, Bárbaro IM, Muniz FRS (2004). Ganho genético por diferentes critérios de seleção em populações segregantes de soja. Pesquisa Agropecuária Brasileira 39:1095-1102.

Cruz CD (2006). Programa Genes: Estatística experimental e matrizes. Editora: UFV, Viçosa.

Cruz CD, Regazzi AJ (1994). Modelos biométricos aplicados ao melhoramento genético. Editora: UFV, Viçosa 390 p.

Cruz CD, Regazzi AJ (2001). Modelos biométricos aplicados ao melhoramento genético. Editora UFV, Viçosa 334 p.

Cruz CD, Vencovsky R, Silva SO, Tosello GA (1993). Comparison of gains from selection among corn progenies, based on different criteria. Revista Brasileira de Genética, Ribeirão Preto 16(1):79-89.

Elston RC (1963). A weight free index for the purpose of ranking or selection with respect to several traits at a time. Biometrics 19:85-97.

Embrapa Milho e Sorgo (2015). Sistema de produção - https://www.spo.cnptia.embrapa.br/conteudo?p_p_id=conteudoportlet_WAR_sistemasdeproducaolf6_1ga1ceportlet&p_p_lifecycle=0&p_p_state=normal&p_p_mode=view&p_p_col_id=column-2&p_p_col_count=1&p_r_p_-76293187_sistemaProducaoId=7905&p_r_p_-996514994_topicoId=8658, ISSN 1679-012X, Versão Eletrônica (9 ed.).

Falconer DS (1978). Introduccion a la genetica cuantitativa. Escuela Nacional de Agricultura, Chapingo 430 p.

Falconer DS, Mackay TF (1996). Introduction to Quantitative Genetics 4th ed. Longman, Harlow. https://www.scirp.org/(S(i43dyn45teexjx455qlt3d2q))/reference/ReferencesPapers.aspx?ReferenceID=1823580

Ferreira A, Cecon PR, Cruz, CD, Ferrão RG (2005). Seleção simultânea de *Coffea canephora* por meio da combinação de análise de fatores e índices de seleção. Pesquisa Agropecuária Brasileira 40:1189- 1195.

Garbuglio DD, Gerage AC, Araújo PM, Fonseca Júnior NS, Shioga OS (2007). Análise de fatores e regressão bissegmentada em estudos de estratificação ambiental e adaptabilidade em milho. Pesquisa Agropecuária Brasileira 42:183-191.

Gonçalves G, Viana AP, Bezerra-Neto FV, Pereira MG, Pereira TNS (2007). Seleção e herdabilidade na predição de ganhos genéticos em maracujá-amarelo. Pesquisa Agropecuária Brasileira 42:193-198.

Granate MJ, Cruz CD, Pacheco CAP (2002). Predição de ganho genético com diferentes índices de seleção no milho-pipoca CMS-43. Pesquisa Agropecuária Brasileira 37:1001-1008.

Hallauer AR, Miranda FJB (1988). Quantitative genetics in maize breeding. Editora: Ames, Iowa State University Press 375p.

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

Lande R, Thompson R (1990). Efficiency of marker-assisted selection in the improvement of quantitative traits. Genetics 124(3):743-756.

Martins IS, Martins RCC, Pinho DS (2006). Alternativas de índices de seleção em uma população de *Eucalyptus grandis* Hill ex Maiden. Cerne 12:287-291.

Moraes NSP (2006). Índices de seleção para famílias de meios-irmãos de *Pinus tecunumanii*. Boletim de pesquisa e desenvolvimento. Embrapa Cerrados. https://ainfo.cnptia.embrapa.br/digital/bitstream/CPAC-2010/27836/1/bolpd-173.pdf

Moro GV (2011). Uso da seleção genômica e fenotípica em linhagens para predição de testecrosses em milho. 116 f. Tese (Doutorado em Genética e Melhoramento de Plantas) - Escola Superior de Agricultura "Luiz de Queiroz", Universidade de São Paulo, Piracicaba, 2011.

Mulamba NN, Mock JJ (1978). Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. Egyptian Journal of Genetics and Cytology 7:40-51.

Oliveira EJ de, Santos VS, Lima DS, Machado MD, Lucena RS, Motta TBN, Castellen MS (2008). Seleção em progênies de maracujazeiro amarelo com base em índices multivariados. Pesquisa Agropecuária Brasileira 43:1543‑1549.

Paula RC, Pires IE, Borges RCG, Cruz CD (2002). Predição de ganhos genéticos em melhoramento florestal. Pesquisa Agropecuária Brasileira 37:159-165.

Pesek J, Baker RJ (1969). Desired improvement in relation to selection indices. Canadian Journal of Plant Science 49:803-804.

Rangel RM, Amaral Júnior AT, Gonçalves LSA, Freitas Júnior SP, Candido LS (2011). Análise biométrica de ganhos por seleção em população de milho pipoca de quinto ciclo de seleção recorrente. Ciência Agronômica 42:473-481.

Rocha RB, Ramalho AR, Teixeira AL, Laviola BG, Silva FCG, Militão JSLT (2012). Eficiência da seleção para incremento do teor de óleo do pinhão‑ manso. Pesquisa Agropecuária Brasileira 47:44- 50.

Santos FS, Amaral Júnior AT, Freitas Júnior SP, Rangel RM, Pereira MG (2007). Predição de ganhos genéticos por índice de seleção na população de Milho-Pipoca UNB-2U sob Seleção Recorrente. Brangantia 66:389-396.

SAS Institute (2012). SAS Proprietary Software, Version 9.3 SAS Institute Inc., Cary, North Carolina, USA.

Smith HF (1936). A discriminant function for plant selection. Annals of Eugenics 7:240-250.

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

Vasconcelos ES, Ferrreira RP, Cruz CD, Moreira A, Rassini JB, Freitas AR (2010). Estimativas de ganho genético por diferentes critérios de seleção em genótipos de alfafa. Revista Ceres 57:205-210.

Vilarinho AA, Viana JMS, Câmara TMM, Santos JF (2003). Seleção de progênies endogâmicas S_1 e S_2 em um programa de melhoramento intrapopulacional de milho pipoca. Acta Scientiarum 24:1419-1425.

Williams JS (1962). The evaluation of a selection index. Biometrics 18:375-393.