

GENETIC PARAMETERS AND PREDICTIVE GENETIC GAIN IN MAIZE WITH MODIFIED RECURRENT SELECTION METHOD

Anderson Afonso Doná¹, Glauco Vieira Miranda^{2*}, Rodrigo Oliveira DeLima²,
Luciana Gonçalves Chaves², and Elto Eugênio Gomes e Gama³

The modified recurrent selection method suggests a less productive population to test the other population more productive and itself aiming to have more genetic gains than tradition recurrent selection method that uses one population to test the other one. The objectives of this work were to estimate the genetic components, to predict and to evaluate the genetic gains of the SynFlint and Syndent populations of maize (*Zea mays* L.), applying a modified recurrent selection method. Two recombination cycles were carried out, with 144 S₁ progeny per cycle. These progenies were test crossed with SynFlint, generating a SynFlint × Syndent inter-population and a SynFlint × SynFlint intra-population. The progenies were evaluated in five environments in the first cycle of selection and in three in the second cycle of selection, in a 12 × 12 lattice. Genetic variability in plant height and ear height, ear weight and prolificacy was observed in the first cycle of selection and in plant height and ear height in the second cycle. The intensity of selection practiced in the first cycle exhausted the genetic variability in ear weight and prolificacy. It can conclude that the two maize populations evaluated do not show adequate levels of genetic variability and predicted genetics gains estimates to allow their use in breeding programs to obtain lines and superior hybrids; and the modified recurrent selection method is inefficient to increase in population performance *per se* for the two populations.

Key words: *Zea mays*, breeding methods, genetic variability.

Maize (*Zea mays* L.) productivity is function of genotype, environment and the genotype × environment interaction (Gonçalves *et al.*, 1999; Deitos *et al.*, 2006; Namorato *et al.*, 2009). The behavior of each genotype varies between regions, which can be capitalized upon to maximize productivity (Fritsche-Neto *et al.*, 2010a; Faluba *et al.*, 2010). Local food security can be increased via the identification of genotypes with improved performance in specific environments such as organic production systems (Oliveira *et al.*, 2011) and soils with low N availability (Souza *et al.*, 2010; Li *et al.*, 2011), low P availability (Fritsche-Neto *et al.*, 2010b; George *et al.*, 2011), and high salinity (Ferreira *et al.*, 2007).

Recurrent selection is a cyclic breeding method that is used to increase the population average and involves obtaining progeny, the evaluation of progeny and the recombination of selected progeny (Comstock *et al.*,

1949). In each cycle of recurrent selection a higher concentration of favorable alleles occurs in the population, with a consequent increase in the average population. This method of selection is very important in maize breeding in order to obtain cultivars and to improve the Brazilian maize populations (Pinto *et al.*, 2003; Santos *et al.*, 2005; Santos *et al.*, 2007; Carvalho and Souza, 2007; Reis *et al.*, 2009; Kist *et al.*, 2010; Souza Jr. *et al.*, 2010; Rovaris *et al.*, 2011).

Recurrent selection differs from other breeding methods because it increases the population average and maintains the genetic variability at levels that are sufficient to obtain genetic gain in subsequent cycles of selection and to simultaneously extract inbred lines for hybrids (Hallauer, 1985). Therefore, this method of selection is designed for use in the medium to long term. The plant population must have genetic variability in the most important traits, with magnitudes that are consistent with the targets required in the program (Souza Jr., 2001; Viana, 2007).

The choice of a specific breeding method will depend on the type of cultivar, whether it is an open-pollinated variety or hybrid, genetic control of the trait, stage of the breeding program, stage of germplasm development, stage of knowledge of the populations, and objectives of the breeding program (Hallauer *et al.*, 2010). If the aim is to obtain open-pollinated varieties or adaptation of exotic

¹Agrícola Wehrmann Ltda., Brasília, Brazil.

²Universidade Federal de Viçosa, Departamento de Fitotecnia, Av. Ph Rolfs, sn, CEP 36570-000, Viçosa, Minas Gerais, Brasil.

*Corresponding author (glaucomiranda@ufv.br).

³Empresa Brasileira de Pesquisa Agropecuária EMBRAPA, Centro Nacional de Pesquisa de Milho Sorgo, Rodovia Estadual MG 424 km 45, CEP 35701-970, Sete Lagoas, Minas Gerais, Brasil.

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germplasm, intra-population methods are recommended. However, when the purpose is to improve the potential of the population for the extraction of inbred lines, inter-population methods are the most appropriate. Several breeding methods have been proposed by maize breeders, especially after quantitative genetic studies showed that the highest proportion of genetic variation in maize populations is due to additive genetic effects (Paterniani and Miranda Filho, 1980; Hallauer, 1985).

