

Estimates of genetic parameter in maize commercial variety IPR 114 at Paraná State, Brazil

Sara Regina Silvestrin Rovaris^{1*}, Pedro Mário de Araújo², Deoclécio Domingos Garbuglio², Cássio Egídio Cavenaghi Prete¹, Valquíria Sheila Zago¹ and Lucas José Ferreira da Silva¹

¹Departamento de Agronomia, Centro de Ciências Agrárias, Universidade Estadual de Londrina, Rod. Celso Garcia Cid, PR-445, Km 380, 86051-990, Londrina, Paraná, Brazil. ²Área de Melhoramento Genético Vegetal, Diretoria Técnico Científica, Instituto Agronômico do Paraná, Londrina, Paraná, Brazil. *Author for correspondence. E-mail: sara_rsr@yahoo.com.br

ABSTRACT. The objective of this study was to estimate the genetic parameters of the IPR 114 maize commercial variety for breeding purpose and the efficiency of the method. It was performed two cycles of half-sib progenic, between 2004 and 2007. The progenies were evaluated in a randomized complete block design with two replications per environments and the plots were composed of one 4 m length row spaced on 0.8 m, and five plants per meter. The trials were carried out in Londrina and Ponta Grossa, Paraná State, Brazil. There were evaluated 173 and 154 progenies for selection cycles 1 and 2, respectively, analyzing the following traits: plant height, ear height, days to flower, prolificacy and predict grain yield. In both cycles verified significant genetic variability between progenies. Significant selection gains were obtained for predict grain yield, showing 6.33 and 5.03% for cycles 1 and 2, respectively. The estimative for genetic parameters obtained in this work justify the selection program continuity of the IPR 114 maize population

Keywords: *Zea mays* L., progeny of maize, genetic gain, intrapopulacional selection.

RESUMO. Estimativas de parâmetros genéticos na variedade comercial de milho IPR 114 no Estado do Paraná, Brasil. O objetivo deste trabalho foi obter estimativas de parâmetros genéticos, na variedade comercial IPR 114 para fins de melhoramento. Realizou-se dois ciclos de seleção recorrente entre e dentro de progênies de meios-irmãos no período de 2004 a 2007. As progênies foram avaliadas em delineamento de blocos casualizados, com duas repetições por local sendo a parcela útil uma linha de 4,0 m de comprimento e 0,8 m entre linhas deixando cinco plantas por metro. Os ensaios foram conduzidos em Londrina e Ponta Grossa, Estado do Paraná. Avaliaram-se 173 e 154 progênies, respectivamente, para os ciclos 1 e 2 de seleção, analisando-se as variáveis: altura de plantas e de espigas, florescimento feminino, prolificidade e peso de grãos. Nos dois ciclos de seleção verificou-se variabilidade genética significativa entre progênies. Para peso de grãos foram preditos ganhos de seleção significativos, sendo para o ciclo 1, de 6,33% e para o ciclo 2, 5,03%. As estimativas dos parâmetros genéticos obtidos neste trabalho justificam a continuidade do programa de seleção na população IPR 114.

Palavras-chave: *Zea mays* L., progênies de milho, ganho genético, seleção intrapopulacional.

Introduction

Maize (*Zea mays* L.) is cultivated in all States of Brazil. Paraná State produced 15.37 million ton in 2008, standing out as the largest national producer (CONAB, 2008).

This cereal presents great genetic plasticity and therefore is grown in several different environments and in different production systems. The selection of more productive cultivars with better adaptation to local or regional conditions consists in a simple and essential technology to increase crop yield, especially by not burdening the costs of production.

According to Sawazaki and Paterniani (2004), before the 60's decade, the cultivated maize cultivars, besides being low productive, were excessively high, lodged easily and did not tolerate high planting density. With the development of breeding programs, expressive changes were obtained not only in productivity, but also in reductions of plant height and life cycle, and increase of plant health. This resulted in better adaptation to water stress conditions, lower lodging, higher resistance to pests and diseases and enhancement in nutrient quality of the grain.

The Agronomic Institute of Paraná (Instituto Agronômico do Paraná - IAPAR) has been

developing breeding in maize populations using different methods of recurrent selection, with emphasis in the method named selection among and within half-sib progenies with remant seeds. According Paterniani (1967), this method is extensively used due to its facility of execution and efficiency in acquiring genetic gains to populations, presenting as an advantage the possibility of estimating the additive genetic variation in intrapopulation level.

