Original Article

GENETIC VARIABILITY AND YIELD POTENTIAL OF THREE SEMIEXOTIC MAIZE (*Zea mays* L.) POPULATIONS

VARIABILIDADE GENÉTICA E POTENCIAL PRODUTIVO EM TRÊS POPULAÇÕES SEMIEXÓTICAS DE MILHO *(Zea mays L.)*

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ABSTRACT: The rapid increase of the maize crop in the last decades in Brazil, mainly in the Central West region, has encouraged the second crop (usually maize after soybean) in the same year. For that reason the need for the exploitation of new sources of germplasm seems to be apparent to attend the challenge to create new cultivars (populations or hybrids) adapted to the extremely varying environments. Following this principle, the objective of the present work was directed to the study of genetic variability and yield potential of three semiexotic populations (CRE-01, CRE-02, CRE-03) under the condition of second crop in the Southwest region of the State of Goiás (Brazil). In addition, one cycle of recurrent selection with half-sib families was completed in each population. Half-sib families from each population (200, 180 and 180, respectively) were evaluated in completely randomized block experiments with three replications in Jataí (GO). Parameters estimates were obtained for ear yield (EY), grain yield (GY), plant height (PH), ear height (EH), ear length (EL) and ear diameter (ED). The population means for GY were 5.68 t/ha, 5.83 t/ha and 5.83 t/ha, which were around 70% of the hybrid check. The coefficients of heritability (family mean basis) varied from 0.36 to 0.70; 0.47 to 0.69; and 0.39 to 0.68 for the respective populations. Estimates of the additive genetic variance for grain yield (g/plant) were 316.1, 266.4 and 258.4; and the expected gain from selection were 11.8%, 10.1% and 9.3%, respectively.

PALAVRAS-CHAVE: Exotic germplasm. Genetic parameters. Recurrent selection. *Zea mays*.

INTRODUCTION

The acreage of the maize crop in Brazil has increased spectacularly in the last decades, thus creating incentives for a second crop (usually maize after soybean) in many important agricultural areas. Such expansion was followed by a better use of modern technologies thus allowing to reach higher levels of productivity. The acreage for second crop maize increased from 356 thousand hectares in 1990 to approximately 1.5 million ha in 1995 (TSUNESHIRO; OKAWA, 1996), reaching 9 million ha and producing 46.2 million tons in the last year (2012/2013); for comparison, the first (normal) crop covered 7 million ha producing 35.2 million tons. The evolution of the second crop was from 24% in 2001/2001 to 56% in the last year. The highest production of the second crop maize is concentrated in the Central West region, represented by the states of Mato Grosso, Mato Grosso do Sul and Goiás, that together cover around 67% of the second crop production of corn (CONAB, 2013).

Even cognizant on the importance of the maize crop (normal and second crop) expansion, other subjects must be taken into account in order to maximize its production and productivity. One important point is the appropriate choice and use of the available germplasm that, by the way, must be in accordance with the objectives of the breeding program. In this sense, broadening the genetic base, by exploiting new sources of germplasm (varieties, populations, composites, synthetics, races, etc.), including exotics, may be a recommended strategy for the conditions of the vast array of environments like those occurring in Brazil. Exotic germplasm has largely contributed to increase the variability and the efficiency of breeding programs for the development of cultivars (MIRANDA FILHO, 1992; REGITANO NETO et al., 1997; SANTOS et al., 2000). The development of commercial hybrids initiated with local germplasm represented by old varieties such as Cateto and Dente Paulista. After that an extraordinary advance occurred with the introduction of exotic germplasm, mainly *Tuxpeño* and related races of Mexico and Central America that largely contributed for the development of high yielding semident hybrids (MIRANDA FILHO; VIÉGAS, 1987). The importance of the introduction of the race *Tuxpeño* for the maize breeding in Brazil was stressed by Paterniani (1990). Several other introductions have contributed to the maize breeding programs along the time. In fact, several authors

have long been emphasized the importance of incorporation of exotic germplasm in maize breeding programs (NASS et al., 2001), but the introductions have been below the acceptable level of adaptation, thus making difficult to attain the desirable objectives. Nevertheless, some experiences have been accumulated and surely will contribute to overcome inherent obstacles (PATERNIANI, 1990; TATER et al., 2004; GOODMAN 2005) in Brazil, most of the introduced germplasm has been from tropical origin, which makes amenable the problem of adaptation.

