Genetic parameters and selection for multiple traits in recurrent selection populations of maize[1]

Érica Munique da Silva[2*], *Márcio Lisboa Guedes*[2], *Ailton José Crispim Filho*[2], *Angelina Luzia Ciappina*[2], *Edésio Fialho dos Reis*[2], *Marcela Pedroso Mendes Resende*[2]

10.1590/0034-737X202370030009

ABSTRACT

The efficiency of recurrent selection depends, among other factors, on the estimation of parameters that guide the breeder to obtain genetic gains for multiple traits. The aim of this research was to estimate genetic and phenotypic parameters of maize populations during the third cycle of recurrent selection for traits of interest. The populations CRE-01 and CRE-02, potential for resistance to corn stunt, were described using genetic and phenotypic parameters of variance components, heritability, variation indices and correlation between 16 agronomic traits. Direct and indirect selection gains were estimated for each trait and considering the Smith and Hazel, Mulamba and Mock and Z index. Both populations have genetic variability for the traits. High heritability estimates were obtained for most of the traits, which associated with the genetic variability, indicate that these populations may show continuous gains with recurrent selection. All selection indexes provided satisfactory genetic gains, but the Z index was the most promising considering the results of both populations.

Keywords: quantitative genetics; heritability; *Zea mays* L; selection index.

INTRODUCTION

Maize (*Zea mays* L.) is one of the cereal grains most used in industry and in human and animal diets (Galvão & Miranda, 2004), and it is second among crops in Brazil in terms of production and planted area (CONAB, 2018). Due to its economic importance, maize is frequently the object of study in agronomic sciences, and plant breeding programs have sought to obtain increasingly high-yielding cultivars. Among breeding methods available, recurrent selection using half-sib progenies is effective and easy to carry out (Hallauer *et al.*, 2010).

The efficiency of recurrent selection depends on various factors, one of which is estimation of genetic and phenotypic parameters during selection cycles. These estimates guide breeding programs in definition of breeding strategies, the intensity of selection to be used, the way of evaluating the diverse traits, and the need for introducing new parents. In addition, this estimation makes it possible to predict genetic gains for future selection cycles and to evaluate the viability of the breeding program (Palomino *et al.*, 2000; Ramalho *et al.*, 2012).

The aim of plant breeding is to obtain gain from selection in superior genotypes that have a set of favorable attributes in relation to yield and market demands (Vasconcelos *et al.*, 2010). However, desired traits are not always positively correlated, impeding selection. Knowing how traits are associated is important for success in selection and in identifying variables that can be used in indirect

---

Submitted on February 10th, 2022 and accepted on September 20th, 2022.

[1] This work is part of the first author's research project funded by CAPES.

[2] Universidade Federal de Goiás, Goiânia, Goiás, Brazil. ericamunique47@gmail.com; marcioguedesbio@gmail.com; ailtonjcf@gmail.com; angelinaciappina@gmail.com; edesiofr7@gmail.com; marcelapmr@ufg.br
*Corresponding author: ericamunique47@gmail.com

selection for other traits (Bernardo, 2010).

Multiple traits can be selected simultaneous through selection indices, which consist of linear combination of the phenotypic values of all the traits in a single value (Ramalho *et al.*, 2012). These indices allow gains to be obtained simultaneously even for negatively correlated traits, which represents a considerable advantage for plant breeding (Santos *et al.*, 2007). Diverse indices have been described in the literature, most notably the indices of Mulamba & Mock (1978), Smith (1936) and Hazel (1943); Williams (1962); and Mendes *et al.* (2009).

In light of the foregoing, the aims of this study were to estimate genetic and phenotypic parameters of half-sib progenies of two maize populations in the third recurrent selection cycle, evaluate the potential of these populations in future selection cycles, and compare the efficiency of different selection indices for simultaneous selection of traits of agronomic importance.

MATERIALS AND METHODS

Two maize populations in the third recurrent selection cycle with potential for resistance to corn stunt were evaluated for grain yield and primary and secondary yield components. These populations originated from crossing of inbred lines coming from the International Maize and Wheat Improvement Center (CIMMYT), introduced in 1999 in the Maize Breeding Program of ESALQ/USP (Escola Superior de Agricultura "Luiz de Queiroz", Universidade de São Paulo). The inbred lines with best expression for resistance to corn stunt were crossed with the commercial hybrid P3041, resistant to corn stunt, and with the CMS14 population, developed by the Maize Breeding Program of EMBRAPA and chosen for its good yield standard. Crossing the lines with the hybrid P3041 gave rise to the CRE-01 population, and crossing with the CMS14 population gave rise to the CRE-02 population, as described in Oliveira *et al.* (2015) and Souza (2015).

In the second crop season of 2017, seeds of CRE-01 and CRE-02 populations were planted in isolated lots of open pollination in the experimental area of the Agronomy School of the Universidade Federal de Goiás in Goiânia, GO (16°35'12"S, 49º21'14"W) to obtain half-sib progenies. Experimental blocks were 300 m², with crop management based on recommendations for maize growing in the region and on crop needs. In July 2017, 160 half-sib families (HSF) were harvested from each population.

Experiments for evaluation of HSF were conducted in the experimental area of the School of Agronomy of the Universidade Federal de Goiás, in Goiânia, GO, in December 2017, using randomized block design with three replications, and plots of one 4-m row with 20 plants at a spacing of 0.20 m between plants and 0.90 m between rows. The progenies were evaluated for male flowering (MF), female flowering (FF), flowering interval (FI), plant height (PH), ear height (EH), relative ear position (REP), prolificacy (PROL), ear diameter (ED), ear length (EL), cob diameter (CD), number of kernels per row (NKR), number of rows per ear (NR), kernel length (KL), ear yield (EY), lodging and breakage (LDBR) and grain yield (GY). EY and GY were adjusted for 13% moisture and ideal stand (20 plants) by covariance analyses, according to Vencovsky & Barriga (1992).

Individual analysis of variance was performed for each trait according to randomized block design. The mean squares of each source of variation were matched with their expected values to obtain the components of the phenotypic variance between progeny means ($\sigma_{\bar{P}}^2$), environmental variance (σ_E^2) and genetic variance among progenies (σ_G^2), according to Regazzi *et al.* (1999). These components were used to estimate the genetic parameters heritability, variation index and genetic gain.

