

# Genetic gain for grain yield and popping expansion in full-sib recurrent selection in popcorn

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## ABSTRACT

A first cycle of full-sib recurrent selection was conducted in a popcorn base population, with the objective of improving popping expansion and grain yield as recommended in a previous study by Pereira and Amaral Júnior (2001). Seventy five full-sib families were obtained and evaluated in a randomized complete block design, with two replications within set, in two distinct environments: Experimental Station at PESAGRO-RIO in Campos dos Goytacazes and in Itaocara, Rio de Janeiro, Brazil. The analysis of variance revealed significant differences for families within set for all evaluated traits, indicating the presence of sufficient genetic variability to be exploited in future recurrent selection cycles. To select the superior families for recombination, the main trait was the popping expansion and at the same time, low grain yield families were avoided. So, the predicted genetic gains were respectively 10.39% and 4.69% for popping expansion and for grain yield. The relatively high genetic gain estimated for both traits is a good indication of the viability of this breeding procedure. Also, the generated population in future cycles must be evaluated in comparison to other genetic materials, to be released as a new improved popcorn variety for the North and Northwest regions of the Rio de Janeiro State, Brazil.

**KEY WORDS:** Popcorn, *Zea mays*, genetic gain, recurrent selection, full-sib family selection.

## INTRODUCTION

Only recently, Brazilian plant breeders have become more interested in popcorn, in order to provide superior varieties to the market and consequently, minimize the need for importation. To emphasize the economic importance of this crop, Pacheco et al. (1998) pointed out that, in the United States of America, this crop is responsible for about half billion dollars a year in revenues.

The most recent information about popcorn breeding in Brazil have emphasized the potentiality of recurrent selection in providing genetic gain for popping expansion, which is the most economically important trait for this crop (Pacheco et al., 1998; Pereira and Amaral Júnior, 2001).

Taking into consideration both popping expansion, a trait typically with additive inheritance (Lyerly, 1942; Dofing et al. 1991; Larish and Brewbaker, 1999; Pereira and Amaral Júnior, 2001) and the fact that the Brazilian varieties have high genetic variability, due to the limited use of breeding methods (Linares, 1987), the intrapopulation recurrent selection procedure constitutes an attractive option for the

development of new varieties (Pacheco et al., 1998).

However, during the application of these selection methods, the truncated selection for popping expansion tends to result in a low yield population, once these two traits, grain yield and popping expansion, are negatively correlated, as indicated by different investigations such as Brunson (1937), Lima et al. (1971), Verma and Singh (1979), Lira (1983) and Andrade (1996).

Based on the estimation of genetic parameters in half-sib progenies in a second cycle of recurrent selection derived from CMS-42 and CMS-43 populations, Pacheco et al. (1998), concluded that it is possible to select genotypes that combine both traits, high yield and good popping expansion. But they consider the improvement for popping expansion easier than for grain yield.

Pereira and Amaral Júnior (2001) estimated the genetic components in a base population, the UNB-2U, and the results showed genetic gains for both traits, popping expansion and grain yield. According to the authors, genetic gains of 27.09% and 9.42%, respectively, for popping expansion and yield, are expected for each cycle of intrapopulation recurrent

selection of full-sib families derived from the UNB-2U population.

The present work was developed to evaluate the genetic gain for popping expansion and for grain yield, during the first cycle of a recurrent selection of full-sib progenies derived from the UNB-2U population, with the objective of obtaining genetic information for the future release of a superior variety adapted to the North and Northwest regions of the Rio de Janeiro State, Brazil.

## MATERIAL AND METHODS

The UNB-2U open pollinated population, originated from the UNB-2 variety, was used in this study, after two cycles of mass selection in Campos dos Goytacazes, Rio de Janeiro, Brazil. The UNB-2 originated from the UNB-1 variety, which came from a 'Composto Indígena' selection donated to UNB (University of Brasília, Brazil) by ESALQ/USP, Piracicaba, São Paulo, Brazil. The UNB-1 was crossed with an American popcorn variety. Selected plants from that cross were crossed with yellow popcorn, a high yield and resistant to *Exserohilum turcicum* genotype. After the second crossing, mass selection was applied to form a population of resistant high yielding and with yellow kernels plants. Such population was then backcrossed three times with the American popcorn variety, eventually originating the UNB-2 open pollinated variety (Bulow, J.F.W.von, unpublished information; Pereira and Amaral Júnior, 2001).