After incorporation or introgression of the exotic germplasm, the next phase is to establish means to get knowledge on the genetic properties of the new population, particularly on the genetic variability of important quantitative traits that are in some extent influenced by the environmental effect. In this sense, the additive genetic variance, the coefficient of heritability and the expected gain from selection are among the most important parameters that will provide information on the genetic structure of the breeding population (VENCOVSKY, 1987; FALCONER, 1981; CRUZ, 2005; HALLAUER et al., 2010). There are several genetic designs that can be used to estimate the genetic variance and its components (HALLAUER et al., 2010). However, the use of half-sib families has been commonly used for that purpose in Brazil (VENCOVSKY et al., 1988). Several other reports have corroborated this fact (CARVALHO et al., 2007; ANDRADE; MIRANDA FILHO, 2008; SOUZA et al., 2009; LIMA NETO; SOUZA JÚNIOR, 2009; FALUBA et al. 2010; KIST et al., 2010; CANDIDO et al., 2011).

The objective of this work was to evaluate the genetic variability and yield potential of three semiexotic populations for their use in recurrent selection programs, toward the development of germplasm specially adapted to the environmental conditions of the Southwestern region of the State of Goías.

MATERIAL AND METHODS

A sample of 682 inbred (S_4) lines previously selected for resistance to *corn stunt* complex were introduced from CIMMYT (*Centro Internacional de Mejoramiento de Maíz y Trigo*, Colombia). A selected sample of 51 lines was crossed with three local testers: **P-3041**, represented by the F_2 generation of the commercial hybrid (Pioneer HyBred Seeds); **CMS-14C**, an open pollinated population derived from *Pool-25* (CIMMYT, Mexico) and released by CNPMS/EMBRAPA; and

ESALQ-PB23, a broad base population obtained from the cross ESALQ-PB2 (dent type) and ESALQ-PB3 (flint type). After evaluation, a sample of testcrosses representing each tester was intercrossed to develop three populations: CRE-01 ≡ 38 lines x **P-3041**; CRE-02 ≡ 39 lines x **CMS-14C**; CRE-02 ≡ 32 lines x **ESALQ-PB23**. After the synthesis of the three semiexotic populations (CRE-01, CRE-02, CRE-03) samples of half-sib families of sizes 50, 70 and 50, respectively, were evaluated in Jataí (GO) in 2008. A mild selection with intensities 13/50, 18/70, and 11/50 was applied and the recombined samples of the selected families represent the base populations in the present project. Isolated blocks from each population were used to generate half-sib families by random open pollination. The number of families were 200, 180 and 180 in the sequence of populations, which were divided into four experiments of 50, 45 and 45 families, respectively. The yield trials were in completely randomized blocks with three replications in one location (Farm *Três Fronteiras*, region of Jataí, GO). Plots were 4.0m long spaced 0.90m apart with 20 plants per plot after thinning. The following traits were analyzed: PH – plant height (cm), EH – ear height (cm), EL – ear length (cm), ED – ear diameter (cm), DR – general disease resistance (notes: 1 – resistant to 9 – susceptible), EY – total ear weight (g/plot) and GY – grain weight (g/plot); both EY and GY were corrected by the linear regression of yield on the number of ears per plot, according to methodology suggested by Miranda Filho, J.B. (apud VENCOVSKY; BARRIGA, 1992). One commercial hybrid (DAS 2B-710) was used as check, intercalated at ten plots in each block. The analyses of variance were performed according to the model $Y_{ij} = m + f_i + b_j + e_{ij}$ where Y_{ij} is the experimental unit referring to the ith family in the jth block, represented by plot total (EY and GY) or sample means of five plants (PH, EH, EL, ED). In the model, m is the general mean, f_i is the random effect of the ith family, b_j is the random effect of the jth block, and e_{ij} is the error term (random effect) for plots. For the purposes of this work, the following expectations are of interest:

$E(f_i) = E(e_{ij}) = 0$, $E(f_i^2) = \sigma_f^2$ (genetic variance among half-sib families), and $E(e_{ij}^2) = \sigma^2$ (plot-to-plot error variance). In the analysis of variance the mean squares for Families and Error have the following expected values: $E(M_f) = \sigma^2 + 3\sigma_f^2$ and $E(M_e) = \sigma^2$. Table 1 shows the procedures for estimating parameters in populations.