Heritability for selection based on progenies means (h^2) were estimated according to the expression $h^2 = \sigma_G^2 / \sigma_{\bar{P}}^2$. The confidence intervals for the heritability estimates were obtained as suggested by Knapp *et al.* (1985), considering a significance of 5%. Variation indices (θ) were obtained as $\theta = CV_g / CV_e$, on what $CV_g = \sigma_G^2 / \bar{y}$ is the genetic variation coefficient, and $CV_e = \sigma_E^2 / \bar{y}$ is the environmental variation coefficient ($\bar{y}$ is the trait mean). Genetic gains were estimated as the expressions:

$$Gs = i\left(\sigma_G^2 / \sqrt{\sigma_{\bar{P}}^2}\right) \text{and}\, Gs(\%) = 100\left(Gs / \bar{y}\right)$$

on what '*i*' was the standardized selection differential for selecting the 20% best progenies (Vencovsky & Barriga, 1992). Genetic (r_{Gxy}), phenotypic (r_{Fxy}) and environmental (r_{Exy}) correlation were also obtained, according to the procedures described in Vencovsky & Barriga (1992).

Simultaneous selection was carried out for multiple traits using the Z index (I_Z) proposed by Mendes *et al.* (2009), the classic index (I_{SH}) of Smith (1936) and Hazel (1943), and the rank summation index (I_{MM}) of Mulamba

& Mock (1978). For the last two methods, the 0 value was used in the economic weight matrix for all traits.

To obtain the coincidence index between the progenies selected by the indices two by two, the expression $IC(\%)=(A-C)/(C-B)x100$ of Hamblin & Zimmermann (1986) was used. The statistical analyses used in the experiments were computed using the GENES (Cruz, 2006) and R computational programs (R Core Team, 2018).

RESULTS AND DISCUSSION

The progenies showed significant differences ($p \leq 0.05$) for all traits in both populations, except for kernel length (KL) and lodging and breakage (LDBR) in the CRE-02 population, indicating that there is variability among the progenies for the traits evaluated, an essential condition for continuity of the recurrent selection program (not shown). The environmental coefficients of variation (CVe) ranged from 2.20% (number of rows per ear - NR) to 23.58% (grain yield - GY) in the CRE-01 population, and from 3.09% (female flowering - FF) to 31.47% (LDBR) in the CRE-02 population (not shown). In spite of the high magnitudes of the CVe for LDBR, these estimates are in agreement with those found in the literature (Moraes & Brito, 2017; Revolti *et al.*, 2016).

In general, the CRE-01 population had higher heritability estimates than the CRE-02 population (Table 1). It is noteworthy that in the CRE-01 population, the heritability estimates were 17.54% higher for ear length (EL) and 24.76% higher for GY. For the CRE-02 population, this superiority was 147% and 14% compared to the data obtained by Souza (2015), who evaluated the second cycle of these populations. According to Ramalho *et al.* (2012), the increase in magnitude of the heritability estimates in the sequence of the cycles is an indication of the accumulation of favorable alleles in the population, showing that recurrent selection is an efficient breeding method.

Table 1: Heritability estimates for selection based on the mean of the progeny (h^2, %), confidence interval for the heritability estimates (IC_{h^2}, %), variation index (θ), and gain from selection (Gs, %) for different traits in the CRE-01 and CRE-02 maize populations

Traits[1]	**CRE-01**				**CRE-02**			
	h^2	IC_{h^2}	θ	**Gs**	h^2	IC_{h^2}	θ	**Gs**
FF	71.62	0.72 - 0.84	0.75	-22.55	54.88	0.61 - 0.78	0.64	-2.50
MF	62.52	0.62 - 0.79	0.92	-20.53	61.30	0.55 - 0.74	0.73	-2.46
FI	47.94	0.48 - 0.71	0.55	-3.19	33.91	0.34 - 0.63	0.41	-10.60
PH	66.59	0.67 - 0.81	0.82	-18.24	37.37	0.37 - 0.64	0.10	-3.17
EH	54.52	0.55 - 0.74	0.63	-12.36	28.69	0.29 - 0.60	0.37	-3.33
REP	47.14	0.47 - 0.70	0.55	-7.21	6.54	0.07 - 0.47	0.15	-1.05
EL	49.38	0.49 - 0.71	0.57	8.41	42.01	0.42 - 0.67	0.49	9.54
KL	35.81	0.36 - 0.64	0.43	5.38	7.98	0.08 - 0.48	0.17	1.00
ED	51.18	0.51 - 0.72	0.59	5.63	39.52	0.40 - 0.66	0.47	9.45
CD	57.60	0.58 - 0.76	0.67	-5.84	40.53	0.41 - 0.66	0.48	-8.46
NR	59.46	0.59 - 0.77	0.70	1.66	44.60	0.45 - 0.69	0.52	7.36
NKR	33.03	0.33 - 0.62	0.41	4.55	24.92	0.25 - 0.57	0.33	6.36
LDBR	48.60	0.49 - 0.71	0.56	-4.19	24.12	0.76 - 0.87	0.33	-7.04
PROL	35.63	0.36 - 0.64	0.43	3.08	35.47	0.35 - 0.63	0.43	1.78
EY	87.45	0.87 - 0.93	1.52	43.90	96.92	0.97 - 0.98	3.24	81.37
GY	86.81	0.87 - 0.93	1.48	45.56	69.58	0.70 - 0.83	0.87	18.47

[1/] FF: female flowering; MF: male flowering; FI: flowering interval; PH: plant height; EH: ear height; REP: relative ear position; EL: ear length; KL: kernel length; ED: ear diameter; CD: cob diameter; NR: number of rows per ear; NKR: number of kernels per row; LDBR: lodging and breakage; PROL: prolificacy; EY: ear yield; GY: grain yield.

The highest estimates of the variation index (θ) occurred for ear yield (EY) in both populations (Table 1). Faluba *et al.* (2010) highlighted that estimates of θ near or higher than 1.00 based on only one location are common, due to genetic variance being inflated by the genotype × environment interaction. However, the high magnitudes of the heritabilities suggest that the indices greater than 1 mean that phenotypic expressions of these traits were mainly due to genetic causes, and not by being overestimated by the interaction (Cruz *et al.*, 2014). These results indicate good perspectives of genetic gain for direct selection (Mistro *et al.*, 2007), and also that simple methods of selection would be sufficient to obtain satisfactory gains.