Reciprocal recurrent selection does not normally result in genetic gains with the same magnitude in two populations (Souza Jr., 1993). Therefore, this author proposed a new modified recurrent selection method using a population with a low yield (B) to evaluate another population with superior performance (A) and itself (B), leading to an average increase in the two populations *per se* and also in heterosis because population A increases the combining ability with population B. Therefore, the increase in heterosis occurs to a lesser extent than in traditional reciprocal recurrent selection, but the two populations will be improved with adequate genetic gains (Arias and Souza Jr., 1998). As the increase in the average inter-population hybrid is a function of improved populations *per se* and heterosis, the modified recurrent selection method is thought to be as efficient as selection in the traditional reciprocal recurrent method.

The objectives of this work were to estimate the genetic parameters, predict and evaluate the genetic gains of the SynFlint and Syndent populations, applying a modified recurrent selection.

MATERIAL AND METHODS

The SynDent and SynFlint synthetic maize populations belonging to Embrapa Maize and Sorghum were used. These populations were formed by recombination of the best inbred lines of flint and dent heterotic groups. The SynFlint CMS 50 was obtained from 15 intercrossed flint inbred lines. The SynDent CMS 28 was obtained by intercrossing with 13 dent inbred lines. Three cycles of phenotypic recurrent selection were used to obtain the synthetic populations.

The modified recurrent selection method was used as proposed by Souza Jr. (1993). He proposed an intra-population method for the low productive population and an inter-population method of the other. The population less productive is the tester for itself and for the other population. This method is different of the original method, because in the original recurrent selection method, genotypes from two populations are evaluated in reciprocal crosses, where each population that is used as the other's tester. The improved populations are generated by intermating superior genotypes of each population that present the best combining abilities with the reciprocal population (Comstock *et al.*, 1949).

In our study, the SynFlint CMS 50 and SynDent

CMS 28 populations are genetically divergent to grain yield, and the SynFlint CMS 50 is lower productive than SynDent CMS 28 population. So, the SynFlint population was used as a male-population to test the SynDent population and SynFlint population. Three hundred plants of each synthetic population were self-pollinated and selected to give 144 S₁ progeny. Part of the seed of each ear was used to produce plants that were crossed and the rest of the seeds at the base of the ears were saved for the recombination of selected progeny. Seeds to sow a 4-m row were sampled from each S₁ progeny, which represented each of the S₀ plants from SynDent CMS 28 population. These half-sib progenies were then grown as females and crossed with pollen from SynFlint CMS 50 in one isolated detasseling blocking. Moreover, seeds to sow a 4-m row were sampled from each S₁ progeny, which represented each the S₀ plants from SynFlint CMS 50 population. These half-sib progenies were then grown as females and crossed with pollen self in one isolated detasseling blocking. The crossing block was composed of rows of 4-m long of each of the 144 selected progeny in isolated field with two rows of female plant for one row of male plant to obtain intra half-sibs and inter half-sibs. Thus, it was produced 144 inter-population half-sib progenies (SynDent × SynFlint) and 144 intra-population half-sib progenies (SynFlint × SynFlint).

The half-sib progenies of first cycle of selection were evaluated in the agriculture season of 2002/2003 at five locations: Goiânia (Goiás, GO), Sete Lagoas (Mato Grosso, MG), Piracicaba (Anhembi Caterpillar and Fazenda Anhembi, São Paulo, SP), and Janaúba (Minas Gerais, MG). Inter and intra population half-sib progenies were evaluated in a 12 × 12 balanced lattice with two replicates per location. Plots were one row 4.0 m long spaced 0.8 m between plots. Plots were overplanted and thinned to 20 plants plot⁻¹ (62 500 plants ha⁻¹). At planting the plots were fertilized at a rate of 300 kg ha⁻¹ of 08-28-16 (N-P-K) and a further application of 100 kg ha⁻¹ of N was made at the fourth and eighth leaf stages. Data were recorded for ear height (EH, cm) and plant height (PH, cm) only in Goiânia and Piracicaba and for ear weight (EW, kg ha⁻¹) and prolificacy (PRL, ears plant⁻¹) in Goiânia, Sete Lagoas, Piracicaba and Janaúba.

According with the average productivity of intra and inter half-sib progenies for all locations was selected the top 15% of each type of progeny. Thus, the respective progenies S₁ of each population were used to form the two news populations (Cycle 1). Recombination was carried out using a ratio of two female rows to one male row, each 5 m in length. The male row was grown from a mixture of seeds of the selected S₁ progeny. In the agriculture season of 2003/2004, the second cycle of modified recurrent selection was carried out, resulting in 144 inter-population half-sib progenies (SynDent × SynFlint) and 144 intra-population half-sib progenies (SynFlint × SynFlint) as in the first cycle of selection. The half-sib progenies of

second cycle of selection were evaluated in the agriculture season of 2004/2005 at three locations: Goiânia (GO), Ipiacu (MG) and Piracicaba (Fazenda Anhembi, SP). As in the first cycle of selection the progenies of the second cycle of selection were evaluated in a 12 × 12 balanced lattice with two replicates per location. Data were recorded for prolificacy (PR, ears plant⁻¹) only in Goiânia and Ipiacu and for weight (EW, kg ha⁻¹) ear height (EH, cm) and plant height (PH, cm) in Goiânia, Ipiacu, and Piracicaba.