Table 1. Formulas for the estimation of quantitative parameters in populations represented by random samples of half-sib families.

Parameters	Estimates
General mean	$m_0 = \frac{1}{IJ} \Sigma Y_{ij}$
Phenotypic variance among half-sib family means	$\hat{\sigma}^2_{HS} = \frac{1}{3} M_f$
Genetic variance among HS families	$\hat{\sigma}^2_f = \frac{1}{3}(M_f - M_e)$
Additive genetic variance (only for HS)	$\hat{\sigma}^2_A = 4\, \hat{\sigma}^2_f$
Error variance	$\hat{\sigma}^2 = M_e$
Coefficient of heritability (family mean basis)	$h^2_f = (M_f - M_e)/ M_f$
Coefficient of variation	$CV\% = 100 \sqrt{M_e}/m$
Genetic coefficient of variation	$CVg\% = 100\, \hat{\sigma}_f /m$
Index of variation	$\theta = CVg/CV$
Expected gain from selection	$G_s = d_s.\, h^2_f$

[$d_s = m_s - m_0$: differential of selection where m_s is the mean of the selected sample for yield; for any other trait (x), m_s is the mean of x in the same sample selected for yield].

RESULTS AND DISCUSSION

The analysis of variance for all traits in the three semiexotic populations showed significance (*F* test; $P < 0.01$) for the variation among families (Table 2). The coefficients of variations were in the range of 4.0% (ear diameter) to 11.1% (grain yield). The set of means for ear yield (t/ha) and grain yield (t/ha) in the sequence [CRE-01, CRE-02, CRE-03] were [7.21, 7.39, 7.48] and [5.68, 5.83, 5.83], respectively. For check means, sets were [9.21, 9.22, 9.54] for EY and [8.01, 8.17, 8.28] for GY, so that in percent of check the family means were in the range of 78.3% to 80.2% for EY and around

71% for GY; it is then clear that the ratio GY/EY for the hybrid check is much higher than for half-sib families in all three populations, averaging 87.5% and 78.5%, respectively.

Ear yield and grain yield of the three semiexotic populations were considered in a good level, expressed as near 80% and around 70% of the hybrid check and this fact is attributable to the genetic base of the three testers used for introgression of the exotic germplasm. The results are similar to those found by Kist et al. (2010) in the open-pollinated population MPA, a wide base composite undergoing recurrent selection in the State of Santa Catarina.

Table 2. Mean squares[k] for Families (M_F) and Error (M_E), coefficients of variation (CV%) and observed means (m) for six traits in three semiexotic populations.

Population	M_F	M_E	CV%	m_o	m_H	m_L	m_C
Plant height (cm)[a]							
CRE-01	299.6 **	191.7	5.6	246.7	281.0	205.0	215.4
CRE-02	277.6 **	148.6	4.9	247.7	284.0	211.0	222.2
CRE-03	222.9 **	136.6	4.5	261.3	300.0	200.0	231.8
Ear height (cm)[a]							
CRE-01	246.6 **	147.7	8.6	141.3	180.0	100.0	112.7