The values of heritability and variation index observed for traits related to height (plant height - PH, ear height - EH and relative ear position - REP) in the CRE-01 population indicate a reasonably favorable condition for selection. In contrast, the values obtained for these traits in CRE-02 indicate that this population has little genetic variability and that the selection for these traits will likely not provide significant gains. When the previous recurrent selection cycles described in Oliveira (2013) and Souza (2015) are compared, a decrease in the magnitude of the heritability estimates was observed, indicating loss of favorable alleles in the CRE-02 population.

Heritability estimates for EL and KL (Table 1) are lower than those reported in the literature by Toledo (2010), Chavaglia (2016) and Chen *et al.* (2016). This may be due to the fact that these traits are highly affected by the environment or to the fact that the genetic variances are small. Since the experiment was conducted in only one environment, the presence of greater environmental effects and, consequently, of greater heritability estimates, is common.

The heritability estimates obtained for ear diameter (ED) and cob diameter (CD) were greater in the CRE-01 population, which can be explained by the estimates of variation index, which for the CRE-01 population was 0.59 (ED) and 0.67 (CD), whereas in the CRE-02 population, they were 0.47 (ED) and 0.48 (CD) (Table 1). Variation index greater than 0.5 indicate that the contribution of the genotype in expression of the phenotype is greater than the contribution of the environmental effect (Vencovsky, 1987). Gains from selection for ED were higher than those obtained by Souza (2015), who in the second recurrent selection cycle in these populations obtained values near zero.

Heritability estimates for LDBR were 48.60% (CRE-01) and 24.12% (CRE-02) (Table 1). The heritabilities of the CRE-01 population were higher than those observed by Pinheiro (2004) for half-sib populations in the second recurrent selection cycle, that ranged from 0.70% to 29.75%. The estimate of θ was greater than 0.5 only in the CRE-01 population, indicating that the selection practiced in the CRE-02 population will not lead to significant gains. According to Andrade & Souza Junior (2017), this trait is difficult to evaluate due to the strong effect of wind, rain, and insect infestation, which makes it difficult to replicate experiments.

Of the 120 pairs of traits (combination of the 16 traits two by two), only 32 had significant genetic correlation in at least one of the two populations (Table 2). The significant phenotypic correlations ranged from weak, below 0.4 (between PH and GY), to very strong, above 0.9 (between REP and CD). LDBR trait did not show significant genetic correlation with the other traits. GY showed genetic correlation with number of kernels per row – NKR (0.59 and 0.734), prolificacy – PROL (-0.505 and 0.439), and EY (0.998 and 0.991) in both populations; with PH (0.384), EH (0.4575), and KL (0.4971) in the CRE-01 population; and with EL (0.463) in the CRE-02 population (Table 2).

The genetic correlation coefficients between EP and EH were positive and of great magnitude in the two populations evaluated (Table 2), indicating that many of the genes involved in determination of EY are also involved in determination of EH. These results corroborate those found by Bianco *et al.* (1987), Pinheiro (2004), and Nzuve *et al.* (2014). These traits not only correlate with each other but also have positive genetic correlation with EY in both populations, and with GY in the CRE-01 population. Thus, some genes that act in promoting the growth of larger plants are connected or also affect yield. In addition, we can affirm that there is a relation between the primary and secondary yield components. These results are different from those found by Souza *et al.* (2008), who did not obtain significant correlations among these traits, and corroborate with the results of Dao *et al.* (2017). PROL showed positive correlation with EY and GY in CRE-02, and negative correlation with these same traits in CRE-01. Initially, this result would indicate that selection for PROL is advantageous in the CRE-01 population and disadvantageous in the CRE-02 population. Negative genetic correlations between PROL and GY were found by Nardino *et al.* (2016), who explain this result based on the negative correlation of PROL with traits that positively affect GY, and that the genes that act to increase PROL are negatively correlated with ED, number of kernel rows and EY. In the present study, the genetic correlation observed between PROL and number of kernel rows was negative in the CRE-01 population and positive in the CRE-02 population (Table 2).

The genetic correlation between PROL and GY should be interpreted carefully. When there is more than one ear on the plant, the second is generally small, with poor kernel set or ear development. PROL does not always result in an increase in GY (Santos *et al.*, 2013). Plants with a greater number of ears may exhibit problems in grain production fields due to the low efficiency of kernel set in the ear (around 30%) when the fasciation rate is high (Durães, 1999). The divergent results obtained for the CRE-01 and CRE-02 populations suggest that PROL should not be considered in selection of higher yielding genotypes in this study.

Table 2: Estimates of the genetic correlation coefficients between multiple traits in the CRE-01 (above the diagonal) and CRE-02 (below the diagonal) maize populations

Traits^{1}	FF	MF	FI	PH	EH	REP	EL	KL	ED	CD	NR	NKR	LDBR	PROL	EY	GY
FF	-	$^{++}$0.83	$^{+}$0.64	0.10	0.11	0.03	0.21	-0.03	0.27	0.36	0.26	-0.05	-0.40	-0.18	-0.04	-0.06
MF	$^{++}$0.85	-	0.10	-0.13	0.00	0.21	0.13	-0.03	0.17	0.24	0.19	-0.10	-0.49	0.13	-0.20	-0.21
FI	0.13	-0.41	-	0.35	0.19	-0.22	0.20	-0.01	0.24	0.31	0.20	0.05	-0.03	-0.50	0.20	0.18
PH	-0.01	-0.04	0.06	-	$^{++}$0.81	-0.22	0.11	0.22	0.32	0.15	0.23	0.23	-0.09	-0.24	$^{+}$0.40	$^{+}$0.38
EH	0.07	-0.06	0.23	$^{+}$0.94	-	0.38	0.17	0.40	0.37	0.04	0.12	0.56	-0.13	-0.18	$^{+}$0.48	$^{+}$0.46
REP	0.23	-0.10	0.59	0.30	0.59	-	-0.04	0.09	0.04	-0.04	-0.12	0.33	0.14	0.05	0.15	0.15
EL	0.15	0.07	0.12	0.44	0.63	0.70	-	0.23	0.33	0.16	0.11	0.54	-0.64	-0.05	0.26	0.25
KL	0.44	0.38	0.05	0.21	0.39	0.69	0.26	-	$^{+}$0.61	-0.28	0.22	0.61	-0.27	-0.23	$^{+}$0.49	$^{+}$0.49
ED	0.28	0.21	0.08	-0.05	-0.21	-0.40	0.12	0.83	-	$^{+}$0.58	$^{+}$0.54	0.38	-0.51	-0.31	0.35	0.34
CD	0.05	0.02	0.05	-0.18	-0.56	$^{++}$1.00	-0.02	0.49	$^{+}$0.90	-	$^{+}$0.43	-0.17	-0.34	-0.13	-0.08	-0.10
NR	0.22	0.11	0.18	-0.12	-0.16	-0.11	-0.25	0.29	0.30	0.19	-	0.35	-0.24	0.01	0.17	0.17
NKR	-0.02	0.01	-0.06	0.65	$^{+}$0.94	$^{++}$1.00	0.62	0.48	0.08	-0.31	-0.39	-	-0.18	-0.17	$^{+}$0.60	$^{+}$0.59
LDBR	0.03	-0.22	0.46	0.50	0.58	0.40	-0.02	0.15	-0.01	-0.14	-0.16	0.14	-	-0.67	0.16	0.13
PROL	-0.15	-0.08	-0.12	0.46	$^{+}$0.64	0.67	0.50	0.06	-0.19	-0.34	$^{++}$0.86	$^{+}$0.80	0.18	-	$^{+}$-0.51	$^{+}$-0.51
EY	-0.33	-0.27	-0.06	0.49	$^{+}$0.61	0.56	0.45	0.53	0.31	0.03	-0.05	$^{+}$0.70	0.13	$^{+}$0.44	-	$^{++}$1.00
GY	-0.39	-0.29	-0.12	0.45	0.60	0.62	$^{+}$0.46	0.61	0.32	-0.03	-0.02	$^{+}$0.73	0.04	$^{+}$0.44	$^{++}$0.99	-

