Genetic gain prediction of the third recurrent selection cycle in a popcorn population

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ABSTRACT. Although Brazil has reduced its importation of popcorn grain in recent years, the availability of improved varieties is still rare. In order to improve a popcorn population and to estimate the prediction of genetic gains, the third cycle of intrapopulation recurrent selection was carried out. One hundred ninety two half-sib families were obtained from the second cycle of the UNB-2U population and tested in a randomized complete block design with two replications within sets in two locations. The presence of statistical significance for sets for grain yield, poorly husked ear and broken plants proved the efficiency and the necessity for the use of the hierarchical statistical model by sets. Except for the poorly husked ear, there was significance for families within sets for the other evaluated traits, showing that there was sufficient genetic variability for exploitation in future cycles. Although the heritability for popping expansion was higher than for grain yield, the predicted genetic gain for the latter was superior to popping expansion because of the higher magnitude of the genetic standard deviation for grain yield. It is expected that in the fifth recurrent cycle, the first popcorn variety with yellow grains may be released for Rio de Janeiro State.

Key words: *Zea mays,* popcorn breeding, genetic gains, yield, popping expansion.

RESUMO. Predição de ganhos genéticos para o terceiro ciclo de seleção recorrente em uma população de milho pipoca. Embora o Brasil tenha reduzido a importação de grãos de milho pipoca, a disponibilidade de variedade melhorada ainda é rara no país. Com o objetivo de melhorar a população UNB-2U de milho pipoca e estimar a predição de ganhos genéticos, implementou-se o terceiro ciclo de seleção recorrente intrapopulacional. Cento e noventa e duas famílias de meios-irmãos foram obtidas e avaliadas em delineamento de blocos casualizados, com duas repetições, dentro de "sets" em dois locais. A presença de significância para "sets", para produção de grãos, espigas mal empalhadas e plantas quebradas, comprovou a eficiência do uso do modelo estatístico hierarquizado por "sets". Com exceção das espigas mal empalhadas, houve significância para famílias dentro de "sets" para as demais características, revelando que há suficiente variabilidade genética a ser explorada em ciclos futuros. Ainda que a herdabilidade para capacidade de expansão (PE) tenha sido superior à da produção de grãos (GY), o ganho predito para GY foi superior a PE, em decorrência da maior estimativa da magnitude do desvio-padrão genético para GY. Espera-se que, no quinto ciclo de seleção recorrente, seja possível a recomendação da primeira variedade de milho pipoca com grãos amarelos para o Estado do Rio de Janeiro.

Palavras-chave: *Zea mays,* melhoramento de milho pipoca, ganhos genéticos, produção de grãos, capacidade de expansão.

Introduction

In the last five years, the Brazilian popcorn market has changed, especially regarding the partnership between producers and packers, which has been reflected in the importation of the product. Until the beginning of the 2003-2004 growing season, national popcorn consumption was approximately 80,000 tons, of which 75% corresponded to imported grains, mainly from Argentina (Galvão *et al*., 2000). In the 2004-2005 growing season, according to information from the packing companies, there was a marked reduction in importation of the product, to 20,000 tons, as a result of the large-scale use of the IAC-112 modified

simple hybrid, developed by the Campinas Agronomic Institute (Sawazaki, 2001).

However, the hybrid popcorn market in Brazil is still incipient, in spite of the importance of the crop that is valued at approximately 1.15 billion dollars annually in the United States of America (Pacheco et al., 1998; Galvão et al., 2000). Yet, obtaining an improved variety from a composite is also rare in Brazil, although the release of varieties derived from composites has been a viable alternative (Vilela et al., 2008). As an example, the variety BRS ANGELA was derived from recurrent selection cycles of the CMS-43 composite, from Embrapa/CNPMS (Pacheco et al., 2000).

The main reason for the dependency on imported popcorn is that breeding programs in the country are rare. As examples can be cited the breeding programs developed in Viçosa and Sete Lagoas (Minas Gerais State), Maringá and Londrina (Paraná State), and Piracicaba and Campinas (São Paulo State). A popcorn breeding program at Campos dos Goytacazes has also been established, aiming at the development of varieties with adaptation for the state of Rio de Janeiro.

The initial program stages involved the assessment of the potential of the UNB-2U population, especially in terms of genetic variance, in order to identify more efficient breeding strategies to produce improved varieties (Pereira and Amaral Júnior, 2001; Vilela et al., 2008). Thus, the first recurrent selection cycle based on full-sib family selection resulted in predicted genetic gains of 4.69% (yield) and 10.39% (popping expansion) (Daros et al., 2002). In the second cycle, based on S_1 families, the predicted genetic gains were 17.8% for popping expansion and 26.95% for yield (Daros et al., 2004).