CRE-02	247.0 **	127.2	7.7	147.4	190.0	100.0	118.2
CRE-03	269.9 **	139.9	7.6	156.6	190.0	113.0	126.9
Ear diameter (cm)[b]							
CRE-01	0.086 **	0.041	4.3	4.7	5.3	4.0	4.9
CRE-02	0.128 **	0.044	4.5	4.7	5.5	4.0	4.8
CRE-03	0.087 **	0.037	4.0	4.7	5.5	4.3	4.9
Ear length (cm)[b]							
CRE-01	2.405 **	1.113	7.0	15.1	19.3	10.0	14.7
CRE-02	2.439 **	1.256	7.3	15.4	19.0	10.8	14.5
CRE-03	2.334 **	1.081	6.8	15.2	19.8	11.8	14.8
Ear yield (t/ha)[b]							
CRE-01	546.5 **	164.1	9.9	7.21	9.78	4.83	9.21
CRE-02	516.3 **	162.9	9.6	7.39	10.1	4.56	9.22
CRE-03	429.4 **	137.1	8.7	7.48	10.1	4.83	9.54
Grain yield (t/ha)[b]							
CRE-01	365.4 **	128.3	11.1	5.68	7.94	3.44	8.01
CRE-02	325.4 **	125.6	10.7	5.83	8.00	3.50	8.17
CRE-03	297.4 **	103.5	9.70	5.83	8.33	3.66	8.28

[k] Degrees of freedom for M_F and M_F: [a] [199 and 199 for CRE-01; 179 and 179 for CRE-02 and CRE-03]. [b] [199 and 398 for CRE-01; 179 and 358 for CRE-02 and CRE-03]. **[Significance of the F test: P<0.01]. m_o: population mean and its range m_H (higher) and m_L (lower); m_C: hybrid check mean.

Figure 1 shows the grain yield (t/ha) of half-sib families and their distribution (percentage) for the three semiexotic populations; a slight superiority on the average of CRE-03 is apparent in Figure 1. In fact, for EY and GY, expressed in percent of the hybrid check, the population means were [78.3, 80.2, 78.4] and [70.9, 71.4, 70.4], respectively, in the sequence [CRE-01, CRE-02, CRE-03]. Even with means around 5.7 t/ha, some families reached yields beyond 7.0 t/ha (~85% of the hybrid check).
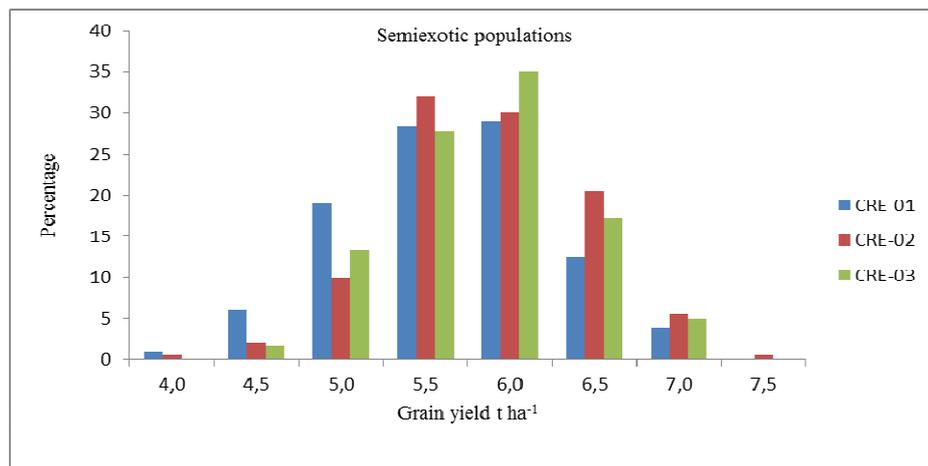
Figure 1. Distribution of means for grain yield (t/ha) in three semiexotic populations (CRE-01, CRE-02, CRE-03). Jataí (GO), 2012.

For both PH and EH family means were in the order CRE-01<CRE-02<CRE-03, averaging 252cm and 148cm, corresponding to 113% and 124% of the check, respectively. The observed means for PH and EH were classified as intermediate to high in the three populations, but the higher values were for CRE-03. In fact, the population used as base for the development of CRE-03 was a wide base composite from typically tropical gemplasm with the well known characteristic of tall plants and high ear placement. All the semiexotic populations also were taller than

49 cultivars evaluated under second crop condition in five locations in the State of Goiás (CAMPOS et al., 2010), thus indicating the need of some strategy to decrease the plant height and ear placement toward a pattern of plant architecture that can be acceptable by the local corn growers.