$^{1/}$ FF: female flowering; MF: male flowering; FI: flowering interval; PH: plant height; EH: ear height; REP: relative ear position; EL: ear length; KL: kernel length; ED: ear diameter; CD: cob diameter; NR: number of rows per ear; NKR: number of kernels per row; LDBR: lodging and breakage; PROL: prolificacy; EY: ear yield; GY: grain yield.
++ and +: Significant at 1% and 5%, respectively, by the bootstrap method with 5000 simulations.

The complexity of genetic control of GY in maize means that selection for this trait is not performed only in a direct manner, but also considering the other yield components. According to Edmeades *et al.* (1998), an ideal secondary component should be genetically correlated and have greater heritability than the trait of interest, be easily measured, be stable within the period of measurement, not be associated with yield penalization under non-severe conditions, preferentially be measurable before or during flowering so that the undesirable parents not be crossed, and be a reliable estimator of yield potential before final harvest.

EY showed very strong and positive correlation with GY, 0.998 for the CRE-01 population and 0.991 for the CRE-02 population, agreeing with results obtained by Lopes *et al.* (2007) and Casarotto (2013), that describe EY as one of the traits with greatest effect on yield.

Differences were observed in the magnitude and in the direction of the phenotypic and environmental correlations between the traits studied in the CRE-01 and CRE-02 populations (Table 3). The significant phenotypic correlations ranged from very weak, below 0.3 (between MF and GY), to very strong, above 0.9 (between EY and GY). Weak phenotypic correlations may have been detected due to the high degree of freedom included in the *t*-test.

In general, positive environmental correlation indicates that the environmental effects that act to increase phenotypic expression in one character also contribute to increase phenotypic expression in another character (Ramalho *et al.*, 2012). For phenotypic correlation, positive values indicate a linear relationship between the variables in general, i.e., an increase in one variable leads to an increase in another (Carvalho *et al.* 2004).

Table 3: Estimates of the genetic correlation coefficients between multiple traits in the CRE-01 (above the diagonal) and CRE-02 (below the diagonal) maize populations

Traits[1]	FF	MF	FI	PH	EH	REP	EL	KL	ED	CD	NR	NKR	LDBR	PROL	EY	GY
FF		**0.77	**0.58	-0.00	0.01	0.02	0.10	-0.04	*0.17	0.26**	**0.22	-0.06	-0.14	-0.15	-0.06	-0.08
MF	**0.74		-0.07	-0.14	-0.05	0.15	0.08	-0.02	0.12	0.17*	*0.17	-0.08	*-0.20	0.06	-0.15	*-0.16
FI	*0.20	**-0.51		*0.18	0.07	-0.17	0.06	-0.04	0.12	0.19*	0.11	-0.00	0.04	**-0.32	0.10	0.08
PH	-0.02	-0.06	0.06		**0.75	-0.11	0.13	0.13	0.224	0.12	0.14	0.22	-0.03	-0.08	**0.37	*0.36
EH	0.02	-0.01	0.05	**0.80		**0.47	0.15	**0.25	**0.24	0.01	0.06	**0.35	-0.06	-0.06	**0.39	**0.37
REP	0.07	0.05	0.01	0.11	**0.68		-0.02	0.10	0.03	-0.078	-0.06	*0.17	-0.02	0.00	0.13	0.13
EL	0.09	0.00	0.11	**0.23	**0.23	0.09		**0.23	**0.31	0.12	0.09	**0.61	**-0.23	-0.02	**0.23	**0.23
KL	0.14	0.09	0.05	0.13	0.10	0.02	**0.28		**0.66	-0.37**	**0.26	**0.37	-0.15	-0.10	**0.35	**0.35
ED	0.15	0.11	0.04	0.03	-0.05	-0.11	**0.29	**0.80		0.45**	**0.51	**0.30	**-0.22	*-0.20	**0.30	**0.30
CD	0.06	0.06	-0.01	-0.09	*-0.19	*-0.20	0.11	-0.03	**0.57		**0.33	-0.07	-0.10	-0.13	-0.05	-0.06
NR	0.12	0.06	0.07	0.01	-0.02	-0.03	-0.00	**0.31	**0.45	0.30**		*0.20	-0.14	-0.04	0.13	0.14
NKR	-0.01	-0.04	0.04	**0.27	**0.30	*0.16	**0.70	**0.33	**0.28	0.02	-0.01		-0.04	-0.11	**0.44	**0.43
LDBR	0.04	-0.04	0.10	0.14	0.14	0.05	-0.04	0.01	-0.01	-0.02	0.00	0.02		**-0.22	0.02	0.00
PROL	-0.09	-0.07	-0.01	**0.21	**0.24	0.13	**0.53	0.05	-0.08	-0.18*	**-0.65	**0.76	0.02		**-0.30	**-0.30
EY	**-0.26	**-0.22	-0.02	**0.31	**0.33	*0.18	**0.34	**0.26	**0.26	0.07	0.02	**0.47	-0.01	**0.35		**0.99
GY	**-0.30	**-0.24	-0.04	**0.29	**0.31	*0.17	**0.34	**0.29	**0.27	0.04	0.05	**0.48	-0.04	**0.34	**0.98	

[1/] FF: female flowering; MF: male flowering; FI: flowering interval; PH: plant height; EH: ear height; REP: relative ear position; EL: ear length; KL: kernel length; ED: ear diameter; CD: cob diameter; NR: number of rows per ear; NKR: number of kernels per row; LDBR: lodging and breakage; PROL: prolificacy; EY: ear yield; GY: grain yield.