The UNB-2U population was planted in February 1999, at the PESAGRO-RIO Experiment Station, Campos dos Goytacazes - RJ. The procedure used for the first cycle was the intrapopulation full-sib recurrent selection, with the recombination of  $S_1$  seeds, corresponding to the superior progenies, as described by Hallauer and Miranda Filho (1988). To obtain the full-sib progenies, and the corresponding  $S_1$  seeds, the population was planted in pairs of rows, and crosses were performed between prolific plants. Normally the first ear (superior) was used for selfing to obtain the  $S_1$  seeds and the second ear to obtain the full-sib progeny. The  $S_1$  seeds were stored and the full-sib progenies were used for testing.

The 75 full-sib progenies obtained as described above were evaluated during the traditional corn planting season (October, 1999 to March, 2000), in a randomized complete block experimental design, with two replications within sets, in two distinct environments: at the PESAGRO-RIO Experimental

Station in Campos dos Goytacazes and in Itaocara, Rio de Janeiro, Brazil. Each progeny was evaluated in a five meter long, two-row plot spaced one meter among rows and 0.20 meter among plants within row.

Data were collected in both environments for sixteen agronomic traits. For simplification reasons, only four traits were analyzed and discussed: a) days from planting to 50 % silk emergence (FLO); b) plant height in cm (PH); c) grain yield in Kg/ha (GY) - about 12 % grain moisture; and d) popping expansion (PE).

The PE was obtained from random samples from the harvested plot. The volume in  $\text{cm}^3$  of 40 g of grain with about 12 to 13 % of moisture was measured before and after popping, producing the corresponding ratio (PE = volume after popping/volume before popping). The PE evaluation was conducted after the corn seeds were submitted to a microwave at maximum power (900 W) for three minutes for each sample. The data were the mean of two samples for each plot.

Analyses of variance (Table 1) were carried out for each trait following the genetic-statistic model  $y_{ijkl} = \mu + E_i + S_j + ES_{ij} + R/ES_{ijk} + F/S_{jl} + EF/S_{jil} + \epsilon_{ijkl}$ , according to Hallauer and Miranda Filho (1988), where  $\mu$  is the mean,  $E_i$  is the effect of the  $i^{\text{th}}$  environment,  $S_j$  is the effect of the  $j^{\text{th}}$  set,  $ES_{ij}$  is the interaction effect of environments and sets,  $R/ES_{ijk}$  is the  $k^{\text{th}}$  effect of replication within interactions between  $i^{\text{th}}$  environment and  $j^{\text{th}}$  set,  $F/S_{jl}$  is the effect of  $l^{\text{th}}$  family (progeny) within  $j^{\text{th}}$  set,  $EF/S_{jil}$  is the interaction effect of environments and families within  $j^{\text{th}}$  set and  $\epsilon_{ijkl}$  is the experimental error. Each set was analyzed separately and then pooled for each environment, over the three sets, and finally pooled over the two environments. All sources of variation, except environments were considered to be random effects. The SAS (1985) program was used to analyze the data.

To select the superior progenies, two traits were considered: PE and GY. However, considering that the UNB-2U is a relatively high yield population, as indicated in recent publication (Pereira and Amaral Júnior, 2001), the trait primarily considered was the PE. So, initially, 50% superior progenies for PE and GY were identified. After that, the selection was based on both traits simultaneously, totaling 28% of the progenies. Then, 21 superior progenies for recombination and a few more families (12%) were selected based on the PE trait only. The recombination to obtain an improved population from the first cycle was performed using the  $S_1$  seeds corresponding to

the 30 selected superior full-sib families.

The predicted genetic gains for the first cycle of full-sib recurrent selection were obtained according to Falconer (1981), using the SAS program (SAS, 1985).

## RESULTS AND DISCUSSION

Table 2 shows the significant effect for environment (E) for all the traits evaluated, indicating that the two environments used on this investigation are distinct.

Different from GY, FLO and PH, the interaction environment by set was significant for PE. Considering that each set has a distinct group of families, such interaction is an indication of genotype by environment interaction. It also indicates an expressive influence of the environment on this trait, contributing to the idea of quantitative inheritance for PE, as suggested initially by Brunson (1937) and Lima et al. (1971). According to these authors, if a large number of ears is tested separately, a normal distribution is obtained for popping expansion.

Alexander and Creech (1977), agree that the expansion phenomenon is a polygenic trait, but subject to a low environmental influence. However, the environmental influence seems to be relevant to PE, once there are evidences that not all the genes that contribute to the endosperm hardness, also contribute to PE, which suggests that the adaptation to the growing area influences the capability of expansion of the popcorn (Robbins Jr and Ashman, 1984; Linares, 1987).

