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Response to the selection in the 11th cycle of reciprocal recurrent selection among full-sib families of maize

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ABSTRACT. The continuous gains in cycles of recurrent selection have raised disagreement among researchers. Two hundred and forty-two full-sib families were obtained from CIMMYT and Piranão populations and evaluated in a simple lattice design in two environments to estimate the response to selection in the 11th cycle of the UENF reciprocal recurrent selection program. No genotype x environment interaction was observed for most of the traits evaluated, indicating that a single recurrent selection program can be conducted for both sites. The population studied exhibited wide genotypic variability and heritability estimates ranged from 33 to 73%, indicating prospects of selection gain for the following cycles. The predicted genetic gain in yield was 12.90%. It is possible to conclude that the populations studied may be promising for the achievement of new selection cycles, which provides a continuous concentration of favorable alleles and the production of hybrids for the North and Northwest regions of the state of Rio de Janeiro.

Keywords: genetic gains, selection index, interpopulation hybrids, longevity of recurrent selection.

Resposta a seleção no 11° ciclo de seleção recorrente recíproca entre famílias de irmãos-completos de milho

RESUMO. A contínua obtenção de ganhos em ciclos de seleção recorrente tem sido motivo de controvérsia entre pesquisadores. 242 famílias de irmãos-completos foram obtidas entre as populações CIMMYT e Piranão, e avaliadas em delineamento látice simples, em dois ambientes para investigar as estimativas da resposta à seleção no 11° ciclo do programa de seleção recorrente recíproca da UENF. Não houve interação genótipos por ambiente para a maioria das características avaliadas, indicando que um único programa de seleção recorrente pode ser conduzido para ambos os locais. A população avaliada revelou ampla variabilidade genotípica, com estimativas de herdabilidade variando de 33 a 73%, indicando perspectivas de ganho de seleção para os próximos ciclos. O ganho genético predito para produtividade foi de 12,90%. Conclui-se que as populações avaliadas são promissoras para a consecução de novos ciclos de seleção, proporcionando concentração contínua de alelos favoráveis e a produção de híbridos para as regiões Norte e Noroeste Fluminense.

Palavras-chave: ganhos genéticos, índice de seleção, híbridos interpopulacionais, longevidade da seleção recorrente.

Introduction

Maize (*Zea mays* L.) is a product of high economic importance. It is grown in almost all agricultural regions of the world for food, for animal feed and, recently, as a source of biofuel (FUZATTO et al., 2002). Brazil is the third largest producer of maize, surpassed only by the United States and China (FAO, 2011). The production of maize in Brazil has significantly increased in recent years.

In a recent past, the economic progress in Northern and Northwestern State of Rio de Janeiro was associated with agriculture, almost exclusively related to sugar cane culture and livestock (RIBEIRO et al., 2009; SILVA, 2006). Today, local agriculture is stagnant and dependent on new alternatives for profitable cultivation, which justified the development of a maize breeding program, aimed at producing cultivars with superior traits and adapted to the conditions of the region.

Among the plant breeding methods, Reciprocal Recurrent Selection is used for two different populations that have complementary traits (COMSTOCK; ROBINSON, 1948). This method favors the achievement of gains due to the additive effects, through the concentration of the favorable alleles in both populations, as well as the dominance deviations, since the genetic distance between the populations is maintained, which allows exploiting the heterosis in crosses between the populations and/or lineages deriving from them (SANTOS et al., 2007; SOUZA JÚNIOR; PINTO, 2000).

The most important goal in a recurrent selection program is the achievement of genetic gains for traits of agronomic interest at each new cycle of selection (HALLAUER et al., 2010), which expresses the progress of the working population in relation to the selection performed. The prediction of gains for each new cycle of selection is a very important criterion, because it guides breeders in the best use of the genetic material available, aiming at obtaining maximum gains for the traits of interest (PAULA et al., 2002). Several authors have reported the effectiveness of recurrent selection in maize breeding programs, mainly for production gains (FARIA et al., 2008; REZENDE; SOUZA JÚNIOR, 2000; SANTOS et al., 2007; SOUZA JÚNIOR; PINTO, 2000; TARDIN et al., 2007).