Analysis of variance (ANOVA) was computed for each location, and the adjusted means and effective mean squared error from each location were used to compute the joint ANOVA. Initially, mean squared errors were submitted to Bartlett's test ($p \leq 0.05$) for homogeneity (Sokal and Rohlf, 2003) and no significance were found for all traits evaluated. All analyses were performed with averages from each plot. PROC GLM from SAS software (SAS Institute, 2003) was used for all analyses.

The pooled ANOVAs were used to estimate the components of genetic variances and covariances (σ_p^2 and $C\hat{ov}_p$) using the method of moments (Searle *et al.*, 1992), i.e., the mean squares were equated to their respective expectations and the estimates of variance and covariance for each cycle of selection were computed. These were used to estimate the intra-population additive genetic variance of the SynFlint population ($\sigma_{A_{11}}^2$), the inter-population additive genetic variance ($\sigma_{A_{12}}^2$), the additive genetic covariance between types of progenies [$C\hat{ov}_{(A_1A_{12})}$], the genetic variance of the deviations from inter-population and intra-population additive effects of the SynDent and SynFlint populations ($\sigma_{\tau_{12}}^2$), and the genetic covariance of the intra-population additive effects with the deviations from the inter-population and intra-population additive effects of the SynDent and SynFlint populations [$C\hat{ov}_{(A_1\tau_{12})}$]. These new variance and covariance components were estimated using a procedure similar to that presented by Arias and Souza Jr. (1998) as follows:

Estimate of intra and inter-population additive genetic variance:

$$\hat{\sigma}_{A_{11}}^2 = [4/(1+F)]\hat{\sigma}_{P_{11}}^2 = 4\hat{\sigma}_{P_{11}}^2, \text{ and } \hat{\sigma}_{A_{12}}^2 = [4/(1+F)]\hat{\sigma}_{P_{12}}^2 = 4\hat{\sigma}_{P_{12}}^2, \text{ because } F \text{ (inbreeding coefficient)} = 0.$$

Estimate of additive genetic covariance between types of progenies:

$$C\hat{ov}_{(A_1A_{12})} = 4C\hat{ov}_{(P_1P_{12})}$$

Estimate of genetic variances of the intra-population additive effects with the deviations from intra-population and inter-population additive effects:

$$\hat{\sigma}_{\tau_{12}}^2 = 4[\hat{\sigma}_{P_{12}}^2 - 2C\hat{ov}_{(P_1P_{12})} + \hat{\sigma}_{P_{11}}^2]$$

Estimate of covariance between additive effects and deviations from intra-population and inter-population additive effects:

$$C\hat{ov}_{(A_1\tau_{12})} = 2[C\hat{ov}_{(P_1P_{12})} - \hat{\sigma}_{P_{11}}^2]$$

Estimates of the heritability coefficients on a progeny-mean basis were computed as $\hat{h}^2 = \hat{\sigma}_p^2 / \hat{\sigma}_{Ph}^2$, where $\hat{\sigma}_{Ph}^2$ is estimate of phenotypic variance among progeny means; and estimates of the genetic gain were computed for SynFlint × SynDent progenies and SynFlint × SynFlint progenies. The unit of recombination was the S₁ progeny. The standardized difference selection used the 15% of progeny with the highest productivity. The genetics gains of intra-population half-sibs (GGIA) and inter-populations half-sibs (GGIE) were estimated as follows:

$$GGIA = \frac{i}{2\hat{\sigma}_{Ph_1}}(\hat{\sigma}_{A_{11}}^2) \text{ and } GGIE = \frac{i}{4\hat{\sigma}_{Ph_1}}[\hat{\sigma}_{A_{11}}^2 + \hat{\sigma}_{\tau_{12}}^2 + C\hat{ov}_{(A_1\tau_{12})}]$$

where, i and $\hat{\sigma}_{Ph_1}$, refer to the intensity of selection (a 15% selection intensity, $i = 1.554$, were used in all instances), and the standard deviation of the unit of selection (half-sib progeny).