Thus, the main objective of this work was to estimate the genetic gain prediction of a third cycle of recurrent selection, and to evaluate the potential of the improved population for future releasing as a new popcorn variety.

Material and methods

One hundred and ninety-two half-sib families were obtained from the C_2 cycle. The field trials were established in December 2004 in Campos dos Goytacazes (21°45'15" S, 41°19'28" W) and in January 2005 in Itaocara (21°40'09" S, 42°04'34" W), in Rio de Janeiro State, Brazil. These environments are contrasting in terms of regions (about 110 kilometers apart), soil types and altitudes.

A completely randomized block design was used,

with six sets, two replications within sets, and each set consisting of 32 families and eight controls. Each family was cultivated in a 5.0 m row with inter-row spacing of 1.0 m and 0.2 m spacing between plants. Initially, fifty seeds were sown per row. One month after sowing, the plants were thinned to 25 plants per row. Soil preparation, fertilizer application and cultural practices were in conformity with the recommendations by Fancelli and Dourado Neto (2000).

The following traits were evaluated: a) popping expansion (PE) – ratio of expanded volume in relation to weight in 30 grams, in mL g^{-1}; b) grain yield (GY) – weight of grain in kg ha^{-1}; c) poorly husked ears (PHE) – number of ears not completely covered by husk; and d) broken plants (BP) – number of plants with stalk broken below the upper ear at harvest.

Popping expansion was assessed in a popcorn machine developed by Embrapa/Instrumentação Agropecuária, incorporating an electronic resistor and thermostat. Two grain samples were obtained and evaluated from each plot.

An analysis of variance was carried out on the measured traits, based on the completely randomized block design with two replications within sets in two environments, according to the genetic-statistical model proposed by Hallauer and Miranda Filho (1981), ie:

$$Y_{ijkl} = \mu + E_i + S_j + ES_{ij} + R/ES_{ijk} + F/S_{jl} + EF/S_{jil} + \xi_{ijkl},$$

where:

μ is the general mean;
E_i is the fixed effect of the ith environment;
S_j is the random effect of jth set;
ES_{ij} is the random effect of environment-by-set interaction;
R/ES_{ijk} is the random effect of the kth replication within the environment-by-set interaction;
F/S_{jl} is the random effect of the lth family within the set;
EF/S_{ijl} is the random effect of environment-by-family interaction within the set; and
ξ_{ijkl} is the experimental error.

Each set was analyzed separated, and then the results from the six sets were grouped for each environment. Finally, the results for all sets were combined for both environments. All sources of variation, with the exception of environment, were assumed to be random. The GENES Program (Cruz, 2006) was used for data analysis.

The genetic parameters, phenotypic $(\hat{\sigma}_f^2)$ and genotypic $(\hat{\sigma}_g^2)$ variance and heritability on the

family mean basis ($\hat{h}^2$) were estimated as follows:

$$\hat{\sigma}_f^2 = \frac{MSF}{re} \; ; \; \hat{\sigma}_g^2 = \frac{MSF - MSE}{re} \; ; \text{ and } \hat{h}^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_f^2} \; ;$$

where: MSF and MSE are, respectively, the family mean square and error mean square; r and e are, respectively, the numbers of replications and environments (Falconer, 1987).

The estimates of genetic gain predictions were obtained by the expression $GS = p \times DP_g \times h \times i$, where p is the parentage control (1 for recombination of remnant seeds of the half-sib families), DP_g is the additive standard deviation among the test units, h is the heritability square root, and i is the selection intensity. The value of i was obtained by the ratio between z (standard curve height at the truncation point) and c (percentage of selected individuals) (Cruz, 2005).

Results and discussion

The coefficients of variation (CV) were considered high for all traits, except popping expansion (Table 1). In the second cycle of recurrent selection of this population (UNB-2U), high values of CV were also observed for these traits (Daros *et al*., 2004). In the CMS-42 and CMS-43 popcorn populations, high magnitudes of CV for the traits percentage of lodged and broken plants were reported by Pacheco *et al*. (1998). The high values of the coefficients of variation are also in accordance with Coimbra (2000) and Santos *et al*. (2007).