Since an elite cultivar combines traits that satisfy both farmers and final consumers simultaneously, it is necessary to apply the selection index methodology when different traits are considered for selection (CRUZ; CARNEIRO, 2006). Selection indexes allow generating an aggregate genotype on which selection is performed, working as an additional trait, resulting from the combination of certain traits selected by breeders, for which simultaneous selection is desired, which allows the separation of superior genotypes, irrespective of whether correlations between traits occur or not (CRUZ; CARNEIRO 2006b; SANTOS et al., 2007).

The estimation of selection gains, regardless of the methodology used, requires a determination of the relative economic value of each trait, as well as the genotypic and phenotypic variances and phenotypic and genotypic covariances between each pair of traits (SANTOS et al., 2007). However, with the advancement of the recurrent selection cycles, changes are expected in the estimates of genetic parameters, including heritability and other genetic components of variance (LIMA NETO; SOUZA JUNIOR, 2009; MARQUEZ-SANCHEZ; HALLAUER, 1970).

A series of studies in different types of maize populations have reported changes in population-genetic parameters (AMORIM; SOUZA, 2005; ANDRADE; MIRANDA FILHO, 2008; CARVALHO et al., 2003; GAMA et al., 2003; GOMES et al., 2004; SALAMI et al., 2007; ZIVANOVIC et al., 2005). Although conflicting results were observed, changes in population-genetic parameters did not decrease genetic variability in most of these studies. However, with the expected concentration of alleles for traits of agronomic interest over successive cycles of recurrent selection, it is necessary to measure the genetic parameters of the work population and verify the genetic progress and possible changes in genotypic variability.

The goals of this work were to estimate the genetic parameters of the populations of CIMMYT and Piranão common maize in the 11th cycle of reciprocal recurrent selection, and to estimate the genetic gain for traits of interest to the program. Three methods of selection indexes were studied in order to identify the most appropriate selection index for the selection of full-sib families to undergo a new cycle of recurrent selection.

Material and methods

Two maize populations belonging to different heterotic groups were used in this experiment: 'CYMMIT', which belongs to the heterotic group 'FLINT', and 'Piranão', which belongs to the heterotic group 'DENT'. Both populations have the brachytic gene. These populations were submitted for five cycles of reciprocal recurrent selection at the common maize program at the Federal University of Viçosa. In 1996, these populations were conveyed to the State University of Norte Fluminense (UENF), and conducted by the full-sib reciprocal recurrent selection from the 5th to the 11th cycle of reciprocal recurrent selection. The work present here is based on the 11th cycle.

The obtainment of full-sib progenies for the two populations was conducted in March 2006, at the Antônio Sarlo State Agricultural High School, in Campos dos Goytacazes, State of Rio de Janeiro. Crosses were performed in prolific plants. For each pair of plants, two self pollinations and two reciprocal crosses were carried out, resulting in 242 full-sib families and 484 self-fertilized progenies (S_1). The S_1 seeds were stored in a cold chamber, and the full-sib families were used for the competition assay.

The 242 full-sib families were evaluated in a simple lattice design with two replications, and two experiments were formed in lattice, with 121 families in each experiment. The experiment was carried out in two environments: the Antônio Sarlo State Agricultural High School, in Campos, Northern Rio de Janeiro and at the Pesagro-Rio Experimental Station, located in Itaocara, Northwestern Rio de Janeiro State. Each experimental unit (family) consisted of a 5.00 m long row, with 1.00 m spacing between rows and 0.20 m spacing between plants.

The progenies obtained were evaluated for the following traits: a) grain yield (GY), converted to kg ha^{-1}; b) plant height (PH): the average height in cm of six plants, measured from ground level to the node of the insertion of the flag leaf; c) height of ear (HE): the average height of ear insertion in cm of six plants measured from ground level to the node of insertion of the upper ear on the stalk; d) number of plants (NPL): the total number of plants per row at harvest; e) number of broken plants (NBP): the number of plants broken below the upper ear, at the time of harvest; f) number of lodged plants (NLP): the number of plants with an inclination angle greater than 45°, at the time of harvest; g) number of ears (NE): the total number of ears harvested; i) number of diseased ears (NDE): the number of ears with symptoms of illness and j) weight of ears (WE): the total weight of husked ears per plot (g $plot^{-1}$).