RESULTS AND DISCUSSION

The locations had a significant effect in both cycles of selection for all traits, except the PH for intra-population progenies in the second cycle (Table 1). The intra and

Table 1. Means square of combined ANOVA for ear weight (EW), plant height (PH), ear height (EH), and prolificacy (PR) for the intra- and inter-populations half-sib progenies in the first and second cycle of selection.

| Source of variations | Intra-populations progenies | | | | Inter-populations progenies | | | |
|---------------------------------------|--|---------------------|-------------------|--------------------------------|--|-------------------|-------------------|--------------------------------|
| | EW ¹ kg ha ⁻¹ | PH cm | EH cm | PR ears plant ⁻¹ | EW ¹ kg ha ⁻¹ | PH cm | EH cm | PR ears plant ⁻¹ |
| First cycle of selection - 2002/2003 | | | | | | | | |
| B/L | 76.61 | 3898 | 2476 | 0.03 | 23.85 | 145 | 769 | 0.04 |
| Locations | 5 453.32* | 204 333* | 152 478* | 2.92* | 10 555.66* | 308 225* | 170 801* | 4.46* |
| Progenies | 55.51* | 268* | 201* | 0.03* | 60.42* | 304* | 214* | 0.04* |
| P × L | 18.72 ^{ms} | 118 ^{ms} | 93 ^{ms} | 0.02 ^{ms} | 23.54 ^{ms} | 134 ^{ms} | 102 ^{ms} | 0.02* |
| Error | 18.22 | 115 | 97 | 0.02 | 20.90 | 141 | 108 | 0.02 |
| Means | 8 178 | 198 | 110 | 1.02 | 9 490 | 204 | 113 | 1.03 |
| CV, % | 16.5 | 5.42 | 8.96 | 12.3 | 15.23 | 5.8 | 9.1 | 12.1 |
| Second cycle of selection - 2004/2005 | | | | | | | | |
| B/L | 9.57 | 712 | 31 | 0.07 | 49.01 | 964 | 326 | 0.11 |
| Locations | 3 799.38* | 3 710 ^{ms} | 16 733* | 10.93* | 32 441.42* | 16 700* | 39 692* | 14.99* |
| Progenies | 25.50 ^{ms} | 281* | 191* | 0.03 ^{ms} | 22.58 ^{ms} | 284* | 252* | 0.03 ^{ms} |
| P × L | 22.65* | 201 ^{ms} | 143 ^{ms} | 0.04 ^{ms} | 20.17* | 222 ^{ms} | 177 ^{ms} | 0.04* |
| Error | 14.86 | 211 | 148 | 0.03 | 16.57 | 202 | 154 | 0.03 |
| Means | 6 909 | 196 | 107 | 0.92 | 7 594 | 202 | 112 | 0.91 |
| CV, % | 17.64 | 7.42 | 11.31 | 19.45 | 16.94 | 7.01 | 11.07 | 17.69 |

¹Means squares multiplied by 10⁶.

^{ms}, non-significant ($p > 0.05$) and $p \leq 0.05$, respectively, by the F test.

inter progenies were significant for all traits in the first cycle of selection and for PH and EH in the second cycle of selection. These results showed that genetic variation among progenies was detected, which can be related to their heterosis, and thus the possibility of obtain of the hybrids highly yield of the lines derived from populations (Hallauer *et al.*, 2010). However, in the second cycle, the intra and inter half-sib progenies showed similar performance for EW and PR, probably due to efficient selection based on the overall results in the first cycle.

The intra-population half-sib progeny by location interaction was significant only for EW in the second cycle. The inter-population half-sib progeny by location interaction was significant only for PR in the first cycle and EW and PR in the second cycle. These results showing the difference in performance of the progenies for these traits in different locations and that the responses to selection differ significantly between locations (Cruz *et al.*, 2004).

The intra-population progenies had the highest EW in Janaúba, Goiânia, and Sete Lagoas, demonstrating good genetic potential and the optimization of the genotypes × locations interaction (Table 2). In the first cycle of selection, the superiority of inter-population progenies in relation to intra-population hybrids for EW was 10.7% in Goiânia, 13.3% in Piracicaba (Anhembi farm), 19.9% in Janaúba, 25.0% in Sete Lagoas, and 8% in Piracicaba (Caterpillar). Prolificacy (PR) was higher in inter-population progenies than intra-population progenies only in Goiânia (4.4%) and Janaúba (5.6%). The superior performance of inter-population progenies (10%) in relation to intra-population progenies in all locations showed the inter-population half-sib progenies vigor. These results are according with the objective of the reciprocal recurrent selection that it is directly related to the improvement of hybrids from inbred lines (Souza Jr., 2001).

In the second cycle, the superiority of inter-population progenies in relation to intra-population progenies for EW was not apparent in Goiânia, and was 35.6% higher in Piracicaba (Anhembi farm) and 8.85% higher

in Ipiacu (Table 2). The PR was higher in the intra-population progenies than in inter-population progenies. The PH and EH of inter-population and intra-population progenies were similar, higher or lower than intra-population progenies depending on the location. The average inter-population progenies are the average of all half-sib progenies derived from crosses of SynFlint with SynDent. As the plant population was uniform, the cause of low prolificacy was probably the absence of ears, due to environmental conditions that were unfavorable for the plant population, water availability, and fertilizers in Ipiacu and Anhembi Farm. This also indicated the inability to use these progenies at a high plant density.