Table 1. Mean squares, general mean, maximum and minimum family mean values and coefficients of variation of the four evaluated traits in the half-sib families, Campos dos Goytacazes and Itaocara, 2005.

| Source | DF | Mean Square | | | |
		PE (mL g⁻¹)	GY (kg ha⁻¹)	PHE (number)	BP (number)
E	1	176.07★★	4447927.81★★	168.25★★	42.23ns
S	5	15.34ns	786828.61★★	5.29★	48.74★★
ES	5	17.32ns	89453.59ns	6.94★★	54.96★★
R/ES	12	24.46★★	692591.00★★	2.36ns	51.00★★
F/S	186	23.72★★	253805.04★★	2.03ns	16.16★
EF/S	186	9.23ns	165124.99★★	2.18ns	13.09ns
Error	372	8.60	132697.00	2.22	13.09ns
Maximum		39.36	3120.00	12.00	12.66
Average		23.24	1135.74	1.76	5.49
Minimum		10.33	380.00	0.00	0.00
CV (%)		12.62	32.07	84.76	64.72

★★, ★Significant by F-test at 1 and 5%, respectively. E is the environment effect; S is the random effect as result of set; ES is the random effect of environment-by-set interaction; R/ES is the random effect of the replication within the environment-by-set interaction; F/S is the random effect of the family within the set; EF/S is the random effect of environment-by-family interaction within the set. DF: degrees of freedom. CV: coefficient of variation.

The analysis of variance results indicate environment effects for the evaluated traits, except for broken plants, showing that the environments differed sufficiently for most of the evaluated traits (Table 1).

Although the effect of environment was significant for GY, there was no significance for the EF/S variation source, showing a tendency to maintain the relative performance of the families in the different environments (Table 1).

Only the trait PE did not show statistical difference for sets, indicating the efficiency and effectiveness for the use of block designs divided into sets. If set effect were not included, it would probably produce variations that could result in loss of experimental accuracy (Table 1).

The source of variation F/S was significant by the F test, for all the evaluated traits, except for PHE (Table 1). This shows there is genetic variability for exploitation in future cycles, enabling progress with selection. Furthermore, it indicated that the recurrent selection objective of improving the population mean maintaining the genetic variability was attained in the third selection cycle.

The selective potential of the UNB-2U population for the main traits, PE and GY, was indicated by the difference in the mean of the selected families compared to the mean of the original population (Table 2). Additionally, the great discrepancy in the mean of the lower and upper limit for the main traits, PE and GY (Table 2), is another indication of the genetic variability in the population UNB-2U that is an essential condition to obtaining superior segregates. Similar results were obtained by Pacheco *et al*. (1998), who also based on the upper and lower limits for PE and GY to predict genetic gains in the CMS-42 and CMS-43 popcorn populations in the second recurrent selection cycle.

Table 2. Estimates of the means of the original population ($\overline{X}_o$), the selected families ($\overline{X}_s$), the controls ($\overline{X}_T$), lower limit (LL) and upper limit (UL) of the evaluated population.

| Estimates | Traits | | | |
	PE (mL g⁻¹)	GY (kg ha⁻¹)	PHE (number)	BP (number)
$\overline{X}_o$	23.30	1135.58	1.76	5.51
$\overline{X}_s$	25.74	1361.92	1.45	4.79
$\overline{X}_T$	19.72	1885.40	1.54	6.17
LL	10.30	380.00	0.00	0.00
UL	39.67	3120.00	12.00	33.00

It is timely to recognize that the upper limit can rise throughout the selection cycle, which means that a maximum value detected in a given cycle can be lower than the maximum for the following cycle, and thus successively with the increase of the frequency of favorable alleles followed by

recombination and generation of advanced cycle populations.

Based on genetic component estimates (Table 3), the heritability estimates of the PE trait are in line with results obtained by Sawazaki (1996), which ranged from 60 to 90% in popcorn half-sib families. Similar estimates for this trait in CMS-43 popcorn population in the second selection cycle among and within half-sib families were obtained by Pacheco et al. (1998).

In the present investigation, PE heritability was superior to that for GY, with values of 68.40 and 50.17%, respectively. Such results are in agreement with previous study conducted by Pereira and Amaral Júnior (2001) using design I (Comstock and Robinson, 1948) in the same base population. These results are also in line with other investigations (Pacheco et al., 1998; Freitas Júnior et al., 2006; Scapim et al., 2006a; Rangel et al., 2007; Rangel et al., 2008). Consequently, as mentioned by Pacheco et al. (1998), greater genetic gains were expected for PE than for GY. However, in the present study, the gain for GY was superior to that predicted for PE because of the estimate of the magnitude of the GY standard deviation, which was much greater than for PE.

Table 3. Phenotypic variance ($\hat{\sigma}_f^2$), genotypic variance ($\hat{\sigma}_g^2$), family mean heritability ($\hat{h}_x^2\%$) and genetic gain (GG%) estimated for the evaluated traits.