An analysis of variance was performed using following statistical model: $Y_{ijkl} = \mu + E_i + R/E_{ij} + B/R/E_{ijk} + G_l + EG_{il} + e_{ijkl,}$ where: $\mu =$ the experimental average; $E_i =$ the fixed effect of the i-th environment; $R_j =$ the effect of the j-th replication; $B/R_{ijk} =$ the effect of the k-ith block within the replication $j_;$ $G =$ the effect of the j-ith genotype; $EG/S_{ijl} =$ the effect of the interaction between environments and genotypes; and $e_{ijkl} =$ experimental error. The effect of environment was considered as fixed and the other effects were considered as random for the model used. The means and mean squares of the error were adjusted for joint analysis of variance in lattice.

After obtaining the expected mean squares, the following genetic parameters were determined: a) genotypic variance: $\hat{\sigma}_g^2 = (QMG - QMR)/er$; b) phenotypic variance: $\hat{\sigma}_f^2 = QMG/er$; c) heritability: $h^2 = \hat{\sigma}_g^2 / \hat{\sigma}_f^2$; d) coefficient of genetic variance: $CV_g(\%) = \left(100.\sqrt{\hat{\sigma}_g^2}\,)/\bar{x}\right)$; e) variation index: $I_v = 100(CV_g / CV_e)$, where: QMG = average square of the genotypes; QMR = average square of the residue; r = the number of replications; e = the number of environments, and; $\bar{x}$ = general average of the trait analyzed.

In the selection of superior families, it was prioritized the selection of more productive families with lower average values for undesirable traits (NBP, NLP and NDE). The following selection indexes were used: a) direct selection; b) classical index (HAZEL, 1943; SMITH, 1936); c) index based on a sum of 'ranks' (MULAMBA; MOCK, 1978) and; d) base index (WILLIANS, 1962). The expected gains by direct selection for yield (GS_{dx}) and for the traits affected by direct selection in yield were measured by the following equation: GS = DS h^{-2} (FALCONER, 1987), as follows: DS = differential selection and h^2 = heritability coefficient.

Random weights were assigned for each trait, by trial, (Table 1) to estimate the selection indexes. These weights refer to the optimal values for obtaining gains in all traits. Statistical analyses and the selection of the 40 best full-sib families were carried out with the aid of the GENES software system (CRUZ, 2006).

Table 1. Values of the weights attributed to different selection indexes for each trait evaluated.

Traits	Smith and Hazel	Mulamba and Mock	Willians
GY	400	2000	500
PH	0	0	0
HE	0	0	0
NPL	100	500	200
NBP	-100	-100	-100
NLP	-100	-100	-100
NE	100	500	200
NDE	-100	-100	-100
WE	100	500	200

[1/]GY = grain yield, PH = plant height; HE = ear height; NPL = number of plants; NBP = number of broken plants; NLP = number of lodged plants; NE = number of ears; NDE = number of diseased ears; and WE = weight of ears.

Results and discussion

Significant differences were observed between the genotypes evaluated for most traits studied (Table 2), except for PH, HE and NDE. These results indicate that genotypic variability exists in the population studied and that genetic gains can be achieved for the current cycle and in subsequent cycles of recurrent selection. The lack of significant differences for PH, HE and NDE is consistent with the expectations for recurrent selection, since these populations have been subjected to 10 selection cycles, and priority was given to the decrease in these traits.

A significant environmental effect was observed for all traits under study (Table 2), which reveals climatic and edaphics variations in the locations of the assessments. No interaction was observed between genotype and environment for most traits, except for NBP and NLP, which indicates that the response to environmental changes was similar for the set of genotypes, without any effects on the ranking of the families studied. So, these hybrids can be developed and recommended to a greater edaphoclimatic area - Northern and Northwestern Rio de Janeiro - based in only one reciprocal recurrent selection program, which saves time, efforts and resources.