Phenotypic correlation is composed of genetic and environmental causes; however, only the genetic associations are inheritable and can be used for direction of plant breeding programs (Faluba *et al.* 2010; Cabral *et al.*, 2011). Thus, in plant breeding, it is indispensable to distinguish and quantify the degree of genetic and environmental association between the traits, i.e., how much the phenotypic correlation is due to genetic correlation and how much is due to environmental correlation. However, traits that are genetically correlated but do not exhibit significant phenotypic correlation might not exhibit response in selection, since selection is performed based on phenotype (Cabral *et al.*, 2011).

EY is phenotypically correlated with KL and ED in CRE-01 population, EL in CRE-02 population, and with plant and EH, NKR and PROL in both populations. The negative correlation between PROL and EY may be due to the second ear being very small, with poor kernel set, and deformed. As commented above, PROL does not always result in an increase in GY (Santos *et al.*, 2013).

GY exhibited positive phenotypic correlation with 10 (CRE-01) and 13 (CRE-02) of the 16 traits evaluated. One specific trait correlated with many others hinders selection of maize genotypes since this creates difficulties in identification of traits of greater interest (Lopes *et al.*, 2007). EL also exhibited significant and positive phenotypic correlation with GY, as already reported by several authors (Alvi *et al.*, 2003; Selvaraj & Nagarajan, 2011; Nzuve *et al.* 2014). The lack of correlation between GY with MF and FF indicates that the cycle of the material did not affect yield (Santos *et al.*, 2002).

Some traits exhibited phenotypic correlation without exhibiting genetic correlation, such as EH with relative REP, KL and EL with NKR in the CRE-01 population, and flowering interval (FI) with male flowering (MF), FF with GY, EH with relative REP, and EL with NKR in the CRE-02 population, which suggests that phenotypic correlation may have occurred due to environmental correlation. However, these results may have arisen from the significance tests applied, bootstrap for the genetic correlation estimates, and the *t*-test for the estimates of phenotypic correlation. According to Silva & Ferreira (2003), the *t*-test tends to show an increase in the probability of occurrence of type II error with the increase in variances. The bootstrap method has an opposite response, i.e., as the variances increase, the probability of type II error declines. The nature and the magnitude of the phenotypic correlations are not always similar to the genetic correlations, and that may lead to erroneous conclusions or to inefficient selection strategies (Nardino *et al.* 2016).

A selection intensity of 20% was applied in each index, which makes for a total selection of 31 progenies of the CRE-01 population and 32 progenies of the CRE-02 population. The greatest coincidence among the progenies selected occurred between the I_{SH} and I_Z, and the lowest coincidence between the I_{MM} and I_{SH} (Table 4). According to Pedrozo *et al.* (2009), the higher the coefficient of coincidence between the selection indices, the greater the agreement of results of selection between them.

Table 4: Coincidence index of the half-sib progenies selected by the Z index (I_Z), the classic index (I_{SH}) and the rank summation index (I_{MM})

Index[1]	Population	
	CRE-01	CRE-02
I_{SH} x I_{MM}	35.48	20.14
I_{SH} x I_Z	71.33	65.28
I_{MM} x I_Z	42.65	27.08

The coincidence of selection among the indices varied according to the population. This may have occurred due to the differences in their genetic constitution, since each population was composed of a different group of genotypes (Pedrozo *et al.,* 2009).

Gains from indirect selection (Gs) and the ratio between the gain from direct selection and gain from indirect selection estimated from the indices varied for the different traits (Table 5). The sum of the gains of all the traits for the indices in the CRE-01 population were 7.06 (I_{SH}), 3.37 (I_{MM}), and 6.52 (I_Z); and in the CRE-02 population, they were 4.23 (I_{SH}), 0.70 (I_{MM}), and 3.96 (I_Z) (Table 5). The comparison between the yield gain obtained by direct selection and by the simultaneous selection indices shows that the gain from direct selection is greater; however, the indices obtain simultaneous gains even for negatively correlated traits, which represents a big advantage for plant breeding (Santos *et al.*, 2007).

The percentage gains predicted (Gs%) for I_{SH} show that positive gains were obtained for all the traits evaluated, except for LDBR (-6.57%) and PROL (-2.07%) in the CRE-01 population (Table 5). The negative gains for these traits are advantageous since LDBR leads to lower EY, compromising the quality of the grain upon entering in contact with the soil, and also losses in mechanized harvest (Schmitz *et al.*, 2010). PROL had negative genetic correlation with GY in the CRE-01 population. The percentage gains predicted for this index in the CRE-02 population allowed positive gains to be obtained for all the traits evaluated, except for LDBR (-2.71%). In both populations, very small positive gains were obtained for the traits PH, EH, and REP; although these gains are considered undesirable due to plant breeding programs looking for smaller plants. The greatest gains were obtained for the EY trait at 40.05% for CRE-01 and 14.05% for CRE-02.

The ratio between gain from direct selection and gain from selection by the indices (ΔG) in GY and in the other traits in both populations imply that although direct selection among progenies provides greater expectation of genetic progress for most of the traits evaluated, the use of the I_{SH} is viable, because it obtained gains more distributed throughout all the traits without detracting from the main trait, which is GY (Table 5).

The results found in the CRE-01 and CRE-02 populations corroborate with those obtained by Gabriel (2006) from reciprocal recurrent selection in full-sib progenies in maize. The author concluded that the gains predicted from the selection index of Smith (1936) and Hazel (1943) are greater than those predicted from the indices of Mulamba & Mock (1978) and Williams (1962). Advantageous results from the use of the I_{SH} were also obtained by Granate *et al.* (2002), in which the I_{SH} was superior to the indices of Pesek & Baker (1969) and Williams (1962).