Very small differences were observed for ED and EL among populations, which were around 4.7cm and 15.3cm; on the average, ED was a little lower and EL a little higher than the hybrid check. Other authors have reported means in the range of 4.2cm to 4.8cm for ED and from 15.0cm to 17.5 cm for EL (ANDRADE; MIRANDA FILHO, 2008; GARBUGLIO et al., 2009). On the other hand, the expression of ED and EL in the three populations did not differ greatly from six commercial hybrids grown in the region of Jataí (MARCHÃO et al., 2005).

In Table 3 are the estimates of parameters for six traits in the three populations. For EY and GY the phenotypic variance among half-sib family means (g/plant) averaged 166 and 110 while the genetic variance among families (σ_f^2) averaged 114 and 70, respectively. The additive genetic variance (σ_A^2) is calculated directly from $\hat{\sigma}_f^2$ and the sets of estimates in the order of populations were [509.9, 471.2, 389.7] and [316.1, 266.4, 258.4] for EY and GY, averaging 456.9 and 280.3, respectively; the averages were close to the upper limit of estimates (450 for EY and 333 for GY) reported by Santos and Miranda Filho (1992) for three semiexotic populations in two locations. For EY the estimate was within the range $250 < \hat{\sigma}_A^2 < 600$ shown by Miranda Filho e Nass (2001); the average of the three populations was similar to the estimate of 581.7 reported by Andrade e Miranda Filho (2008). Also, for GY the estimate was similar to the average (306.1 g^2) of 45 estimates in Brazilian populations reported by Miranda Filho (1985) ; and close to 276.8 (average of three locations) given by Kist et al. (2010). For comparison, it is worthwhile to mention the estimates of σ_A^2 for GY reported by Hallauer & Miranda Filho (1988), as 469.1 on the average of 99 estimates; the authors also mentioned 188.0 as the average of four experiments in the population BSSS (*Iowa Stiff Stalk Synthetic*) and 241.2 as the average in seven cycles of recurrent selection in the BSK(S) population. Other estimates at the interpopulation level were also given, as 386.3 (BSSS x BSCB1 as

tester) and 373.8 (BSCB1 x BSSS as tester) in eight cycles of reciprocal recurrent selection.

The results of the three semiexotic populations under study, referring to variance estimates, indicate a good pattern of genetic variation for enabling them as base populations for a recurrent selection program in the Southwest region of the State of Goiás.

Estimates of the additive genetic variance ($\hat{\sigma}_A^2$) for PH and EH were within the range $170cm^2 < \hat{\sigma}_A^2 < 260$ cm², with low variation among populations, averaging 215.5 cm² and 232.4 cm²; the estimates were a little lower for PH and a little higher for EH, as compared to estimates (323.8 and 170.3) given by Andrade & Miranda Filho (2008) and were also similar to the average (321.0 and 218.0 cm², respectively) of 16 estimates summarized by Miranda Filho (1985) in Brazilian populations. The estimates were, however, greater for PH and about the same for EH in relation to 45 estimates summarized by Hallauer & Miranda Filho (1988). Estimates higher than those herein observed were found by Candido et al. (2011) in the population Isanão (a brachytic composite) in which the higher variability may be the result of different expression of the brachytic gene (*br₂*) in the homozygous state in different genotypes. For PH the estimates also were very smaller than the average (579.3 cm², over three locations) reported by Kist et al. (2010).

The sets of estimates of σ_A^2 (x10^2) for ED and EL were [6.00, 11.20, 6.67] and [172.3, 157.7, 167.1], averaging 7.96 and 165.7, which are higher than the averages (3.9 and 142.3) of four experiments of BSSS population reported by Hallauer e Miranda Filho (1988); the same authors gave the average of 36 estimates as 4.6 and 152.4. The estimates given by Andrade e Miranda Filho (2008) for the population ESALQ-PB1 were 4.40 and 264.0, respectively. For EL, Santos e Miranda Filho (1992) reported values of 139.4, 96.2 and 191.6 in the local population E (ESALQ-PB1) and crosses E x EC (race *Cravo*) and E x EE (race *Entrelaçado*), respectively. Even with a restricted amount of information, the results clearly indicate that the populations under study have expressive variability for changing ear length and ear diameter by selection.