Thus, breeding of maize populations aims the enhancement of frequency of favorable alleles inside the population. According to Vencovsky (1987), the probability of obtaining a superior crop line depends on the frequency of favorable alleles of this population. The frequency of those alleles can be gradually increased through successive selection cycles, which are an efficient way of enhancing varieties aiming both commercial use and line extraction.

Several works using half-sib progenies have been reported in literature. Proving the efficiency of this method, Carvalho et al. (2002) emphasize that, in addition of being practical, it is capable of maintaining sufficient genetic variability to promote progress during the selection cycles.

The objective of this work was to obtain estimatives of genetic parameters of IPR 114 maize variety and to evaluate the population potential for breeding purposes.

Material and methods

The IPR 114 commercial maize variety was developed at IAPAR through diallelic cross between a group of commercial hybrids resulting in a synthetic variety (its genetic constitution involves less than 16 inbreds), being subsequently submitted to two recombination cycles. It is a population of open pollination, presenting the following characteristics: early cycle, low plant height and ear insertion, good tolerance to lodging and staking, good ear coverage, wide adaptation, good productive potential and semi-flint yellow-orange colored grains.

This population was subsequently submitted to two selection cycles among and within half-sib progenies with remant seeds. The following traits were evaluated: plant and ear height (PH and EH, respectively) in centimeters, female flowering (FF) in days, prolificacy (PRO) in units and grain yield (GY) in kg ha^{-1} , correcting the grain humidity to 14,5%. In order to obtain the genetic parameter estimative, GY data were converted to g plant^{-1} . This conversion was necessary due to the fact that most data presented in literature use that unit, which

allows comparison with results obtained by other authors.

The experiment was conducted at IAPAR, at the main Londrina Station and at the Experimental Station of Ponta Grossa, Paraná State, Brazil.

Two selection cycles among and within half-sib progenies with remant seeds were performed using a selection intensity of about 20%. In both cycles, the recombination of selected progenies was done in isolated field. The method consists in bulked of a sample of the selected progenies seeds to generate the male lines. This lines were planted in two periods with 10 days of difference, to effectively guarantee the recombination among all selected progenies. At the flowering time, individualized progenies were detasselled, constituting in this way the female lines. At the end of the cycle, the best plants within the lines were selected for further agronomic evaluations.

The evaluation of selection cycle 1 of this population started at 2004/2005 season, using as checks the following cultivars: IPR 115 Simple Hybrid synthesized at IAPAR; BRS 1010 Simple Hybrid of Embrapa Maize and Sorghum Research Center; and P30F33 Simple Hybrid by Pioneer, this completing 182 entries.

Based on this evaluation, it was performed the selection among progenies. Were selected 40 progenies with the best yield means, which were recombined at 2005/2006 season in isolated field. Simultaneously, the selection within progenies was performed, thus completing one selection cycle. At this stage, 154 ears were selected to constitute the progenies for new evaluations in field trial, starting this way the selection cycle 2. Along with this evaluation, the genetic parameters and the selection gain estimative were also obtained.

The evaluation of second cycle 2 occurred at 2006/2007 season, in which the treatments were constituted by 154 selected progenies using as checks: IPR 115, IPR 114-SB – Basic Seed; IPR114-SG – Genetic Seed; DKB 390 – Simple Hybrid by Monsanto; DOW 2B 710 – Simple Hybrid by Dow Agroscience; and P30F53 – Simple Hybrid by Pioneer, totalizing 160 treatments. At 2007/2008 season the selected progenies were recombined, finishing the second selection cycle.

In both selection cycles 1 and 2, progenies were evaluated in completely randomized complete block design with two replication at each locations (Ponta Grossa e Londrina, Paraná State). The experimental plots were represented by single rows 4 m long spaced 0.80 m apart with 25 plants per plot after thinning.

After evaluation assays between progenies of cycles 1 and 2, single and joint variance analyses

were performed, considering that the effects of genotypes and environments were randomized. Analyses were carried out using the Genes v. 2007.0.0 software (CRUZ, 2007).

The variance components were estimated with the expected means square of variance analysis (VENCOVSKY, 1987). It was estimated the heritability coefficient at average level (h_m^2), the additive genetic variance for half-sib progenies, which corresponds with $4\sigma_a^2$, and variation index b that is estimated by the relation between the genetic variation coefficient and environment variation coefficient (CRUZ et al., 2003).

The selection gains were estimated in g plant⁻¹ and in percentage, according to the following expressions, respectively:

$$(\bar{X}_1 - \bar{X}_0)h_m^2 \text{ and } \frac{SG}{\bar{X}_0} \cdot 100$$

where:

- \bar{X}_1 = means of selected progenies;
- \bar{X}_0 = means of all tested progenies;
- σ_a^2 = variance among progenies;
- σ_F^2 = phenotypic variation;
- GY = predict selection gain.