The I_{MM} of Mulamba & Mock (1978) showed the lowest gains related to GY, 11.99% for CRE-01 and 4.70% for CRE-02; and also related to EY, 13.68% for CRE-01 and 6.15% for CRE-02, which are the main traits of interest in a maize breeding program. In the CRE-02 population, only this index led to negative gains for FF (-0.38%), MF (0.25%), and FI (-0.52%). Reduction in the days of these traits generates individuals with shorter cycles, reducing the time of the crop in the field and making it more suitable for use in a second crop season (Chavaglia, 2016).

The results obtained for the ratio between gain from direct selection and gain from selection by the indices in GY for selection through the I_{MM}, (25.74 in CRE-01 and 25.43 in CRE-02), suggest that acquisition of gains that are more distributed in all the traits evaluated had a very negative effect on the main trait. Divergent results were obtained by Berilli *et al.* (2013), who used the indices of Smith (1936) and Hazel (1943), Mulamba & Mock (1978), and Williams (1962) in full-sib progenies and obtained better fitted predictions of gains from selection with the I_{MM}, which led to greater gain in yield and reduced or negative gains in deleterious traits. Entringer *et al.* (2016) carried out selection of S1 progenies of sweet corn and obtained greater gains using the Mulamba & Mock (1978) index compared to the indices of Smith (1936) and Hazel (1943), Williams (1962), and Pesek & Baker (1969).

Table 5: Estimates of gains from indirect selection performed from the] I_{SH}, I_{MM}, and $I_{Z,}$ (Gs and Gs%), and ratio between gain from direct selection and gain from selection by the indices (ΔGs%) for the diverse traits in the CRE-01 and CRE-02 populations

VARI-ABLE	**SMITH & HAZEL**						**MULAMBA & MOCK**						**Z INDEX**					
	CRE-01			**CRE-02**			**CRE-01**			**CRE-02**			**CRE-01**			**CRE-02**		
	Gs	**Gs%**	**ΔGs**	**Gs**	**Gs%**	**ΔGs**	**Gs**	**Gs%**	**ΔGs**	**Gs**	**Gs%**	**ΔGs**	**Gs**	**Gs%**	**ΔGs**	**Gs**	**Gs%**	**ΔGs**
FF	0.53	0.86	0.00	0.68	1.04	-42.55	0.46	0.76	0.00	-0.25	-0.38	15.35	0.63	1.02	0.00	0.56	0.88	-35.25
MF	0.24	0.40	0.00	0.72	1.11	-46.12	0.15	0.25	0.00	-0.16	-0.25	10.33	0.32	0.53	0.00	0.54	0.85	-34.54
FI	0.17	1.55	-159.65	0.06	0.49	-0.38	0.20	1.83	-188.20	-0.06	-0.52	0.40	0.17	1.59	-163.43	0.09	0.74	-0.56
PH	0.04	1.72	-1.50	0.02	1.01	-32.59	0.04	1.81	-1.58	0.02	0.70	-22.14	0.06	3.03	-2.65	0.03	1.30	-40.90
EH	0.02	1.88	-13.17	0.02	1.29	-40.42	0.02	1.98	-13.90	0.01	0.87	-26.11	0.03	2.99	-20.98	0.02	1.60	-47.92
REP	0.00	0.32	-10.50	0.00	0.14	-30.43	0.00	0.39	-12.66	0.00	0.08	-17.77	0.00	0.50	-16.05	0.00	0.15	-33.20
EL	0.44	2.61	3.19	0.37	2.12	0.15	0.35	2.04	2.50	0.08	0.46	0.03	0.45	2.67	3.27	0.35	2.14	0.14
KL	0.01	1.20	22.20	0.00	0.39	40.14	0.01	0.80	14.79	0.00	0.33	32.87	0.02	1.91	35.34	0.01	0.57	56.42
ED	0.07	1.58	8.07	0.05	1.08	0.12	0.08	1.80	9.18	0.04	0.89	0.09	0.10	2.07	10.56	0.08	1.82	0.19
CD	0.05	1.68	-23.30	0.01	0.41	-0.58	0.07	2.51	-34.82	0.01	0.34	-0.48	0.05	1.84	-25.49	0.03	1.11	-1.56
NR	0.33	2.20	888.03	0.04	0.29	0.28	0.21	1.37	552.15	0.03	0.24	0.23	0.40	2.65	1070.44	0.15	1.05	0.99
NKR	0.51	1.51	5.68	0.34	0.95	0.01	0.40	1.19	4.46	0.20	0.57	0.01	0.56	1.67	6.27	0.43	1.27	0.02
LDBR	-0.13	-6.57	208.29	-0.03	-2.71	217.92	-0.14	-7.15	226.70	0.01	1.07	-95.18	-0.05	-2.43	77.00	-0.03	-2.24	200.43
PROL	-0.02	-2.07	-73.97	0.03	1.22	172.32	-0.03	-2.48	-88.60	0.02	0.66	90.69	-0.02	-1.84	-65.92	0.03	1.04	142.02
EY	2.70	40.05	89.24	1.26	14.05	20.11	0.92	13.68	30.48	0.47	6.15	7.56	2.13	31.56	70.33	1.10	14.42	17.64
GY	2.09	40.35	86.59	0.66	9.43	58.73	0.62	11.99	25.74	0.28	4.70	25.43	1.65	31.89	68.44	0.57	9.53	51.35
Total	**7.05**			**4.23**			**3.36**			**0.70**			**6.50**			**3.96**		

[1]/FF: female flowering; MF: male flowering; FI: flowering interval; PH: plant height; EH: ear height; REP: relative ear position; EL: ear length; KL: kernel length; ED: ear diameter; CD: cob diameter; NR: number of rows per ear; NKR: number of kernels per row; LDBR: lodging and breakage; PROL: prolificacy; EY: ear yield; and GY: grain yield.

Garcia & Souza Junior (1999) stated that the use of the I_{MM} is very simple since phenotypic values are not used directly, but rather a number associated with each one of them. Thus, variance is the same for all the traits, avoiding transformations of data. However, it is not known if the differences between the means are significant or not, which may lead to erroneous interpretations.

The gains in percentage predicted for the I_Z allowed positive gains to be obtained for all the traits evaluated, except for LDBR (-2.43%) and PROL (-1.84%) in the CRE-01 population. In the CRE-02 population, they allowed positive gains to be obtained for all the traits evaluated, except for LDBR (-2.24%). In the CRE-02 population, the I_Z had greater gains for EY (14.42%) and GY (9.53%) compared to the other indices. The results in both populations indicate that more distributed gains were obtained in all the traits evaluated, without a negative effect on the main trait, making the use of the I_Z viable.