Table 3. Estimates of the phenotypic variance among family means ($\hat{\sigma}^2_{HS}$), genetic variance among families ($\hat{\sigma}^2_{f}$), additive genetic variance ($\hat{\sigma}^2_{A}$), coefficient of heritability (h^2_f: family mean basis), genetic coefficient of variation (CVg%), index of variation (θ), expected gain from selection (Gs) and expected gain from selection in percentage (Gs%) for six traits in half-sib families of three semiexotic populations. Jataí (2012).

Population	Parameters estimates							
	$\hat{\sigma}^2_{HS}$	$\hat{\sigma}^2_{f}$	$\hat{\sigma}^2_{A}$	h^2_f	CVg%	θ	G_s	$G_s\%$
	Plant height (cm)							
CRE-01	149.8	53.98	215.9	0.36	2.98	0.53	-1.04	-0.42
CRE-02	138.8	64.53	258.1	0.47	3.24	0.66	2.02	0.81
CRE-03	111.4	43.11	172.4	0.39	2.51	0.56	0.12	0.05
	Ear height (cm)							
CRE-01	123.3	49.42	197.7	0.40	4.97	0.58	-1.32	-0.93
CRE-02	123.5	59.93	239.7	0.49	5.25	0.69	1.32	0.83
CRE-03	134.9	64.99	259.9	0.48	5.15	0.68	-0.64	-0.41
	Ear diameter (cm)							
CRE-01	2.85	1.50	6.00	0.53	2.59	0.61	0.04	0.84
CRE-02	4.25	2.79	11.20	0.66	3.56	0.80	0.07	1.40
CRE-03	2.90	1.68	6.67	0.58	2.73	0.68	0.04	0.84
	Ear length (cm)							
CRE-01	8.01	4.30	172.3	0.54	4.34	0.62	0.32	2.12
CRE-02	8.13	3.94	157.7	0.49	4.09	0.56	0.20	1.27
CRE-03	7.78	4.17	167.1	0.54	4.25	0.62	0.04	0.26
	Ear yield (g/plant)							
CRE-01	182.2	127.5	509.9	0.70	8.70	0.88	14.98	11.54
CRE-02	172.1	117.8	471.2	0.69	8.16	0.85	14.12	10.62
CRE-03	143.1	97.43	389.7	0.68	7.33	0.84	11.95	8.870
	Grain yield (g/plant)							
CRE-01	121.8	79.03	316.1	0.65	8.70	0.79	12.07	11.81
CRE-02	108.5	66.60	266.4	0.61	7.77	0.73	10.63	10.12
CRE-03	99.12	64.61	258.4	0.79	7.66	0.79	9.731	9.274

The coefficient of heritability (h^2_f) for family means indicates directly the level of expected response by selection of each trait under study. For the yield traits (EY and GY) the estimates were in the range of 0.60 to 0.80, that can be considered in a good level for selection purposes; these estimates are much higher than the average of 0.34 and 0.35 given by Kist et al. (2010) and Miranda Filho e Nass (2001), for GY and EY, respectively. For plant and ear height, estimates of h^2_f were much lower (0.36 to 0.49) than for the yield traits. Generally, the heritability is higher for PH and EH than for yield traits (EY and GY) because the later are more affected by the dominant gene action (HALLAUER; MIRANDA FILHO, 1988); in the present case, the results are explained by the genetic structure of the semiexotic populations, rather than on type of gene

action controlling the trait. For the ear traits (ED and EL), the estimates of h^2_f were considered relatively high (around 0.5), which are similar to the 0.56 and 0.66 reported by Andrade & Miranda Filho (2008).