Results and discussion

The joint variance analyses of progenies for both selection cycles revealed significant differences for: FF, PH, EH and GY, showing persistence of genetic variation at the IPR 114 population (Table 1).

It was also observed that mean square of locations for FF presented highly significant differences at 1% probability level in both selection cycles. This result was observed due to the great difference grouch degree day acumulation between the locations interfering in the progenies cycle.

Ponta Grossa is located at a mild climate environment, where the accumulation of degree days happens in a slower manner, resulting in longer vegetative cycle.

The mean square of P x L interaction for GY was not significant in both selection cycles, evidencing that besides location presented edafoclimatic differences, progenies obtained similar performances. The populations will have the best progenys recombined, searching a population with major adeptness for all regions of the Paraná State. The experimental variation coefficients were considered low for FF and PRO and intermediate for the other traits, demonstrating a good performace of the trial (PIMENTEL-GOMES, 1976; SCAPIM et al., 1995).

Average GY for progenies were of 7,648 kg ha⁻¹ on cycle 1 and 8,500 kg ha⁻¹ on cycle 2, equivalent to 78.13% of the IPR 115 control productivity used on both cycles.

The genetic parameters estimatives obtained on both selection cycles of IPR 114 population allow evidencing a decrease in genetic variability from cycle 1 to cycle 2 for all five traits analyzed (Table 2). Comparable data have been observed in similar breeding works that utilize this kind of progenies (CARVALHO et al., 2000; CARVALHO; SOUZA, 2007; PATERNIANI, 1967; SANTOS; NASPOLINI FILHO, 1986).

As emphasized by Ramalho (1977 apud CARVALHO; SOUZA, 2007), this happens due to the maximum utilization of free variability existing among polygenic blocks. From cycle 2 on, it is used the latent genetic variability present within polygenic blocks and which is gradually dispensed, throughout genetic crossing-over.

Table 1. Mean squares of joint variance analyses and variation coefficients on two selection cycles of progenies of maize IPR 114 population, in Londrina and Ponta Grossa, 2004 to 2007.

Variation Source	1 st Cycle					
	Mean Square					
	F	FF	PH	EH	PRO	GY ¹
Progenies (P)	172	16**	285.3**	194.6**	0.1781**	566.95**
Locations (L)	1	2177.4**	27754*	9501.2**	0.452	3189.90
P x L	172	44.9**	122.8	109.6*	0.0089	276.31
Mean error	362	3.2	102.7	85.2	0.0081	322.39
Means	-	74.3	211.2	104.7	1.08	122.37
C.V.(%)	-	2.4	4.8	8.8	8.52	14.82
Variation Source	2 nd Cycle					
	Mean Square					
	F	FF	PH	EH	PRO	GY ¹
Progenies (P)	153	4.9**	206.5**	186.4*	0.0113	635.5**
Locations (L)	1	12843**	214988**	121467**	2.4267*	221445**
P x L	153	2.3	114.5	135.9**	0.0088	363.2
Mean error	318	1.8	94.2	91.5	0.0074	303.4
Means	-	65.8	212.5	113.3	0.9664	136.0
C.V.(%)	-	2.0	4.5	8.4	8.92	12.8

¹g plant⁻¹; **, *: Significant by F test t 1 at 1 and 5% pobability level.

Table 2. Obtained estimatives referred to additive variance of progenies, variance of progenies x locations interaction, mean heritability coefficient, genetic variation coefficient, and genetic gains within progenies in % and g plant⁻¹.

Genetic Parameters	1 st Cycle				
	FF Days	PH -----cm-----	EH	PRO un	YG g pl ⁻¹
$\hat{\sigma}_A^2$	11.600	162.500	85.060	0.0088	290.610
$\hat{\sigma}_{pl}^2$	0.5861	9.26	11.938	0.0002	-15.968
CV _g	2.29	3.02	4.40	4.31	7.20
b	0.93	0.62	0.49	0.50	0.49
$h^{2\%}$	72.06	56.95	43.70	49.60	51.26
Selection Gains (SG)	0.23	1.70	-0.87	0.02	7.49
Selection Gains % (SG%)	0.31	0.83	-0.83	2.04	6.33
Genetic Parameters	2 nd Cycle				
	FF Days	PH -----cm-----	EH	PRO un	PG ¹ g pl ⁻¹
$\hat{\sigma}_A^2$	2.720	92.000	50.542	0.0248	272.380
$\hat{\sigma}_{pl}^2$	0.2050	11.775	21.517	0.0006	29.222
CV _g	1.25	2.25	3.13	2.58	6.12
B	0.60	0.50	0.36	0.28	0.47
$h^{2\%}$	54.84	44.55	27.10	21.83	42.85
Selection Gains (SG)	0	1.13	0.71	0.008	6.82
Selection Gains % (SG%)	0	0.53	0.61	0.833	5.06