The genetic variance estimates ($\hat{\sigma}_{P11}^2$ and $\hat{\sigma}_{P12}^2$) of both progenies were similar to the first cycle for PH and EH (Table 3). For EH in the second cycle, the genetic variance estimate for inter-population progenies ($\hat{\sigma}_{P12}^2$) was 50% higher than that for intra-population progenies ($\hat{\sigma}_{P11}^2$), however, the reverse was observed for PH. In both cycles, the genetic variance estimates were lower than the

Table 3. Estimates of genetic variance within intra-populations ($\hat{\sigma}_{P11}^2$) and inter-populations ($\hat{\sigma}_{P12}^2$), estimates of covariance [$C\hat{O}v_{(p1p12)}$] and estimates of locations × progenies interaction variance and covariance [$\hat{\sigma}_{P11}^2$, $\hat{\sigma}_{P12}^2$, $C\hat{O}v_{(p1p12)}$] in the first and second cycle of selection.

| Parameters | Traits | | | |
|--|---------------------|-------|-------|--------------------------|
| | EW | PH | EH | PR ¹ |
| | kg ha ⁻¹ | cm | | ears plant ⁻¹ |
| First cycle of selection - 2002/2003 | | | | |
| $\hat{\sigma}_{P11}^2$ | 367 838 | 25.05 | 18.12 | 1.00 |
| $\hat{\sigma}_{P12}^2$ | 368 874 | 28.39 | 18.67 | 2.00 |
| $C\hat{O}v_{(p1p12)}$ | 18 031 | -4.97 | -2.88 | -0.25 |
| $\hat{\sigma}_{P11}^2$ | 25 246 | 1.50 | -2.00 | 0 |
| $\hat{\sigma}_{P12}^2$ | 131 697 | -3.50 | -3.00 | 0 |
| $C\hat{O}v_{(p1p12)}$ | 36 597 | -2.47 | -4.86 | 0 |
| Second cycle of selection ² - 2004/2005 | | | | |
| $\hat{\sigma}_{P11}^2$ | - | 13.33 | 8.00 | - |
| $\hat{\sigma}_{P12}^2$ | - | 10.34 | 12.25 | - |
| $C\hat{O}v_{(p1p12)}$ | - | 5.15 | 7.66 | - |
| $\hat{\sigma}_{P11}^2$ | 389 316 | -5.00 | -2.00 | 5.00 |
| $\hat{\sigma}_{P12}^2$ | 179 985 | 10.00 | 11.50 | 5.00 |
| $C\hat{O}v_{(p1p12)}$ | -64 487 | 7.99 | 5.09 | -2.48 |

¹Estimates multiplied by 10³.

²Traits no significant by the F test (p > 0.05) for progenies effect.

EW: ear weight; PH: plant height; EH: ear height; and PR: prolificacy.

Table 2. Mean of ear weight (EW), plant height (PH), ear height (EH) and prolificacy (PR) for intra and inter-population progenies in the first and second cycle of selection evaluated.

| Locations ¹ | Intra-populations progenies | | | | Inter-populations progenies | | | |
|---------------------------------------|-----------------------------|-----|-----|--------------------------|-----------------------------|-----|-----|--------------------------|
| | EW | PH | EH | PR | EW | PH | EH | PR |
| | kg ha ⁻¹ | cm | | ears plant ⁻¹ | kg ha ⁻¹ | cm | | ears plant ⁻¹ |
| First cycle of selection - 2002/2003 | | | | | | | | |
| PC | 7 041 | - | - | 0.95 | 7 630 | - | - | 0.93 |
| SL | 8 400 | - | - | 1.07 | 10 557 | - | - | 1.05 |
| GO | 9 007 | 194 | 130 | 1.13 | 9 978 | 195 | 133 | 1.18 |
| PA | 6 555 | 173 | 85 | 0.88 | 7 430 | 176 | 86 | 0.88 |
| JA | 9 885 | 225 | 114 | 1.06 | 11 852 | 240 | 120 | 1.12 |
| Means | 8 177 | 197 | 110 | 1.06 | 9 489 | 203 | 113 | 1.03 |
| Second cycle of selection - 2004/2005 | | | | | | | | |
| GO | 10 740 | 193 | 100 | 1.06 | 10 201 | 193 | 100 | 1.01 |
| PF | 6 469 | 193 | 115 | - | 8 773 | 208 | 124 | - |
| IP | 3 516 | 200 | 106 | 0.78 | 3 828 | 205 | 111 | 0.76 |
| Means | 6 908 | 195 | 107 | 0.92 | 7 600 | 202 | 112 | 0.88 |

-: Traits no evaluated in these locations.