Genetic Parameters	Traits			
	PE	GY	PHE	BP
$\hat{\sigma}_f^2$	6.28	68875.00	0.54	4.15
$\hat{\sigma}_g^2$	4.29	34559.52	0.00	0.75
$\hat{h}_x^2\%$	68.42	50.18	0.00	18.12
GG%	11.40	17.97	0.00	10.39

The genetic gain for the PE trait was 11.40% for the third selection cycle. Based on the initial mean, such gain is equivalent to an increase of 1.84 units year^{-1}. In relation to GY, the predicted gain was of 17.97% in comparison to the original population. Such gain is equivalent to an increase of 134.28 kg ha^{-1} year^{-1} (Table 3).

When the means obtained for PE and GY in the three first cycles were compared with the predicted mean for the third cycle, it was observed that there were increases in PE and GY as a result of the favorable allele concentration (Table 4). Linear regression analysis showed the evolution of gains in the successive selection cycles (Figures 1 and 2). It was observed that the selection strategy to obtain C_3 using half-sib families resulted in satisfactory gains for popping expansion and grain yield, which increased to desirable magnitudes. The use of S_1

families in a previous cycle (Daros et al., 2004) did not compromise the genetic gains once after selection; the selected families are recombined, overcoming the inbreeding depression and recovering the vigor of the population (Scapim et al., 2006b).

Table 4. Obtained means in the C_0, C_1, C_2 and predicted mean in the C_3 cycles[1/] of recurrent selection in UNB-2U population for the popping expansion (PE) and grain yield (GY) in Campos dos Goytacazes and Itaocara.

Cycle	PE (mL g^{-1})	GY (kg ha^{-1})
C0	20.28	1960.00
C1	21.68	1990.00
C2	23.44	2025.00
C3	25.11	2080.00

[1/] C_0 = mass selection; C_1 = full-sib recurrent selection; C_2 = S_1 families recurrent selection; and C_3 = half-sib recurrent selection.
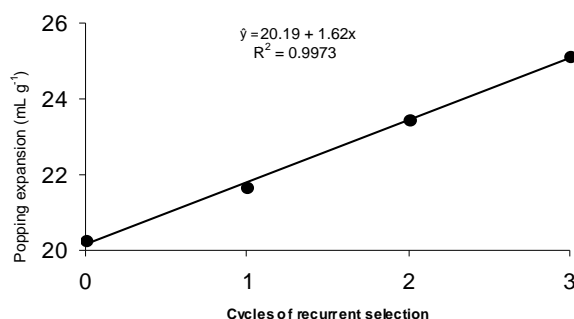

Figure 1. Obtained Means in the three first cycles (0, 1 and 2) and predicted mean in the third cycle (3) of recurrent selection in UNB-2U population for the trait PE (mL g^{-1}).
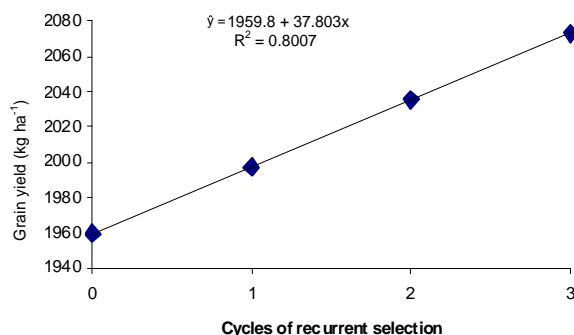

Figure 2. Obtained Means in the three first cycles (0, 1 and 2) and predicted mean in the third cycle (3) of recurrent selection in UNB-2U population for the trait GY (kg ha^{-1}).

Judging from the progress of the first three cycles, it is expected that with two more cycles of recurrent selection, the resulted population will present desirable popping expansion and grain yield magnitudes that will propitiate the future release of the first bred variety of popcorn with yellow grains in Rio de Janeiro State. Also, it is expected that, in addition to the magnitude of the desirable traits, the improved population should also retain enough

genotypic variability to justify the continuity of recurrent selection procedures with the correspondent genetic gains.

Conclusion

The significance of the source of variation F/S for most of the traits showed that there is genetic variability for exploitation in future cycles, enabling progress with selection.

Although the heritability for PE was superior to GY, the predicted gain for the latter was superior to the former, resulting from the greater estimates of the genetic standard deviation for GY.

It is expected that after the fifth recurrent selection cycle, it will be possible to release the first popcorn variety with yellow grains for Rio de Janeiro State.

Acknowledgement

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