Table 2. Values and significances of the average squares of the joint analysis of variance for the different traits.

Traits $^{1/}$	FV						
	Environment (E)	Rep/E	Block/Rep/E	Genotype (G)	G★E	Residue	CV(%)
GY	376475388.00★	1731567,75	1702671,5	2044070.45★	1178710,05^{ns}	900944.00	20,00
PH	6.37★	0,17	0,12	0,05^{ns}	0,02^{ns}	0,01	5,00
HE	5.80★	0,02	0,06	0,04^{ns}	0,01^{ns}	0,01	8,00
NPL	3175,07★★	20,49	11,52	10,68★	7,45^{ns}	6,66	12,00
NBP	445,13★★	15,15	17,28	10,92★	8,31*	6.49	60,00
NLP	331,47★	16,00	29,79	11,73★	11,22*	7,82	72,00
NE	4268,53★★	56,90	23,12	36,84★★	20,27^{ns}	17,02	17,00
NDE	29,47★	27,55	2,52	3,52^{ns}	2,18^{ns}	2,03	72,00
WE	118225240.35★	570363.7	567425.20	662799,05★	382173,65^{ns}	304597,65	20.00

$^{1/}$GY = grain yield (kg ha^{-1}), PH = plant height (cm); HE = ear height (cm); NPL = number of plants; NBP = number of broken plants; NLP = number of lodged plants; NE = number of ears; NDE = number of diseased ears; and WE = weight of ears in g plot^{-1}. ★,★★ Significant at 5% and 1% probability by the F test, respectively. ^{ns} Non- significant.

In addition, significant interactions between genotype x environment in the traits NBP and NLP were observed in the same location by Daros et al. (2004), Tardin et al. (2007), Santos et al. (2008) and Freitas Júnior et al. (2009).

According to the classification proposed by Scapim et al. (1995), the variation coefficients obtained in this study are presented as average values for most traits. These variation coefficients indicate good experimental accuracy for all traits, except for NBP, NLP and NDE (Table 2). The magnitude of the estimates of CV% for NBP, NLP and NDE is due to the nature of these characteristics, whose average includes either null values or different positive values, without a normal distribution. Daros et al. (2004), Santos et al. (2008) and Freitas Júnior et al. (2009) evaluated S_1 full-sib families in popcorn and found high values of CV% for these same traits.

The estimates of genotypic variances were high (Table 3), suggesting that most of the phenotypic variance observed is due to genetic effects rather than environmental effects. The genotypic variance values for most traits evaluated are also close to the values obtained for the variance of the genotype x environment interaction (Table 3).

Table 3. Estimates related to the genotypic (σ_g^2) and phenotypic (σ_f^2) variance of the genotype x environment interaction (σ_{ga}^2), heritability coefficient (h^2), variation index (Iv) and the averages of the nine traits.

Traits$^{1/}$	σ_g^2	σ_f^2	σ_{ga}^2	h^2 (%)	I_v	Average
GY	285781.61	511017.61	225236	56.00	60.00	4478
PH	0.01	0.01	0.01	73.00	0.90	221
HE	0.01	0.01	0.01	73.00	0.82	137
NPL	1.00	2.66	1.66	38.00	4.00	21
NBP	1.10	2.73	1.62	41.00	44.00	4
NLP	1.00	2.94	1.95	33.00	35.00	4
NE	4.95	9.20	4.25	54.00	65.46	20
NDE	0.37	0.88	0.50	42.00	42.50	2
WE	89550.35	165699.76	76149.5	54.00	52.83	2833

$^{1/}$GY = grain yield (kg ha^{-1}), PH = plant height (cm); HE = ear height (cm); NPL = number of plants; NBP = number of broken plants; NLP = number of lodged plants; NE = number of ears; NDE = number of diseased ears; and WE = weight of ears in g plot^{-1}.

