



ARTICLES

Genetic gains in popcorn by full-sib recurrent selection

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ABSTRACT – *The purpose of this study was to investigate the genetic progress in the fourth selection cycle of full-sib popcorn families. Two hundred families were evaluated for six agronomic traits, including grain yield (GY) and popping expansion (PE), in a random block design with two replications, in sets in two different environments: Campos dos Goytacazes and Itaocara, in the State of Rio de Janeiro. There were significant differences among families within sets in all traits, indicating the presence of genetic variability to be exploited in the future cycles. The family by environment in the sets for GY and PE was significant but simple, indicating the possibility of conducting a single breeding program for both locations. The release of the improved variety for producers of the Northern and Northwestern regions of the State of Rio de Janeiro is expected after the fifth cycle.*

Key words: *Zea mays*, recurrent selection, genetic gains, variety release.

INTRODUCTION

Although popcorn breeding in Brazil and USA was initiated at about the same time, Brazil is still largely dependent on improved genotypes which, even when not directly imported, were mostly bred in the USA and are grown in Brazil in partnership with producers of companies such as Yoki and Hikari (Rangel et al. 2008).

The first national variety was released in 1941, bred in mass selection cycles from the base population "South American Mushroom" (SAM), derived from "South American" from the USA. However, research work was only resumed in the country in the early 80s, culminating in 1988 in the release of the simple modified hybrid IAC-112, from a combination of lines of the variety SAM with lines from the intervarietal hybrid Guarani x UFV Amarelo (Sawazaki et al. 2000, Sawazaki 2001) and almost simultaneously, the release of the triple

hybrid Zélia, marketed by Pioneer. Of the 206 corn varieties available in Brazil in the 2004/2005 growing season, only two were popcorn, namely RS 20 and Zélia. This contrasts sharply with the crop profit potential – the market value of popcorn is about three times as high as that of common corn.

More recently, new popcorn breeding programs have been developed, particularly by public institutions. In the 90s, the following genotypes were released: IAC-112, which is bound to a partnership agreement with the company Hikari, IAC-125, a simple hybrid derived from IAC-112, registered in April 2006, as well as the open-pollinated varieties BRS Angela, obtained from recurrent selections with composite CMS-43, but with the drawback of a white grain color; RS 20, developed by IPAGRO and marketed by AGROESTE-SC; and UFVM2-Barão Viçosa (Sawazaki 2001, Rangel et al. 2007, Freitas Júnior et al. 2006).

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The reduced genetic basis of the crop, which may be a result of the selections of corn types such as flint (Kantety et al. 1995), is an aspect that has concerned researchers when implementing breeding programs. As an example we cite the study of Miranda et al. (2008), who concluded that although it is possible to increase grain yield by using local genotypes, it is difficult to breed commercial hybrids from these genotypes in Brazil due to the poor performance in terms of popping expansion. Nevertheless, Capentieri-Pípolo et al. (2003) evaluated the genetic divergence in nine popcorn genotypes by means of cluster analysis and detected the formation of only two groups, with only one genotype in group I and four in Group II. Consequently, only four superior hybrids can be bred, which reduces the possibility of exploring the 36 possible hybrids among all genotypes included in the study considerably.

Studies for breeding procedures in popcorn focused on combining ability have received attention of researchers in Brazil. Zanette (1989) for example examined the performance of six North American popcorn hybrids and detected no significant heterosis for grain yield and popping expansion. On the other hand, significant effects of general and specific combining ability in popcorn were reported by Andrade et al. (2002), Scapim et al. (2002), Viana and Matta (2003), Freitas Júnior et al. (2006), Scapim et al. (2006), Rangel et al. (2007), Viana et al. (2007) and Rangel et al. (2008).

Strategies of evaluating genotypes as possible compounds of a composite with broad genetic variability to be used in breeding programs (Rangel et al. 2007), as well as the evaluation of natural populations to investigate the genetic potential for use in breeding programs have been a focus of research in Brazil. For example the estimation of genetic parameters in the population DFT1-Ribeirão in the study of Coimbra et al. (2002), who evaluated 121 half-sib families in a lattice square design, resulting in an estimated reduction of the high yield from 4918.00 Kg ha⁻¹ to 4724.00 Kg ha⁻¹ and an increased expansion volume from 20.00 to 23.00 g mL⁻¹, after the recombination of progenies selected for the first cycle of recurrent selection.

The Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) has been developing a recurrent selection program with popcorn, with a view to release a variety with desirable traits, adapted to the north and northwestern regions of Rio de Janeiro. The program was initiated with the evaluation of the potential of the

population UNB-2U by Pereira and Amaral Júnior (2001) and the observation that the strategy of recurrent selection among full-sib families is the most efficient to breed improved varieties, for both expansion volume and grain yield.

In view of the selection potential of UNB-2U, three recurrent selection cycles were performed with selection gains in grain yield and popping expansion of, respectively, 10.39% and 4.69% in the first cycle (Daros et al. 2004a), 26.95% and 17.80% in the second cycle (Daros et al. 2004b) and 10.00% and 7.16% in the third cycle (Santos et al. 2007), without any evidence of a narrowing of the genetic basis of the population, as verified by Vilela et al. (2008).

This study aimed to continue the program to recurrent selection of the UENF with the evaluation of full-sib UNB-2U families in the fourth selection cycle, to estimate the expected genetic progress, in particular for grain yield and expansion volume, and to investigate the possibility of the release of an improved variety.

MATERIAL AND METHODS

The experiments were conducted in the 2005/2006 growing season, at the Colégio Estadual Agrícola Antônio Sarlo, in Campos dos Goytacazes, in the north of the State of Rio de Janeiro, at an altitude of 11 m asl, and at the Experimental Station of PESAGRO-RIO in Itaocara, at 60 m asl, 110 Km away from each other.

To obtain the full-sib progenies, 300 rows of a balanced mixture of recombined seeds of the third cycle were sown. Rows and plants were numbered to facilitate the identification of the pairwise crosses that were performed. This procedure resulted in 200 families with two ears per family.

In the evaluation of the 200 full-sib families, the populations UNB C0-2U, 2UC1-UNB, UNB-2U C2, UNB-2U C3 and variety BRS Angela were included for comparison. The plants were sown in November 2004 in 5.00 m long rows, spaced 1.00 m apart, with 25 plants spaced 0.20 m away from each other in a randomized block design, with two replications within sets.

The following traits were evaluated: grain yield (GY), ear weight with grains (EW), number of diseased ears (NDE), number of ears attacked by pests (NEP), number of partially husked ears (PHE) and popping expansion (PE). The PE was determined in the laboratory, according to the method recommended by Pacheco et

al. (1998), using an electric popper of EMBRAPA-Instrumentação Agropecuária.

The data of the traits were used for the analysis of variance according to the statistical model $Y_{ijkl} = m + A_i + S_j + AS_{ij} + R/AS_{ijk} + F/S_{jl} + AF/S_{jil} + x_{ijkl}$, where: m is the mean, A is the fixed effect of the i^{th} environment; S_j is the effect of the j^{th} set; AS_{ij} is the effect of the interaction between environments and sets; R/AS_{ijk} is the effect of k^{th} replication within the interaction between the i^{th} environment and j^{th} set; F/S_{jl} is the random effect of i^{th} genotype in the j^{th} set; AF/S_{jil} is the effect of the genotype-environment interaction in the j^{th} set; and x_{ijkl} is the experimental error. The SAS program (SAS 1995) was used for the statistical analysis.

The components of variance were obtained, based on the genotypic variance between families estimated by: $\sigma_p^2 = \frac{MSF - MSR}{ra}$, where: MSF : = mean square of families within sets; MSR : = residual mean square; r = replication; and a = environment. The heritability based on the mean of families was estimated by $h_x^2 = \frac{\sigma_G^2}{\sigma_P^2}$.

where $\sigma_p^2 = \frac{MSF}{re}$, which corresponds to the estimator of the phenotypic variance between families. The coefficient of genetic variation in percentage (CVg) was determined by: $CVg = 100 \sqrt{\frac{\sigma_g^2}{MSR}}$; and the variation index by the ratio (Cruz and Carneiro 2003).

The decomposition of the partly complex interaction was based on the expression: $C = \sqrt{(1-r)^3} \sqrt{Q_1 Q_2}$, as proposed by Cruz and Castoldi (1991), where Q_1 and Q_2 are the mean squares of the genotypes in environments 1 and 2, respectively, and r is the correlation between genotype means in the two environments.

RESULTS AND DISCUSSION

There was a significant environmental effect for all traits (Table 1), but this significant difference between the environments was no restriction to the implementation of a single breeding program for the two locations. According to Daros et al. (2004a,b) and Santos et al. (2007), what matters for selection is the expression of the phenotypic means of families in both environments. The significance of environments for

popping expansion (PE) was also stated by Vendruscolo et al. (2001), in an evaluation of 15 genotypes (varieties and inter-varietal hybrids) in 15 environments in central-southern Brazil.