The I_Z exhibited greater gains for the main traits than the I_{MM} did, and was thus more efficient. This result corroborates those obtained by França *et al.* (2016), who carried out simultaneous selection in sweet sorghum progenies and also obtained better results with the I_Z. Compared to the I_{SH}, the I_Z exhibited greater total gains in the CRE-02 population and lower gains in the CRE-01 population. However, in the CRE-01 population, the I_Z allowed gains to be obtained with distribution that was more in fitting with the purposes of selection.

In general, the I_{SH} led to better gains in the CRE-01 population, and the I_Z was more efficient for the CRE-02 population. Nevertheless, good results were also obtained from the use of the I_Z in the CRE-01 population. Due to the ease of obtaining the I_Z and the satisfactory gains for this index in both populations, the I_Z is most recommended for selection of multiple traits in maize breeding programs (França *et al.*, 2016),

CONCLUSIONS

The CRE-01 and CRE-02 populations have genetic variability for primary and secondary yield components.

The high heritability of most of the traits associated with genetic variability of the populations indicate that these populations have potential for providing continuity to the recurrent selection program and achieving gains from selection.

The Z index allows positive gains to be obtained for primary and secondary yield components and is recommended for selection of multiple traits in maize breeding programs.

ACKNOWLEDGEMENTS, FINANCIAL SUPPORT AND FULL DISCLOSURE

The authors would like to thank to Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for granting a scholarship. The authors declare that there is no conflict of interesting carrying this research and publishing this manuscript.

REFERENCES

Alvi MB, Rafique M, Tariq MS, Hussain A, Mahmood T & Sarwar M (2003) Character Association and Path Coefficient Analysis of Grain Yield and Yield Components Maize (*Zea mays* L.). Pakistan Journal of Biological Sciences, 6:136-138.

Andrade MT & Souza Junior CL (2017) Epistasia e parâmentros genéticos em ambientes com e sem estresse hídrico em milho. Doctoral Thesis. Universidade de São Paulo, Piracicaba. 148p.

Berilli APCG, Pereira MG, Trindade RDS, Costa FRD & Cunha KSD (2013) Response to the selection in the 11th cycle of reciprocal recurrent selection among full-sib families of maize. Acta Scientiarum Agronomy, 35:435-441.

Bernardo R (2010) Breeding for quantitative traits in plants. 2º ed. Woodbury, Stemma Press. 390p.

Bianco S, Tosello GA & Souza Junior CL (1987) Correlações genéticas e fenotípicas em duas populações de milho (*Zea mays* L.) braquítico e suas implicações no melhoramento do teor de óleo no grão. In: Anais da Escola Superior de Agricultura Luiz de Queiroz, São Paulo. Proceedings, FapUNIFESP. p.801-810.

Cabral PDS, Soares TCB, Lima ABP, Soares YJB & Silva JAD (2011) Análise de trilha do rendimento de grãos de feijoeiro (*Phaseolus vulgaris* L.) e seus componentes. Revista Ciência Agronômica, 42:132-138.

Carvalho FIF, Lorencetti C & Benin G (2004) Estimativas e implicações da correlação no melhoramento vegetal. Pelotas, Editora Universitária da UFPel. 142p.

Casarotto G (2013) Relações lineares entre caracteres fenológicos, morfológicos e produtivos. Master Dissertation. Universidade Federal de Santa Maria, Santa Maria. 76p.

Chavaglia AC (2016) Potencial produtivo, variabilidade genética e depressão por endogamia em população derivada de híbridos comerciais de milho. Master Dissertation. Universidade Federal de Goiás Regional Jataí, Jataí. 73p.

Chen J, Zhang L, Liu S, Li Z, Huang R, Li Y, Cheng H, Li X, Zhou B, Wu S, Chen W, Wu J & Ding J (2016) The Genetic Basis of Natural Variation in Kernel Size and Related Traits Using a Four-Way Cross Population in Maize. Plos One, 11:01-12.

CONAB – Companhia Nacional de Abastecimento (2018) Acompanhamento da safra brasileira de grãos. Available at: <https://www.conab.gov.br/info-agro/safras/graos/boletim-da-safra-de-graos?start=40>. Accessed on: August 31rst, 2018.

Cruz CD (2006) Programa GENES: Biometria. Viçosa, Editora UFV. 382p.

Cruz CD, Regazzi JA & Carneiro PCS (2014) Modelos biométricos aplicados ao melhoramento genético. 3ª ed. Viçosa, Editora UFV. 480p.

Dao A, Sanou J, Traore EVS, Gracen V & Danquah EY (2017) Selection of Drought Tolerant Maize Hybrids Using Path Coefficient Analysis and Selection Index. Pakistan Journal of Biological Sciences, 20:132-139.

Durães FOM (1999) Prolificidade. Revista Cultivar, 1:36-37.

Edmeades GO, Bolaños J, Banziger M, Ribault JM, White JW, Reynolds MP & Lafitte HR (1998) Improving crop yields under water deficits in the tropics. In: 2ª Internatinal Crop Science Congress, New Delhi. Proceedings, Oxford/IBH. p.437-451.

Entringer GC, Vettorazzi JCF, Santos EA, Pereira MG & Viana AP (2016) Genetic gain estimates and selection of S1 progenies based on selection indices and REML/BLUP in super sweet corn. Australian Journal of Crop Science, 10:411-417.

Faluba JDS, Miranda GV, DeLima RO, Souza LVD, Debem EA & Oliveira AMC (2010) Potencial genético da população de milho UFV 7 para o melhoramento em Minas Gerais. Ciência Rural, 40:1250-1256.

França ÁEDD, Parrella RADC, Souza VFD, Bastos GQ, Nunes JAR & Schaffert RE (2016) Seleção simultânea em progênies de sorgo-sacarino por meio de índices de seleção. Pesquisa Agropecuária Brasileira, 51:1737-1743.

Gabriel APC (2006) Seleção recorrente recíproca em famílias de irmãos completos em milho (*Zea mays* L.) assistida por marcadores moleculares. Master Dissertation. Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes. 112p.

Galvão JCC & Miranda GV (2004) Tecnologias de produção de milho. Viçosa, Editora UFV. 366p.