Analyzing Table 2 we can observe that the estimatives for additive genetic variances obtained on cycle 1 for PH and EH traits were of 162.5 and 85.05 (cm plant⁻¹)², respectively, and on cycle 2 were of 91.20 and 50.52 (cm plant⁻¹)², being considered high when compared to values obtained by Silva et al. (2001) in the ESAM-1 maize composite. According to Paterniani (1967), it is of interest that the additive genetic variance is maintained as high as possible to allow the achievement of substantial gains by selection. The same occurs with values obtained for the estimatives for FF and PRO, which were low on both cycles. However, these are expected values, since the IPR 114 variety was synthesized from hybrids that present low height, early cycle and small prolificacy.

In breeding of population of open pollination, the additive genetic variance contribute significantly in answer of selection of population. Many works (CARVALHO et al., 2002; HALLAUER; MIRANDA FILHO, 1988; PATERNIANI, 1967; WEBEL; LONQUIST, 1967) reports, in that populations there are existence of additive genetic variance, that is the principal component of genetic variance of grain yield.

For GY, additive genetic variance was of 290,61 (g plant⁻¹)² and can be considered high when compared to the value obtained by Carvalho and Souza (2007), which was of 147,7 (g plant⁻¹)² from BR 5011 Sertanejo variety.

The negative variance value of the progenies x locations interaction obtained on cycle 1 for GY was due to its reduced mean square value, which was lower than the mean square of the error. This still lead to an increase in progenies variance, considering

that the estimative was obtained through the expected mean squares of progenies and errors, causing the enhancement of average heritability coefficient for GY, on selection cycle 1. However, for the other traits the value of $\hat{\sigma}_{pl}^2$ was positive, but it is noticed a decrease from cycle 1 to cycle 2.

Due to the fact that the progenies evaluations were performed in two locations, the magnitudes of the obtained estimatives presented less influenced by the progenies x location interaction. Hallauer and Miranda Filho (1988) mention that the estimatives of genetic and phenotypic parameters obtained in only one location can be overestimated, as being influenced by the progenies x location interaction.

The b index was close to 1.0 only for FF on both selection cycles, presenting values of 0.93 and 0.60 on cycles 1 and 2, respectively. According to Vencovsky and Barriga (1992), when b coefficient reaches a value equal or superior than 1.0 in experiments with half-sib progenies, there is a very favorable situation for selection.

Nevertheless, in this work, the genetic variation coefficients presented for both selection cycles reflect the wide variation existing among half-sib progenies, the same as the values for selection gains indicate the viability for the recurrent selection program with IPR 114 population, especially for yield enhancement.

In general, from cycle 1 to cycle 2 it was observed that heritability coefficient at average level decreased. The same happened for selection gains for GY in percentage and in g plant⁻¹. This decrease can be explained by the reduction in genetic variability that occurs through selection from cycle 1 to cycle 2.

The heritability coefficients at average level estimated in IPR 114 population for GY on both selection cycles presented superior values than the ones obtained by Silva et al. (2001), which showed 31.55%, and Cardoso et al. (2003) for the CMS 47 and BR 5039 population, that was of 18.57 and 2.56%, respectively.

The selection gain estimated in percentage to GY was 6.33% in cycle 1 and 5.03% in cycle 2. This estimated gains can be considered intermediate, however, they are superior to the values obtained by Cardoso et al. (2003), that were of 4.88 and 0.78% for CMS 47 and BR 5039, respectively, and inferior to the value observed by Carvalho and Souza (2007), which was of 27% for BR 5011 Sertanejo population. Still, the values here estimated are in agreement with the mean reported by Hallauer and Miranda Filho (1988) in a survey done with several works that utilized this selection method, in which the gain varied from 2 to 13%.

For EH, on cycle 1 it was obtained a negative selection gain, meaning that the height of ear insertion decreased with the selection process, which is a characteristic of great agronomic interest.

Conclusion

The magnitude of genetic parameters estimatives obtained indicates the possibility of continuous gains for grain yield in the IPR 114 population, without greater alterations in the other characteristics, thus justifying the continuity of the selection process.

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