Several studies indicate that genetic variance increases with increasing cycles of reciprocal recurrent selection (HOLTHAUS; LAMKEY, 1995; REZENDE; SOUZA JÚNIOR, 2000; SCHNICKER; LAMKEY, 1993; STUCKER; HALLAUER, 1992; VILELA et al., 2005, 2008). However, Santos et al. (2007) compared cycles zero and three of reciprocal recurrent selection in full-sib families of maize, that were generated by the interbreeding between the populations IG-1 and IG-2, and found significant reductions in the estimates of the genotypic variance and the heritability coefficients for grain yield, plant height, height of ear insertion and prolificacy.

The wide heritability estimates based on the average of families (h^2) ranged between 33 and 73%. These results are in line with the expectations for all traits evaluated (Table 3). The traits NPL, NBP, NLP and NDE have lower heritability values (Table 3).

Attention should be paid to the h^2 value for GY (56% - Table 3). Although results with heritability values of 81.69, 94 and 93.95% for yield were obtained by Amorim and Souza (2005), Câmara et al. (2007) and Rangel et al. (2008), respectively, the value of heritability for yield observed in this experiment is an estimate of high magnitude, considering the quantitative and polygenic nature of this character (HALLAUER et al. 2010; HOLTHAUS; LAMKEY, 1995). These results confirm the genetic variability of the populations under study and the possibility of obtaining superior genotypes with significant genetic gain.

The estimated values for the indexes of variation (I_V) were satisfactory for most traits, except for PH, HE and NPL. This parameter helps in the indication of the presence of genetic variability in the population under study, and in the selection of the method to be used for genetic breeding.

Inference on genetic gain for grain yield (GY), with direct selection (Table 4), was 14.10%, which is considered significant in comparison to previous cycles of selection with these populations. On the other hand, indirect gains for the traits number of broken plants (NBP) and number of lodged plants (NLP) (3.22 and 3.90, respectively) were undesirable, indicating that selection by considering grain yield alone may increase the rate of breaking and lodging in maize populations.

Table 4. Original average of the individuals selected, gains by direct selection and gains provided by three different simultaneous selection indexes.

Traits$^{1/}$	Xo	GS(%)			
		Direct	Mulamba	Smith	Willians
GY	4778	14.10	12.90	10.76	12.80
PH	221	1.94	1.35	0.80	1.80
HE	137	2.65	2.44	2.40	1.80
NPL	21	2.70	2.32	2.60	1.78
NBP	4	3.22	-4.54	1.75	-3.00
NLP	4	3.90	2.60	5.90	2.78
NE	20	9.65	7.45	5.30	7.45
NDE	2	-3.60	-4.65	-0.89	-3.60
WE	2833	12.10	11.95	9.00	12.15

Comparison between the yield gain predicted in direct selection and that of the indexes of simultaneous selection demonstrates that the gain from direct selection is superior to that obtained by simultaneous selection (Table 4). However, it should be noted that direct selection based on a single trait can cause undesirable changes in other traits and hinder the achievement of favorable gains by selection in a set of traits, as observed for NDE (Table 4) (CRUZ; CARNEIRO, 2006). In this case, the simultaneous selection indexes are more advantageous because of the better distribution of favorable gains in the other traits.

Based on the estimates generated by the use of three different selection indexes in full-sib families, it is possible to observe that the procedure proposed by Mulamba and Mock (1978) promoted the most adjusted predictions of selection gains for maize breeding, and stood out due to higher GY and reduced or negative gains in deleterious traits, such as NBP, NLP and NDE (Table 4).

The predicted gain estimated for GY, by the Mulamba and Mock (1978) selection index was 12.90%, which is higher than the gains obtained by Smith and Hazel (SMITH, 1936; HAZEL, 1943) and the Willians (1962) indexes but lower than those obtained through direct selection. Tardin et al. 2007 found estimated gains of 18.80 and 14.58% for the same population, in the eighth and tenth cycles of recurrent selection, respectively. However, in the ninth selection cycle, the estimated gain for the same populations was only 4.68%, which was explained by the difference in the intensity of selection applied in the ninth cycle, which was approximately 23% (TARDIN, et al. 2007).