The environmental influence on the differentiated expression of PE, in popcorn, was also found by

Vendruscolo et al. (2001), that verified significant effect of genotype by environmental interaction on 15 genotypes (varieties and inter-variety hybrids), evaluated in 15 locations in the Central Southern region of Brazil.

The potential for obtaining genetic gain from the recurrent selection UENF's popcorn program is evidenced by the occurrence of significance for family within set for all the evaluated traits (Table 2), demonstrating the existence of sufficient genetic variability to be exploited in successive cycles of selection, increasing the favorable alleles in such population, the main reason for the recurrent selection.

The selective potential of the UNB-2U population for GY and PE is indicated by the difference of the mean of the selected families in relation to the original population (Table 3). Yet, expressive progresses are expected in future cycles, once this is the principle (continuous gains) of the recurrent selection procedure. The future progress is indicated by the existence of families with mean values superior to the mean of the selected progenies (Table 3). The continuous progress in future cycles is obtained once with the increase of the frequency of favorable alleles, superior segregants are expected in successive cycles.

In general, the occurrence of a large discrepancy in the mean for the inferior and superior limits of GY and PE (Table 3), is an indicative of the genetic variability of the UNB-2U base population, which is an essential condition for obtaining superior segregants.

Pacheco et al. (1998), in their investigation of popcorn

**Table 1.** Analyses of variance table for the evaluated agronomic traits.

SV	DF	E (MS) <sup>1/</sup>
Environments (E)	e - 1	$\sigma^2 + fr\theta\sigma_{ES}^2 + f\theta\sigma_{R/ES}^2 + r\theta\sigma_{EF/S}^2 + fsr\Phi_E$
Sets (S)	s - 1	$\sigma^2 + r\theta\sigma_{EF/S}^2 + f\theta\sigma_{R/ES}^2 + er\sigma_{F/S}^2 + fer\sigma_S^2$
E x S	(e - 1) (s - 1)	$\sigma^2 + r\theta\sigma_{EF/S}^2 + f\theta\sigma_{R/ES}^2 + fr\sigma_{LS}^2$
Replications (R) / E x S	es (r - 1)	$\sigma^2 + f\theta\sigma_{R/ES}^2$
Families (F) / S	s (f - 1)	$\sigma^2 + er\sigma_{F/S}^2$
E x F / S	s (f - 1) (r - 1)	$\sigma^2 + r\theta\sigma_{EF/S}^2$
Error	es (f - 1) (r - 1)	$\sigma^2$
Total	efrs - 1	

$$1/ \theta = \frac{e}{e-1}; \quad \Phi_E = \frac{\sum E_i^2}{e-1}$$

**Table 2.** Mean squares for the four evaluated traits on the full-sib families of popcorn derived from the first cycle of intrapopulation recurrent selection.

SV	DF	Mean Squares <sup>1/</sup>			
		GY	FLO	PH	PE
E	1	0.3649 <sup>3/</sup>	865.4882 <sup>3/</sup>	0.4185 <sup>3/</sup>	312.1135 <sup>3/</sup>
S	2	0.0817 <sup>ns</sup>	26.8253 <sup>3/</sup>	0.3044 <sup>3/</sup>	1.9588 <sup>ns</sup>
E x S	2	0.0908 <sup>ns</sup>	9.1964 <sup>ns</sup>	0.0411 <sup>ns</sup>	13.0191 <sup>3/</sup>
R / E x S	6	0.0433 <sup>ns</sup>	16.0169 <sup>3/</sup>	0.0661 <sup>3/</sup>	5.2748 <sup>2/</sup>
F / S	72	0.1029 <sup>3/</sup>	15.9558 <sup>3/</sup>	0.0473 <sup>3/</sup>	10.2649 <sup>3/</sup>
E x F / S	72	0.0558 <sup>ns</sup>	24.1691 <sup>3/</sup>	0.0199 <sup>2/</sup>	6.9668 <sup>3/</sup>
Error	140	0.0437	4.4574	0.0139	2.2837
CVe (%)		39.1782	3.5019	6.2923	13.676

<sup>1/</sup> FLO: days from planting to 50 % silk emergence; PH: plant height; GY: grains yield and PE: popping expansion;

<sup>2/</sup> Significant at the 0.05 level; <sup>3/</sup> Significant at the 0.01 level; <sup>ns</sup> Not significant at the 0.05 level.

**Table 3.** Estimated means for population ( $\bar{X}_o$ ), selected families ( $\bar{X}_s$ ) inferior limit (IL) and superior limit (SL) of the evaluated progenies for grain yield (GY) and for popping expansion (PE) in the first cycle of intrapopulation full-sib recurrent selection of popcorn.