Garcia AA & Souza Júnior CLD (1999) Comparação de índices de seleção não paramétricos para a seleção de cultivares. Bragantia, 58:253-267.

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, Carena MJ & Miranda Filho JB (2010) Quantitative genetics in maize breeding. 6ª ed. New York, Springer. 515p.

Hamblin J & Zimmermann MDO (1986) Breeding common bean for yield in mixtures. Plant breeding reviews, 4:245-272.

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

Knapp SJ, Stroup WW & Ross WM (1985) Exact confidence intervals for heritability on a progeny mean basis. Crop Science, 25:192-194.

Lopes SJ, Lúcio ADC, Storck L, Damo HP, Brum B & Santos VJ (2007) Relações de causa e efeito e espigas de milho relacionadas aos tipos de híbridos. Ciência Rural, 37:1536-1542.

Mendes FF, Ramalho MAP & Abreu ÂFB (2009) Índice de seleção para escolha de populações segregantes do feijoeiro-comum. Pesquisa Agropecuária Brasileira, 44:13121318.

Mistro JC, Fazuoli LC & Gallo PB (2007) Estimates of genetic parameters in Arabic coffee derived from the Timor hybrid. Crop Breeding and Applied Biotechnology, 7:141-147.

Moraes DF & Brito CH (2017) Análise de possível correlação entre as características morfológicas do colmo do milho e o acamamento. Plant Biotechnology Journal, 15:1439-1452.

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.

Nardino M, Baretta D, Carvalho IR, Follmann DN, Konflanz VA, Souza VQ, Oliveira AC & Maia LC (2016) Correlações fenotípica, genética e de ambiente entre caracteres de milho híbrido da região sul do Brasil. Revista Brasileira de Biometria, 34:379-394.

Nzuve F, Githiri S, Mukunya DM & Gethi J (2014) Genetic Variability and Correlation Studies of Grain Yield and Related Agronomic Traits in Maize. Journal of Agricultural Science, 6:166-176.

Oliveira AS (2013) Variabilidade genética e potencial produtivo em três populações semiexóticas de milho (*Zea Mays* L.). Master Dissertation. Universidade Federal de Goiás, Jataí. 82p.

Oliveira AS, Miranda Filho JB & Reis EF (2015) Variability and inbreeding in semiexotic maize populations. Genetics and Molecular Researchm, 14:1184-1199.

Palomino EC, Ramalho MAP & Ferreira DF (2000) Tamanho da amostra para avaliação de famílias de meios-irmãos de milho. Pesquisa Agropecuária Brasileira, 35:1433-1439.

Pedrozo CA, Benites FRG, Barbosa MHP, Resende MDV & Silva FL (2009) Eficiência de índices de seleção utilizando a metodologia REML/BLUP no melhoramento da cana-de-açúcar. Scientia Agraria, 10:31-36.

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

Pinheiro MH (2004) Melhoramento intrapopulacional recorrente de milho-pipoca, utilizando famílias de meios-irmãos. Doctoral Thesis. Universidade Federal de Viçosa, Viçosa. 67p.

R Development Core Team (2018) R: A language and environment for statistical computing. Available at: <https://www.gbif.org/pt/tool/81287/r-a-language-and-environment-for-statistical-computing>. Accessed on: August 15th, 2019.

Vencovsky R (1987) Herança quantitativa. In: Paterniani E & Viegas GP (Eds.) Melhoramento e produção do milho. 2ª ed. Campinas, Fundação Cargill. p.137-214.

Ramalho MAP, Abreu AF, Santos JB & Nunes JAR (2012) Aplicações da genética quantitativa no melhoramento de plantas autógamas. Lavras, Editora UFLA. 522p.

Regazzi AJ, Silva HD, Viana J, Soriano M & Cruz CD (1999) Análises de experimentos em látice quadrado com ênfase em componentes de variância. Pesquisa Agropecuária Brasileira, 34:1987-1997.

Revolti LTM, Moraes KE, Amaral CB, Dutra SMF, Silva FAM, Caprio CH & Môro GV (2016) Correlação entre caracteres de milho de ciclo super precoce. Ciência & Tecnologia: Fatec-JB, 8:01-06.

Santos FS, Amaral Júnior AT, Freitas Júnior SP, Rangel RM & Pereira MG (2007) Predição de ganhos genéticos por índices de seleção na população de milho pipoca UNB-2U sob seleção recorrente. Bragantia, 66:389-396.

Santos LPD, Aquino LA, Marques PH, Nunes P & Xavier FO (2013) Doses de Nitrogênio na cultura do milho para altas produtividades de grãos. Revista Brasileira de Milho e Sorgo, 12:270-279.

Santos PG, Juliatti FC, Buiatti AL & Hamawaki OT (2002) Avaliação do desempenho agronômico de híbridos de milho em Uberlândia, MG. Pesquisa agropecuária brasileira, 37:597-602.

Schmitz TH, Bertoncelli P, Ortiz S, Piran Filho FA, Jesus E & Martin TN (2010) Correlação entre as variáveis morfológicas e de produção na cultura do milho. In: Seminário: Sistemas de Produção Agropecuária - Ciências Agrárias, Animais e Florestais, Dois vizinhos. Proceedings, SSPA. p.01-04.

Selvaraj CI & Nagarajan P (2011) Interrelationship and Path-coefficient Studies for Qualitative Traits, Grain Yield and other Yield Attributes among Maize (*Zea mays* L.). International Journal of Plant Breeding and Genetics, 5:209-223.

Silva RBV & Ferreira DF (2003) Alternativas para o teste t com variâncias heterogêneas avaliadas por meio de simulação. Ciência e Agrotecnologia, 27:185-191.

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

Souza AC (2015) Variabilidade genética em três populações de milho. Master Dissertation. Universidade Federal de Goiás Regional Jataí, Jataí. 62p.

Souza ARR, Miranda GV, Pereira MG & Souza LV (2008) Correlação de caracteres de uma população crioula de milho para sistema tradicional de cultivo. Revista Caatinga, 21:183-190.

Toledo FHRB (2010) Controle genético e interrelação de um caracter de limiar e outros componentes da espiga do milho. Master Dissertation. Universidade Federal de Lavras, Lavras. 60p.

Vasconcelos ES, Ferreira 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.

Vencovsky R & Barriga P (1992) Genética biométrica aplicada ao fitomelhoramento. Ribeirão Preto, Sociedade Brasileira de Genética. 496p.

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