The index of variation (θ) is also related to the expected gain from selection and were above 0.5 for all traits in the three populations. Vencovsky e Barriga (1992) indicated that values of θ near or above 1.0 assure a favorable condition for selection. Here, the estimates were the lower (0.53 < θ̂ < 0.68) for PH and EH, and medium (0.56 < θ̂ < 0.80) for ED and EL. For EY and GY, the sets of θ estimates were [0.88, 0.85, 0.84] and [0.79, 0.73, 0.79] averaging 0.857 and 0.770, respectively , in the sequence of populations. In the present work, θ estimates did not follow the usual pattern of other studies. In fact, KIST *et al.* (2010) reported θ̂ < 0.5

(0.418 on the average) for GY in three experiments of the population MPA; for EH $\hat{\theta}$ values were around 1 (average 1.061). In the same way, Miranda Filho & Nass (2001) reported results from five semiexotic populations, showing estimates in the range of $0.361 < \hat{\theta} < 0.661$ for EY, $0.702 < \hat{\theta} < 0.934$ for PH, $0.735 < \hat{\theta} < 0.987$ for EH, $0.190 < \hat{\theta} < 0.664$ for EL and $0.416 < \hat{\theta} < 0.793$ for ED; averaging 0.528, 0.827, 0.852, 0.463 and 0.598, respectively.

After a final analysis of all the parameters related to genetic variability, it seems clear that yield traits were identified as the most promising for an effective selection. In fact, selection of the 20 higher yielding families was practiced in the three populations (CRE-01, CRE-02, CRE-03), representing selection intensities of 10.0%, 11.1% and 11.1%, respectively. After recombination of the selected families in isolated blocks with open-pollination, the expected effective size in the improved populations should be Ne ~ 80 that is considered an appropriate number in recurrent selection programs. The expected gain from selection, as explained above, were 11.8%, 10.1% and 9.3%, respectively, averaging 10.40%. After one cycle of selection considering 10% yield gain, the expected means (t/ha) would be 6.25, 6.41 and 6.41, representing around 78% of the check yield. Under the same conditions (hypothesis of no changes in the genetic and environmental parameters), the expected mean of populations after two cycles of recurrent selection would be around 85% of the hybrid check.

The overall results of this work thus indicate that the three populations can be used successfully as base for a recurrent selection program toward the enhancement of their yield level, and agronomic traits at a less extent. The main purpose of this project seems to be achieved, that is to open the opportunity to make use of an interesting source of exotic germplasm, identified by the resistance to the *corn stunt* complex, by incorporation into local and adapted maize populations. In addition, because the tropical origin of the introduced germplasm, it can contribute immediately to widen the genetic variability of known or unknown characteristics of local breeding populations.

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RESUMO: O rápido aumento da cultura do milho nas últimas décadas no Brasil, principalmente na região Centro-oeste, causou incentivo para o milho "safrinha" (segunda cultura, geralmente milho após soja) no mesmo ano agrícola. Por esta razão, a necessidade de explorar novas fontes de germoplasma parece óbvia para atender ao desafio de criar novas cultivares (populações ou híbridos) adaptadas aos ambientes extremamente variáveis. Seguindo esta diretriz, o objetivo do presente trabalho foi direcionado ao estudo da variabilidade e do potencial produtivo de três populações semiexóticas (CRE-01, CRE-02, CRE-03) sob a condição de cultura de "safrinha" na região Sudoeste do Estado de Goiás (Brasil). Além disso, foi completado um ciclo de seleção recorrente com famílias de meios irmãos em cada população. As famílias de meios irmãos de cada população (200, 180 e 180, respectivamente) foram avaliadas experimentalmente em blocos casualizados com três repetições em Jataí (GO). Foram obtidas estimativas de parâmetros para produção de espigas (EY) e de grãos (GY), altura da planta (PH) e da espiga (EH) e comprimento (EL) e diâmetro (ED) da espiga. As médias populacionais para GY foram, respectivamente, 5,68 t/ha, 5,83 t/ha e 5.83 t/ha, equivalendo a cerca de 70% do híbrido testemunha. Os coeficientes de herdabilidade (médias de famílias) variaram de 0,36 a 0,70; 0,47 a 0,69; 0.39 a 0,68 para as respectivas populações. As estimativas da variância aditiva para produção de grãos (g/planta) foram 316,1; 266,4 e 258,4; e os ganhos esperados por seleção foram de 11,8%, 10,1% e 9.3%, respectivamente, para as três populações.

PALAVRAS-CHAVE: Germoplasma exótico. Parâmetros genéticos. Seleção recorrente,. *Zea mays*.

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