Piracicaba (Caterpillar-PC and Anhembi Farm-PA), Sete Lagoas (SL), Goiânia (GO), Janaúba (JA), and Ipiacu (IP).

limits reported by Pinto *et al.* (2000). For EH, Pinto *et al.* (2000) found a genetic variance of 49.19 (cm plant⁻¹)² with a lower limit of 25.07 (cm plant⁻¹)² in the BR 106 population and a genetic variance of 56.85 (cm plant⁻¹)² and a lower limit of 28.35 (cm plant⁻¹)² in the BR105 population. For PH they found a variance of 97.66 (cm plant⁻¹)² with a lower limit of 43.59 (cm plant⁻¹)² in the BR 106 population and a variance of 91.13 (cm plant⁻¹)² with a lower limit of 49.75 (cm plant⁻¹)² for the BR105 population. This could be because these authors worked with populations that have genetics base wider than used in this work. This work was used populations synthetic formed a few inbred lines selected for these traits.

In the second cycle, there was no genetic variability ($\hat{\sigma}_{P11}^2$ and $\hat{\sigma}_{P12}^2$) in EW, which may be because the selection in the previous cycle was based on this trait. Another factor that may have contributed to the lack of genetic variability is the number of progeny used for recombination to produce the progenies for the next cycle (Santos *et al.*, 1993).

In the first cycle, additive genetic variance estimates ($\hat{\sigma}_A^2$, $\hat{\sigma}_{A11}^2$ and $\hat{\sigma}_{A12}^2$) for PH and EH were similar for both progenies (Table 4). In the second cycle, the $\hat{\sigma}_A^2$ estimates for PH for intra-population progenies were higher than those for inter-population progenies and the reverse occurred for EH. There was reduction of about 50% in the $\hat{\sigma}_A^2$ for PH and EH from first cycle to second cycle of selection. These $\hat{\sigma}_A^2$ for EH and PH in second cycle were smaller than those found by Arias and Souza Jr. (1998): 127.45 and 185.74 (cm plant⁻¹)², respectively, for the BR 105 population and 74.04 and 109.31 (cm plant⁻¹)², respectively, for the BR 106 population.

The additive genetic variance estimates ($\hat{\sigma}_{A11}^2$ and $\hat{\sigma}_{A12}^2$) of EW in the first cycle were similar between the intra and inter population progenies (Table 4). Arias and Souza Jr. (1998) found an $\hat{\sigma}_{A11}^2$ of 376 (g plant⁻¹)² and an $\hat{\sigma}_{A12}^2$ of 281 (g plant⁻¹)² for the BR 106 dent population and an $\hat{\sigma}_{A11}^2$ of

442 (g plant⁻¹)² and $\hat{\sigma}_{A12}^2$ of 522 (g plant⁻¹)² for the BR 105 flint population. The $\hat{\sigma}_{A12}^2$ for prolificacy were also low, which hampers genetic gain in the breeding program. The occurrence of inbreeding during the formation of populations and the use of non-prolific plants to establish the plant population may have been a cause of the low prolificacy (Hallauer *et al.*, 2010).

The parameters $\hat{\sigma}_{\tau12}^2$ and $C\hat{\sigma}_{V(A1\tau12)}$ are related to the genetic divergence of the base populations and to the level of dominance of traits (Souza Jr., 1993). The $\hat{\sigma}_{\tau12}^2$ will always be positive, but when the favorable allele in population A is more common than the favorable allele in population B the $C\hat{\sigma}_{V(A1\tau12)}$ will be positive and vice-versa. The magnitudes of $\hat{\sigma}_{\tau12}^2$ were five and eight times larger in the first than the second cycle for PH and EH, respectively, and both the signs were positive (Table 4). The estimates obtained by Arias and Souza Jr. (1998) for EH were -1.48 ± 9.97 (cm plant⁻¹)² for BR106 and 110.37 ± 23.28 (cm plant⁻¹)² for BR 105; for PH they were 18.57 ± 20.92 (cm plant⁻¹)² for BR106 and 164.24 ± 35.38 (cm plant⁻¹)² for BR 105. These were lower in magnitude and in some cases had opposite signs to those observed in this work.

The values of $C\hat{\sigma}_{V(A1\tau12)}$ were negative for all traits (Table 4). Note that the PH and EH covariance for the first cycle had the same sign but different magnitudes. These negative values interfere directly in the genetic gain in the inter-population progenies, because they are directly involved in the response to indirect reciprocal recurrent selection in the populations *per se* and for intra-population recurrent selection (Souza Jr., 1993).