The PE is reported to be strongly influenced by the environment, contributing to the assumption of quantitative inheritance, as originally suggested by Brunson (1937). In this context, Alexander and Crech (1977) agree that the popping expansion is a polygenic trait, although influenced by a low environmental effect. The environmental influence on popping expansion of popcorn is justified by the fact that not all genes that contribute to endosperm hardness contribute to grain expansion volume as described in detail by Robbins and Ashman (1984).

The traits EW, GY, PE and PHE were significantly different in the sets (S) (Table 1). The block design with partition into sets is therefore efficient; an absence of this partition would expectedly induce variations that could result in a loss of experimental accuracy.

The source of variation for F/S was significant for all traits (Table 1), which shows that there is genetic variability that may be explored in future cycles, with a view to selection progress. Moreover, this indicates that the objective of population improvement by recurrent selection without loss of genetic variability was achieved in the population of the fourth recurrent selection cycle in full-sib families.

The values of CVe (%) ranged from 9.99% for NEP to 84.82% for NDE. The second highest percentage was found for PHE, with a value of 84.82%. Arnhold et al. (2007) also obtained high CVe (%) values for PHE in a study with recurrent selection in popcorn. High CVe (%) values for NDE, NEP, PHE and GY had also been observed in the previous recurrent selection generations (Daros et al. 2004b, Santos et al. 2007). In this study, for the key traits to improve the crop, the experimental coefficient of variation for grain yield was moderate (20.00%) and low for popping expansion (8.26%).

The significance for all traits in relation to the interaction FxE/S indicated the type of interaction. The interaction of most traits was complex, below 20.00%; only the values of NDE, NEP and PHE exceeded this percentage, but were always lower than 50.00%. In particular, the estimated percentage of complex interactions for traits NDE, NEP, EW, GY, PE, and PHE were, respectively: 20.23%, 33.57%, 19.15%, 18.55%, 15.06% and 21.67%, which demonstrates the superiority

Table 1. Mean squares and mean coefficients of variation of six traits evaluated in two environments in progenies of the fourth cycle of intrapopulation recurrent selection of full-sib popcorn families

SV	DF	MS ^{1/}					
		NDE	NEP	EW	GY	PE	PHE
Environment (E)	1	25.0227**	0.6787 ^{ns}	371911525.0000**	22242737.5000**	28.5456*	124.2660**
Set (S)	7	9.8529 ^{ns}	6.2781 ^{ns}	2236207.6000**	956764.5000**	40.0827**	9.9749**
E x S	7	12.6212 ^{ns}	17.3892**	2062223.9000**	1225771.7000**	5.2867 ^{ns}	7.7351**
Repl. (R) / E x S	16	14.0621*	27.5411**	1782337.5000**	1499974.0000**	10.8446**	5.0351**
Family (F) / S	193	10.3142*	7.6780**	7080099.8000**	532241.0000**	43.6911**	4.1951**
E x F / S	192	8.7951 ^{ns}	5.4388 ^{ns}	508407.6000**	368325.1000**	12.5215**	3.1914**
Error	383	7.7937	5.2606	319199.2000	229460.4000	4.2850	2.1042
Mean		3.2912	22.9400	2971.4800	2393.9800	25.0600	1.9900
CVe (%)		84.8200	9.9900	19.0100	20.0000	8.2600	72.7500

^{1/} NDE = number of diseased ears; NEP = number of ears attacked by pests; EW = ear weight with grains; GY = grain yield; PE = popping expansion; and PHE = number of partially husked ears. ^{ns} = non significant at 1% and 5% probability by the F test; * = significant at 5% probability; and ** = significant at 1% probability.

of simple over complex interaction and confirms that a single breeding program is possible for the different environments considered here.

Based on the means and limits (Table 2), ear weight with grains (EW) was the trait with widest range of variation, which is of interest in breeding programs, since this is a yield component. For the agronomic traits of greatest importance, GY and CE, the discrepancy between the lower and upper limits was great, with lower limits of 910.00 Kg.ha⁻¹ and 11.20 mL g⁻¹ and upper limits of 4.510.00 Kg.ha⁻¹ and 35.90 mL g⁻¹, respectively.