However, the estimates of gains in selection for yield achieved in this experiment are comparable or superior to those observed in the literature. Souza Júnior and Pinto (2000) obtained a direct yield gain of 7.2%, with reciprocal recurrent selection for half-sib families of common maize, which may be related to the fact that selection in half-sib families explores only half the additive variance, while the selection of full-sib families allows the full exploration of additive variance. In turn, Santos et al. (2005) obtained 4.07% of direct gain for yield, while working with maize populations IG-1 and IG-2, subjected to three cycles of reciprocal recurrent selection.

It is important to point out that the negative values of gains in NBP and NDE estimated by Mulamba and Mock (1978) are interesting for the breeding of maize, due to the deleterious effect of these traits on yield.

It should also be said that, among full-sib progenies, which is the case of this work, part of the dominance variance is also capitalized, thus allowing higher gains for selection, compared to the use of half-sib families (HALLAUER et al., 2010; SANTOS et al., 2007; SOUZA JÚNIOR; PINTO, 2000). Therefore, both the additive variance and the deviations of dominance contribute to the estimated gains via selection indexes and for the gains expressed by the progenies evaluated, the different values of selection pressure applied to the populations and the number of families obtained, since the higher the number, the greater the gains, since a greater selection pressure will not compromise the genetic variability of a working population of a large number of individuals.

Conclusion

On the basis of the estimated gains for morphoagronomic traits evaluated by selection indexes, it is concluded that the reciprocal recurrent selection enhanced by simultaneous selection of traits was effective in improving the interpopulation hybrids from crosses between CYMMIT and Piranão populations.

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References

AMORIM, E. P.; SOUZA, J. C. Híbridos de milho inter e intrapopulacionais obtidos a partir de populações S_0 de híbridos simples comerciais. **Bragantia**, v. 64, n. 3, p. 561-567, 2005.

ANDRADE, J. A. C.; MIRANDA FILHO, J. B. Quantitative variation in the tropical mayze population

ESALQ-PB1. **Scientia Agricola**, v. 65, n. 2, p. 174-182, 2008.

CÂMARA, T. M. M.; BENTO, D. A.; ALVES, G. F.; SANTOS, M. F.; MOREIRA, A. J. U. V.; SOUZA JÚNIOR, C. L. Parâmetros genéticos de caracteres relacionados à tolerância à deficiência hídrica em milho tropical. **Bragantia**, v. 66, n. 4, p. 595-603, 2007.

CARVALHO, H. W. L.; LEAL, M. L. S.; SANTOS, M. X. Estimativas de parâmetros genéticos na população de milho CPATC-3 em dois locais de Sergipe. **Pesquisa Agropecuária Brasileira**, v. 38, n. 1, p. 73-78, 2003.

COMSTOCK, R. E.; ROBINSON, H. F. The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. **Biometrics**, v. 4, n. 1, p. 254-266, 1948.

CRUZ, C. D. **Programa genes**: versão windows: aplicativo computacional em genética e estatística. Viçosa: UFV, 2006.

CRUZ, C. D.; CARNEIRO, P. C. S. **Modelos biométricos aplicados ao melhoramento genético**. 2. ed. Viçosa: Editora UFV, 2006.

DAROS, M.; AMARAL JÚNIOR, A. T.; PEREIRA, M. G.; SANTOS, F. S.; GABRIEL, A. P. C.; SCAPIM, C. A.; FREITAS JÚNIOR, S. P.; SILVÉRIO, L. Recurrent selection in inbred popcorn families. **Scientia Agricola**, v. 61, n. 6, p. 609-614, 2004.

FALCONER, D. S. **Introdução à genética quantitativa**. Translation by Martin de Almeida e Silva and Jose Carlos Silva. Viçosa: Editora UFV, 1987.

FAO-Food and Agriculture Organization of the United Nations. **Statistical Database**. Available from: <http://www.faostat.fao.org/site/612/default.aspx#ancor>. Accesse on: Feb. 12, 2011.

FARIA, V. R.; VIANA, J. M. S.; SOBREIRA, F. M.; SILVA, A. C. Seleção recorrente recíproca na obtenção de híbridos interpopulacionais de milho-pipoca. **Pesquisa Agropecuária Brasileira**, v. 43, n. 12, p. 1749-1755, 2008.