Estimates	Traits <sup>1/</sup>	
	GY	PE
$\bar{X}_o$	0.53	11.04
$\bar{X}_s$	0.57	12.52
IL	0.19	7.79
SL	0.84	15.32

<sup>1/</sup> GY: grains yield and PE: popping expansion.

based on the superior and inferior limits for popping expansion and grain yield, predicted superior segregants for the CMS-42 and CMS-43 populations in the second cycle of the recurrent selection.

Based on the genetic component estimates (Table 4), the magnitude of  $\sigma_g^2$  is superior to  $\sigma^2$  for PE and the opposite for GY ( $\sigma^2$  superior to  $\sigma_g^2$ ). As a result, the heritability for PE was superior than for GY, with values of 77.75 % and 57.48 %, respectively.

In fact, the superiority of the heritability for PE in relation to that for GY was expected in the present study, which is in agreement with the results previously obtained by Pereira and Amaral Junior (2001) on the same population (UNB2-U). Such results are also in agreement with other popcorn investigations (Lira, 1983; Pacheco et al., 1998). So, as mentioned by Pacheco et al. (1998), more genetic gains are expected for popping expansion than for grain yield in popcorn breeding programs.

**Table 4.** Estimates of phenotypic variance ( $\sigma_f^2$ ), genotypic variance ( $\sigma_g^2$ ), environmental variance ( $\sigma^2$ ), broad sense heritability ( $h_b^2$ ) and genetic gain (GG) in percentage for grain yield (GY) and for popping expansion (PE) in the first cycle of intrapopulation full-sib recurrent selection of popcorn.

Genetic Parameters	Traits <sup>1/</sup>	
	GY	PE
$\sigma_f^2$	0.0257	2.5662
$\sigma_g^2$	0.0147	1.9953
$\sigma^2$	0.0437	1.1418
$h_b^2$	57.4845	77.7500
GS	4.6969	10.3990

<sup>1/</sup> GY: grains yield and PE: popping expansion.

Despite the fact that genetic progress can be greater in breeding programs carried out under each particular environmental conditions, in the case of recurrent selection procedures it would be too time consuming. Fortunately, in the present situation, the genetic gains for GY and for PE, based on the mean for both environments, Campos dos Goytacazes and Itaocara, were positive (Table 4). So, only one improved population was generated by the recombination of superior families allowing the continuation of just one recurrent selection program in future cycles, for both environments.

The positive genetic gains for both traits, GY and PE (Table 4) were possible in the present study, as a result of the selection strategy adopted. A tandem selection was performed, once these traits are negatively

correlated, and a truncated selection would probably result in desirable genetic gains for just one of the traits.

The relatively high genetic gain estimated for both traits, 4.69% and 10.39, respectively, for grain yield and for popping expansion (Table 4), is a good indication for the viability of this breeding procedure. Also, the generated population in future cycles must be evaluated against other genetic materials, and, finally be released as new improved popcorn varieties for the North and Northwest regions of the Rio de Janeiro State, Brazil.

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## RESUMO

### Progressos Genéticos para Capacidade de Expansão e Produção de Grãos em Milho Pipoca sob Seleção Recorrente

Com o objetivo de estimar os progressos genéticos possíveis com a implementação do primeiro ciclo de seleção recorrente na população-base de milho pipoca UNB-2U, previamente identificada por Pereira e Amaral Júnior (2001) com potencialidade para geração de segregantes superiores, setenta e cinco famílias de irmãos completos foram obtidas e avaliadas em blocos completos casualizados com duas repetições dentro de grupos, em dois ambientes distintos: Estação Experimental da PESAGRO-RIO, em Campos dos Goytacazes e em Itaocara, Rio de Janeiro, Brasil. A análise de variância revelou diferenças significativas para famílias dentro de grupos para todas as características avaliadas, demonstrando haver suficiente variabilidade a ser explorada nos sucessivos ciclos de seleção recorrente. Na seleção das progênies para recombinação, procuraram-se aquelas com maior potencial de expansão possível, e ao mesmo tempo, que não apresentassem médias de produtividade em nível inferior, o que possibilitou a expectativa de progresso

genético de 10,39 % para capacidade de expansão e 4,69 % para produção de grãos com o primeiro ciclo de seleção recorrente. Conclui-se pela expectativa de sucesso do Programa de Melhoramento de Milho Pipoca da UENF para o futuro lançamento de variedade melhorada para as regiões Norte e Noroeste Fluminense.

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