With the exception of EW in the second cycle, the estimates of inter-population phenotypic variance among progeny means ($\hat{\sigma}_{Ph12}^2$) was higher than the estimates of intra-population phenotypic variance among progeny means ($\hat{\sigma}_{Ph11}^2$) (Table 5). The differences between the cycles for $\hat{\sigma}_{Ph11}^2$ of EH and PH were small, with a reduction for EH and an increase for PH in the estimates between the first and second cycle of selection. The $\hat{\sigma}_{Ph12}^2$ increased for EH and decreased for PH between the first and second cycles. The phenotypic variance estimates of prolificacy for both types of progenies were higher in the second cycle than in the first cycle of selection. Differently from the genetic variance, the phenotypic variance did not change a lot between first and second cycle of selection, especially for PH and PR (Santos *et al.*, 2005)

In the first cycle of selection the estimates of the heritability coefficients differed significantly ($p < 0.05$) from zero for all traits (Table 5). Estimates of the heritability coefficients for all traits in intra-and inter-population progeny in the first cycle were similar those reported in the literature for this type of progenies in maize, with values around 50% (Santos *et al.*, 2005; Carvalho and Souza, 2007; Faluba *et al.*, 2010). Thus, if some breeding method is used to improve these populations, it will result resulted in genetic gain for

Table 4. Estimates of additive genetic variance within intra-populations ($\hat{\sigma}_{A11}^2$) and inter-populations ($\hat{\sigma}_{A12}^2$), covariance between them [$C\hat{\sigma}_{V(A1\tau12)}$], genetic variances of deviations from intra-population and inter-population additive effects ($\hat{\sigma}_{\tau12}^2$) and covariance between additive effects and deviations from intra-population and inter-population additive effects [$C\hat{\sigma}_{V(A1\tau12)}$] in the first and second cycle of selection.

| Parameters | EW | PH | EH | PR ¹ |
|--|---------------------|--------|--------|--------------------------|
| | kg ha ⁻¹ | cm | | ears plant ⁻¹ |
| First cycle of selection - 2003/2004 | | | | |
| $\hat{\sigma}_{A11}^2$ | 1 471 351 | 100.20 | 72.48 | 4.00 |
| $\hat{\sigma}_{A12}^2$ | 1 475 498 | 113.56 | 74.68 | 14.00 |
| $C\hat{\sigma}_{V(A1\tau12)}$ | 72 124 | -19.88 | -11.52 | -1.00 |
| $\hat{\sigma}_{\tau12}^2$ | 2 802 600 | 253.52 | 170.20 | 22.04 |
| $C\hat{\sigma}_{V(A1\tau12)}$ | -699 613 | -60.03 | -42.00 | -3.84 |
| Second cycle of selection ² - 2003/2004 | | | | |
| $\hat{\sigma}_{A11}^2$ | - | 53.35 | 32.01 | - |
| $\hat{\sigma}_{A12}^2$ | - | 41.36 | 49.00 | - |
| $C\hat{\sigma}_{V(A1\tau12)}$ | - | 20.60 | 30.64 | - |
| $\hat{\sigma}_{\tau12}^2$ | - | 53.48 | 19.72 | - |
| $C\hat{\sigma}_{V(A1\tau12)}$ | - | -16.36 | -0.68 | - |

¹Estimates multiplied by 10³.

²Traits no significant by the F test ($p > 0.05$) for progenies effect.

EW: ear weight; PH: plant height; EH: ear height; and PR: prolificacy.

Table 5. Estimates of progeny phenotype variance ($\hat{\sigma}_{Ph11}^2, \hat{\sigma}_{Ph12}^2$), heritability ($\hat{h}_{11}^2, \hat{h}_{12}^2$) and genetic gain of intra-population half-sibs (GGIA) and inter-population half-sibs (GGIE) obtained by the modified recurrent selection method for the traits in the first and second cycle of selection.

| Parameters | Traits ¹ | | | |
|-------------------------|--|---------------|---------------|--------------------------|
| | EW | PH | EH | PR |
| | kg ha ⁻¹ | cm | | ears plant ⁻¹ |
| | First cycle of selection - 2002/2003 | | | |
| $\hat{\sigma}_{Ph11}^2$ | 555 076 | 44.66 | 33.5 | 0.003 |
| $\hat{\sigma}_{Ph12}^2$ | 604 242 | 50.66 | 35.6 | 0.004 |
| | 66.27 | 56.04 | 54.09 | 55.67 |
| \hat{h}_{11}^2 | [56.70;66.39] | [41.86;67.11] | [38.91;65.44] | [14.42;49.12] |
| | 61.05 | 56.00 | 52.23 | 50.00 |
| \hat{h}_{12}^2 | [50.00;70.27] | [41.80;67.07] | [37.06;64.39] | [35.82;61.84] |
| GGIA | 1 534.48 | 11.65 | 9.73 | 0.060 |
| GGIA, % | 18.76 | 5.88 | 8.85 | 5.86 |
| GGIE | 737.44 | 6.20 | 4.86 | 0.025 |
| GGIE, % | 7.77 | 3.04 | 4.30 | 2.42 |
| | Second cycle of selection ² - 2004/2005 | | | |
| $\hat{\sigma}_{Ph11}^2$ | 425 064 | 46.80 | 31.83 | 0.008 |
| $\hat{\sigma}_{Ph12}^2$ | 376 332 | 47.34 | 42.00 | 0.008 |
| | - | 28.49 | 25.13 | - |
| \hat{h}_{11}^2 | - | [5.55;46.56] | [1.14;44.07] | - |
| | - | 21.84 | 29.16 | - |
| \hat{h}_{12}^2 | - | [-3.22;41.61] | [7.26;41.61] | - |
| GGIA | - | 6.06 | 4.41 | - |
| GGIA, % | - | 3.09 | 4.12 | - |
| GGIE | - | 2.33 | 2.94 | - |
| GGIE, % | - | 1.16 | 2.62 | - |