FREITAS JÚNIOR, S. P.; AMARAL JÚNIOR, A. T.; RANGEL, R. M.; VIANA, A. P. Genetic gains in popcorn by full-sib recurrent selection. **Crop Breeding and Applied Biotechnology**, v. 9, n. 1, p. 1-7, 2009.

FUZATTO, S. R.; FERREIRA, D. F.; RAMALHO, M. A. P.; RIBEIRO, P. H. E. Divergência genética e sua relação com os cruzamentos dialélicos na cultura do milho. **Ciência e Agrotecnologia**, v. 26, n. 1, p. 22-32, 2002.

GAMA, E. E. G.; SANTOS, M. X.; FERRÃO, R. G.; MEIRELES, W. F.; PACHECO, C. A. P.; PARENTONI, S. N.; GUIMARÃES, P. E. O. Potencial genético de um sintético de milho de grãos duros para formação de híbridos. **Ciência Rural**, v. 33, n. 4, p. 44-52, 2003.

GOMES, M. S.; VON PINHO, R.; RAMALHO, M. A. P.; FERREIRA, D. V.; BRITO, A. H. Variabilidade genética em linhagens de milho nas características relacionadas com a produtividade de silagem. **Pesquisa Agropecuária Brasileira**, v. 39, n. 9, p. 879-885, 2004.

HALLAUER, A. R.; CARENA, M. J.; MIRANDA, J. B. **Quantitative genetics in maize breending**. 3rd ed. Iowa: Iowa State University Press/Springer Science, 2010.

HAZEL, L. N. The genetic basis for constructing selection indexes. **Genetics**, v. 28, n. 1, p. 476-490, 1943.

HOLTHAUS, J. F.; LAMKEY, K. R. Population means and genetic variances in selected and unselected Iowa Stiff Stalk maize populations. **Crop Science**, v. 35, p. 1581-1589, 1995.

MARQUEZ-SANCHEZ, F.; HALLAUER, A. R. Influence of sample size on the estimation of genetic variances in a synthetic variety of maize for grain yield. **Crop Science**, v. 10, p. 357-361, 1970.

MULAMBA, N. N.; MOCK, J. J. Improvement of yield potential of the Eto Blanco maize (*Zea mays* L.) population by breeding for plant traits. **Egypt Journal of Genetic and Cytology**, v. 7, n. 1, p. 40-51, 1978.

LIMA NETO, F. P.; SOUZA JÚNIOR, C. L. Number of recombinations and genetic properties of a maize population undergoing recurrent selection. **Scientia Agricola**, v. 66, n. 1, p. 52-58, 2009.

PAULA, R. C.; PIRES, I. E.; BORGES, R. C. G.; CRUZ, C. D. Predição de ganhos genéticos em melhoramento florestal. **Pesquisa Agropecuária Brasileira**, v. 37, n. 6, p. 1020-1028, 2002.

RANGEL, R. M.; AMARAL JÚNIOR, A. T.; SCAPIM, C. A.; FREITAS JÚNIOR, S. P.; PEREIRA, M. G. Genetic parameters in parents and hybrids of circulant diallel in popcorn. **Genetics and Molecular Research**, v. 7, n. 4, p. 1020-1030, 2008.

REZENDE, G. S. P.; SOUZA JÚNIOR, C. L. A reciprocal recurrent selection procedure outlined to intgrate hybrid breeding programs in maize. **Journal of Genetics Breeding**, v. 54, n. 1, p. 57-66, 2000.

RIBEIRO, A. C.; ATHAYDE, K. R.; CASTRO, R. A. R. Novo ciclo da agroindústria canavieira brasileira: perspectivas de inserção do estado do Rio de Janeiro. **Revista Inovare**, v. 8, n. 1, p. 111-126, 2009.

SALAMI, A. E.; ADEGOKE, S. A. O.; ADEGBITE, O. A. Genetic variability among cultivars grown in Ekiti-State, Nigéria. **Middle-East Journal of Scientific Research**, v. 2, n. 1, p. 9-13, 2007.