A comparison of the means of the control (BRS Angela) with the means of the selected progenies shows

Table 2. Estimates of means of the original population (\bar{X}_o), the selected families (\bar{X}_s), the controls (\bar{X}_r), the lower (LL) and the upper limit (UL) of progenies in the fourth cycle of intrapopulation recurrent selection of full-sib popcorn families

Traits ^{1/}	\bar{X}_o	\bar{X}_s	\bar{X}_r	LL	UL
NDE	3.2900	2.7100	2.9300	0.0000	21.0000
NEP	3.2500	2.8700	4.3400	0.0000	13.0000
EW	2791.4800	3383.1600	2635.5000	910.0000	5620.0000
GY	2393.9800	2772.5000	1955.0000	670.0000	4510.0000
PE	25.0600	28.0000	30.2100	11.2000	35.9000
PHE	1.9900	1.8100	0.8700	0.0000	13.0000

^{1/} NDE = number of diseased ears; NEP = number of ears attacked by pests; EW = weight of ears with grains; GY = grain yield; PE = popping expansion; and PHE = number of partially husked ears

that for the trait GY the means of the selected plants were by 30.00% higher than of the control. In particular

for PE, the variety BRS Angela exceeded the mean of the selected progenies by 7.31%, which is not a relevant factor, since BRS Angela is a variety that has already been recommended by EMBRAPA-Milho e Sorgo. For other traits the control means were lower than of the selected progenies, as in the case of NDE and NEP, which is favorable for improvement, since the disease index and ears attacked by pests tend to be lower in the families.

The estimates of the genetic parameters (Table 3) indicated a high possibility of obtaining superior segregating generations for EW, since the h^2 estimate was the highest. The expectation of selecting superior genotypes that carry ears full of grains is therefore high.

For the traits of greatest economic interest, GY and PE, only for GY the value of σ^2_e was greater than of the component σ^2_e , indicating the greater environmental influence for GY. This had been expected since GY is a quantitative trait and therefore more sensitive to environmental effects. Moderate and high h^2 values (58.88% and 90.19%, respectively) were recorded for GY and PE. The higher h^2 for trait PE than for GY shows that the procedure of intrapopulation recurrent selection led to a considerable concentration of alleles with additive effects in the population. Considering heritability only, high and moderate gains are to be expected, respectively, for PE and GY, in the population under selection.

An interesting fact is that the values of I_v for number of diseased ears and number of ears attacked by pests are the lowest (Table 3), due to genetic

coefficients of variation similar to the experimental (Table 1). This may be explained by the fact that the values of genotypic variances were not significant in comparison with the phenotypic, resulting in low values of heritability based on the sets means. For NDE and NEP the h_x^2 values (24.11% and 16.47%, respectively) are promising results, since they predict a low expectation for a transfer of the genes responsible for pest and disease susceptibility to the next generation. Also, the moderate h_x^2 value for PHE indicates that the transfer of undesirable genes that would affect good husk cover of the ears is not very likely.

The estimated gains with the selection of full-sib families were negative for NDE, NEP and PHE (Table 3), which is favorable for the breeding of an improved population, where the number of diseased plants, of plants attacked by insects and with partially hulled ears tends to be lower.

The percentage gains with truncation selection were highest, in decreasing order, for EW, PE and GY (20.23%, 10.58% and 7.71%, respectively). In other words, the expectation for C5 is to contain genotypes with PE of 30.80 mL g⁻¹ and GY of 2.986.25 Kg ha⁻¹. With a view to the release of a variety these values are acceptable, and therefore it is expected that the population of the next recurrent selection cycle can be recommended for producers in the northern and northwestern region of the State of Rio de Janeiro.

In a comparison of the means obtained for PE and GY in the cycles C0, C1, C2, C3 and predicted for C4, a continuous increase in PE and GY was observed (Figures 1 and 2). The R² value for the equation of the

straight line in Figure 1 is high, which is an indication that the regression model represented a consistent statistical adjustment. Figure 1 also shows the evolution of gains by intrapopulation recurrent selection, where in cycle C0 the population had an PE of 19.00 mL g⁻¹ and reached 28.00 mL g⁻¹ in C4, which is equal to an increase of 47.00% in popping expansion in only four cycles of recurrent selection, as a result of the increase in the frequency of favorable alleles in the population. Similarly for GY, there was an increase of 63.00% from C0 to C4 (from 1,700.00 to 2,772.00 Kg ha⁻¹) (Figure 2).