¹Confidence intervals at the 95% probability level between brackets.

²Traits non-significant by the F test ($p > 0.05$) for progenies effect.

EW: ear weight; PH: plant height; EH: ear height; and PR: prolificacy.

these traits in these environments conditions. However, estimates of the heritability coefficients for EH, PH were considerably lower in the second cycle and heritability coefficients for PH in inter-population progeny did not differ from zero ($p \leq 0.05$). This indicates that the selection of these traits was very intensive and the genetic variability should be increased in the populations for new cycles of selection.

In the first cycle of selection, for the intra-population half-sib progenies, the expected genetic gain from selection was 8.85% for EH, 5.88% for PH, 5.86% for PR, and 18.76% for EW (Table 5). For inter-population half-sib progenies, the expected gain due to selection was 4.30% for EH, 3.04% for PH, 2.42% for PR, and 7.77% for EW. However, in the second cycle of selection, genetic gain was only observed for PH and EH in intra-population progeny, with average values of 3.09% and 4.72%, and for EH in inter-population progenies with average value of 2.62%. For EH and PH in the second cycle, the expected genetic gain was very small for both progenies. An increase in mean PH and EH is not agronomically advantageous, since plants that have a high EH and PH may be more vulnerable to lodging, which is a problem in modern agriculture.

The truncated selection and intensity of selection led to a lack of genetic variability for EW and PR in intra- and inter-population half-sib progenies in the second cycle. Such intense selection has been used by different maize breeders to obtain genetic gain for traits associated with productivity (Bernardo, 1996; Rezende and Souza Jr.,

2000; Santos *et al.*, 2005; Reis *et al.*, 2009). Therefore, if genetic gains are required in subsequent cycles, it will be necessary to increase the genetic variability of progenitor populations.

CONCLUSION

For the conditions in which this work was carried out, we can conclude that: the two maize populations evaluated do not show adequate levels of genetic variability and predicted genetics gain estimates allow their use in breeding programs to obtain lines and superior hybrids.

The modified recurrent selection method is inefficient to increase in population performance *per se* for the two populations evaluated and the inter-population progenies.

The continuity of the maize breeding program depends on increasing the genetic variability in the populations of both parents, which can be achieved with the introduction of genotypes from population base.

Parámetros genéticos y ganancia genética predicha en maíz con el método de selección recurrente modificado.

El método de selección recurrente modificado sugiere el uso de una población menos productiva para probar otra población más productiva y a sí misma que difiere del método de selección recurrente tradicional en que usa una población para probar otra. Los objetivos de este trabajo fueron estimar los componentes genéticos, predecir y evaluar los avances de la ganancia genética y las poblaciones SynFlint y Sydent de maíz (*Zea mays* L.) con un método modificado de selección recurrente. Dos ciclos de recombinación fueron realizados con 144 S₁ progenies por ciclo obtenidas de cruzamiento con SynFlint, generando una población SynFlint × Sydent y otra SynFlint × SynFlint. Las progenies se evaluaron en cinco ambientes en el primer ciclo de selección y en tres en el segundo ciclo de selección, en un lattice 12 × 12. La variabilidad genética fue significativa para la altura de la planta y altura de mazorca, peso de mazorca y prolificidad en el primer ciclo de selección y en altura de la planta y altura de inserción de mazorca en el segundo ciclo. La intensidad de la selección practicada en el primer ciclo acabó con la variabilidad genética del peso de mazorca y de prolificidad. Se puede concluir que las dos poblaciones de maíz evaluadas no muestran niveles adecuados de variabilidad genética ni estimaciones de ganancias genéticas predichas para permitir su uso en programas de mejoramiento genético para obtener líneas e híbridos superiores; y que el método modificado de selección recurrente es ineficaz para aumentar el rendimiento en la población por sí y entre las poblaciones.

Palabras clave: *Zea mays*, métodos de mejoramiento genético, variabilidad genética.

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