SANTOS, F. S.; AMARAL JÚNIOR, A. T.; FREITAS JÚNIOR, S. P.; RANGEL, R. M.; SCAPIM, C. A. Genetic gain prediction of the third recurrent selection cycle in a popcorn population. **Acta Scientiarum. Agronomy**, v. 30, n. 5, p. 651-65, 2008.

SANTOS, F. S.; AMARAL JÚNIOR, A. T.; FREITAS JÚNIOR, S. P.; RANGEL, R. M.; PEREIRA, M. G. Predição de ganhos genéticos por índices de seleção na população de milho-pipoca UNB-2U sob seleção recorrente. **Bragantia**, v. 66, n. 3, p. 389-396, 2007.

SANTOS, M. F.; MORO, G. V.; AGUIAR, A. M.; SOUZA JUNIOR, C. L. Responses to reciprocal recurrent selection and changes in genetic variability in IG-1 and IG-2 maize populations. **Genetics and Molecular Biology**, v. 28, n. 4, p. 781-788, 2005.

SANTOS, M. F. T.; CÂMARA, M. M.; MORO, G. V.; COSTA, E. F. N.; SOUZA JÚNIOR, C. L. Responses to selection and changes in combining ability after three cycles of a modified reciprocal recurrent selection in maize. **Euphytica**, v. 157, n. 2, p. 185-194, 2007.

SCAPIM, C. A.; CARVALHO, C. G. P.; CRUZ, C. D. Uma proposta de classificação dos coeficientes de variação para a cultura do milho. **Pesquisa Agropecuária Brasileira**, v. 30, n. 4, p. 683-686, 1995.

SCHNICKER, B. J.; LAMKEY, K. R. Interpopulation genetic variance after reciprocal recurrent selection in BSSS and BSCB1 maize populations. **Crop Science**, v. 33, n. 1, p. 90-95, 1993.

SILVA, L. C. Reconfiguração do Norte Fluminense a partir dos anos 70: a chegada do petróleo e suas conseqüências na dinâmica de crescimento regional. **Revista Plurais**, v. 1, n. 4, p. 167-187, 2006.

SMITH, H. F. A discriminant function for planta selection. **Annals of Eugenics**, v. 7, n. 1, p. 240-250, 1936.

SOUZA JÚNIOR, C. L.; PINTO, R. M. C. Responses to a short-term reciprocal recurrent selection procedure in maize. **Maydica**, v. 45, n. 1, p. 21-28, 2000.

STUCKER, D. S.; HALLAUER, A. R. Genetic variability as affected by selection in Iowa stiff stalk synthetic maize. **Journal of Heredity**, v. 83, n. 2, p. 410-418, 1992.

TARDIN, F. D.; PEREIRA, M. G.; GABRIEL, A. P. C.; AMARAL JÚNIOR, A. T.; FILHO, G. A. S. Selection index and molecular markers in reciprocal recurrent selection in maize. **Crop Breeding and Applied Biotechnology**, v. 7, n. 3, p. 225-233, 2007.

VILELA, F. O.; AMARAL JÚNIOR, A. T.; PEREIRA, M. G.; DAHER, R. F.; SCAPIM, C. A.; PACHECO, C. A. P. Viability of the UENF popcorn improvement program based on morphoagronomic and molecular divergence in S1 families of the second recurrent selection cycle. **Crop Breeding and Applied Biotechnology**, v. 5, n. 2, p. 215-222, 2005.

VILELA, F. O.; AMARAL JÚNIOR, A. T.; PEREIRA, M. G.; SCAPIM, C. A.; VIANA, A. P.; FREITAS JÚNIOR, S. P. Effect of recurrent selection on the genetic variability of the UNB-2U popcorn population. **Acta Scientiarum. Agronomy**, v. 30, n. 1, p. 25-30, 2008.

WILLIANS, J. S. The evaluation of a selection index. **Biometrics**, v. 18, n. 1, p. 375-393, 1962.

ZIVANOVIC, T.; SECANSKI, M.; TODOROVIC, G. Components of genetic variability and heritability of the number of rows per ear in silage maize. **Biotechnology in Animal Husbandry**, v. 21, n. 1, p. 109-121, 2005.

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