A comparison of the gains expected by Daros et al. (2004b), for the second cycle of recurrent selection, and Santos et al. (2007) for the third cycle is interesting, since the increase for GY was even higher when the recombined population mean was compared with the estimated mean. In this respect, a mean yield of 1140.00 Kg ha⁻¹ was predicted for C2 and when the real mean was obtained the GY reached 2,497.81 Kg ha⁻¹, which represents an increase of 119.00%, compared to the expected mean. Similarly, in the C3 cycle a mean grain yield of 2,156.00 Kg ha⁻¹ was expected, but with the real mean the increase was 27.00%, since the yield was 2,741.88 Kg ha⁻¹. If this tendency continues in the recombination cycle C4, over 2,986.25 Kg ha⁻¹ can be obtained, which meets the quality standard for a release of the genotype.

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Table 3. Estimates of phenotypic variance (σ_f^2), genotypic variance (σ_g^2), residual variance (σ_r^2), the heritability on the basis of families (h_x^2), the coefficient of genetic variation (CV_g), the index of variation (I_v) and selection gain in percentage (SG) for the population UNB-2U in the fourth cycle of intrapopulation recurrent selection

Traits	σ_f^2	σ_g^2	σ_r^2	h_x^2	CV_g	I_v	SG (%)
NDE	2.5786	0.6301	7.7937	24.45000	24.1100	0.2842	-4.3103
NEP	1.2384	0.2867	3.8068	23.1500	16.4700	0.2747	-2.7006
EW	1770024.9500	1690225.1500	319199.2000	95.4900	43.7500	2.3014	20.2399
GY	133060.2500	75695.1500	229460.4000	56.8800	11.4900	0.5745	7.7140
PE	10.9227	9.8515	4.2850	90.1900	12.5200	1.5157	10.5809
PHE	1.0487	0.5227	2.1042	52.2700	36.3300	0.4993	-4.7279

^{††} NDE = number of diseased ears; NEP = number of ears attacked by pests; EW = weight of ears with grains; GY = grain yield; PE = popping expansion; and PHE = number of partially husked ears

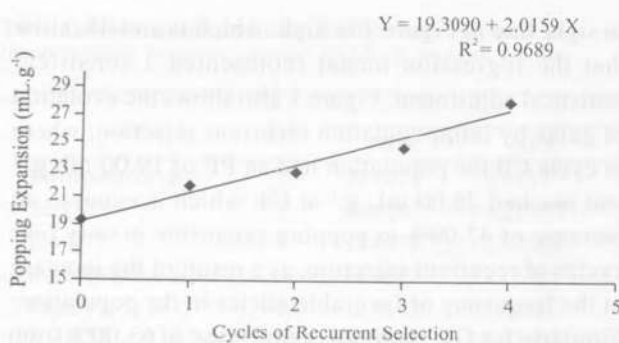


Figure 1. Evolution of the means in the cycles C0, C1, C2, C3 and predicted in C4 for popping expansion

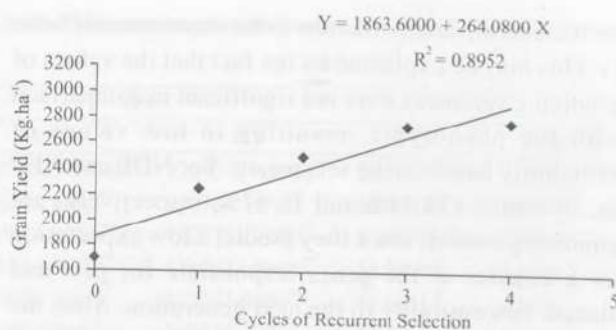


Figure 2. Evolution of the means in the cycles C0, C1, C2, C3 and predicted in C4 for grain yield

Ganhos genéticos em população de milho pipoca sob seleção recorrente

RESUMO - Objetivou-se estimar o progresso genético no quarto ciclo de seleção recorrente com famílias de irmãos-completos de milho pipoca. Duzentas famílias foram avaliadas quanto a seis características agrônômicas, incluindo rendimentos de grãos (RG) e capacidade de expansão (CE), em delineamento em blocos ao acaso com duas repetições dentro de "sets" em dois ambientes distintos: Campos dos Goytacazes e Itaocara, no Estado do Rio de Janeiro. Houve diferenças significativas para famílias/"sets" em todas as características, indicando a presença de variabilidade genética a ser explorada nos futuros ciclos. A interação foi significativa para famílias x ambientes / "sets", em relação a RG e CE, mas do tipo simples, favorecendo a condução de um único programa de melhoramento para ambos os locais. Para o próximo ciclo espera-se o lançamento de variedade melhorada para os produtores do Norte e Noroeste Fluminense.

Palavras-chave: Zea mays, seleção recorrente, ganhos genéticos, lançamento de variedade.

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MATERIAL AND METHODS