Genetic parameters of soybean populations obtained from crosses between grain and food genotypes

Cleber Vinicius Giaretta Azevedo1, Bruno Henrique Pedroso Val1, Lilian Cristina Andrade de Araújo1, Ana Cristina Pinto Juhász2, Antonio Orlando Di Mauro1 and Sandra Helena Unêda-Trevisoli1

1Faculdade de Ciências Agrárias e Veterinárias de Jaboticabal, Departamento de Produção Vegetal, Universidade Estadual Paulista Júlio de Mesquita Filho, Via de Acesso Professor Paulo Donato Castelane, s/n, Vila Industrial, 14884-900, Jaboticabal, São Paulo, Brazil. 2Departamento de Genética e Melhoramento, Empresa de Pesquisa Agropecuária de Minas Gerais, Uberaba, Minas Gerais, Brazil. 1Author for correspondence. E-mail: cvg.azevedo@gmail.com

ABSTRACT. In addition to the agronomic traits of interest, soybean cultivars destined for human consumption must have specific attributes that meet the demands of the consumer market. To meet this demand, this study aimed to select progenies with agronomic and commercial traits of interest from soybean populations obtained from crosses between different food and grain genotypes and to estimate the genetic parameters of these populations. The F3.4 and F4.5 progenies that originated from the two crosses were evaluated in the 2015/16 and 2016/17 agricultural years, respectively, using the pedigree method. The experimental design utilized augmented blocks, while statistical analyses were performed by using the REML/BLUP methodology. The evaluated traits were plant height at maturity (APM), insertion height of first pod (AIV), lodging (AC), agronomic value (VA), number of pods per plant (NV), number of days to maturity (NDM), number of branches (NR), number of nodes (NN), 100-seed weight (PCS), and grain yield per plant (PG). The best progenies were selected, and the following genetic parameters were estimated: genetic variance, phenotypic variance, heritability, and selective accuracy. The estimates of the genetic parameters indicate the presence of high genetic variance in these populations. Heritability was high for most of the traits, indicating good potential for the selection of superior genotypes.

Keywords: Glycine max; pedigree method; REML/BLUP; variance components.

Introduction

Conventional breeding is the most widely used method for selecting genotypes with specific combinations of desirable agronomic and commercial traits (Jauregui, Chen, & Scaboo, 2011).

Usually, the selection methods used for autogamous plants such as soybean combine the traits of interest by crossing elite lineages and/or exotic germplasms from two to four parents. Subsequently, the progenies of these populations are selected during generations of inbreeding or after reaching homozygosis, depending on the selected method, so that superior genotypes are identified based on the evaluated traits of interest (Volpato et al., 2017).

The genealogical method is based on the selection of superior progenies from the initial generations (F2 to F3), which causes genotypes with low agronomic potential to be eliminated, and only the superior progenies are used in the next generation (Carvalho, Neto, & Geraldi, 2008). This method is based on the principle that the progeny performance in the initial generations is a good predictor of the performance of the derived lineages (Bernardo, 2003).

In addition to the traditional agronomic traits of the crop, the genotypes of soybean cultivars used for human consumption should present specific traits for the consumer market, such as ideal physical characteristics in terms of the seed coat, hilum color, size, and texture. Furthermore, attributes that improve the flavor of the grain, such as higher starch, sucrose, fructose, glutamic acid, alanine, and protein content, the absence of lipoygenase enzymes, and low content of the Kunitz trypsin inhibitor, which allows reducing heat treatment, are also desirable (Castoldi, Charlo, Vargas, Braz, & Carrão-Panizzi, 2011; Zoldan, Braga, Fonseca, & Carrão-Panizzi, 2014).

However, since most of these traits are quantitative in nature and strongly influenced by the environment, it is essential to determine how much of the phenotypic variability observed in the experiments is inheritable, i.e., of a genetic nature, to choose the best selection strategy for obtaining higher gains.

The objective of this work was to select superior progenies and to estimate the genetic parameters of two soybean populations from crosses between grain and food genotypes using the genealogical method.
Material and methods

Genetic Material

The F3:4 and F4:5 soybean progenies obtained from the crossings of four cultivars, BRSMG 810C x BRSMG 790A (population A) and BRSMG 810C x BRSMG 800A (population B), were evaluated. The parents were selected to obtain new soybean cultivars with agronomic and commercial traits of interest for human consumption and resistance to the soybean cyst nematode (SCN), which was obtained from the cultivar BRSMG 810C.

The cultivar BRSMG 810C is a genotype classified as a grain type, with determined growth, a medium-length growth cycle (114 - 140 days), lodging resistance, a yellow seed coat, a black hilum, high protein content, and resistance to cyst nematode species 1 and 3, frog eye leaf spot, stem canker, and bacterial pustules.

The cultivar BRSMG 790A has organoleptic, nutritional, and industrial characteristics favorable for human consumption and the food industry, with determined growth, a medium-length growth cycle (110 - 130 days), a yellow seed coat and hilum, high carbohydrate content, and a mild flavor. It is also resistant to frog eye leaf spot, stem canker, and root-knot nematodes (Meloidogyne incognita) but is susceptible to SCN.

The cultivar BRSMG 800A has determined growth, a medium-length grown cycle (120 - 140 days), and resistance to lodging. Its seed coat is brown, which after cooking has physical characteristics similar to those of ‘carioca’ beans, making it highly acceptable for human consumption as food.

Experimental site

The experiments were conducted during the 2015/16 and 2016/17 agricultural years in Jaboticabal, located in northern São Paulo State, Brazil, at 21°15'22" S and 48°18'58" W and an approximately 605 m altitude. The predominant soil of the area is classified as Eutrophic Red Latosol. The regional climate is classified as Cwa, according to Köppen, with a hot and humid summer, a dry winter, a 22.2°C average annual temperature, and 1,451 mm average annual rainfall (Vianna, Desideriosup, de Santiagosup, Juniorsup, & Ferraudosup, 2013).

Crop conditions

Soybean was sown directly by using a no-tillage system. The soil was fertilized by applying 350 kg ha−1 NPK (00-20-20). At the time of sowing, the seeds were inoculated with Bradyrhizobium japonicum.

Insects and diseases were managed throughout the crop cycle by applying insecticides and fungicides, respectively. Weed control was performed by hand weeding. Additionally, sprinkler irrigation was performed in the initial stages of development as necessary.

Evaluated traits

Six individual plants were selected from each plot to evaluate the following traits. The plant height at maturity (APM, cm) was measured from the soil surface to the apex of the main stem, and the insertion height of the first pod (AIV, cm) was measured from the soil surface to the insertion of the first pod. Lodging (AC) was rated using a visual score scale, varying from 1 (almost all plants erect) to 5 (all plants down). The agronomic value (VA) was also evaluated visually using a score scale ranging from 1 (poor plant) to 5 (excellent plant). Counts were performed to determine the number of pods per plant (NV); number of nodes (NN); number of branches (NR); number of branches derived from the main stem; number of days to maturity (NDM); and number of days between germination and maturity at stage R8. Additionally, yield variables such as the 100-seed weight (PCS) in grams, the grain yield (PG), the total grain weight of each plant in grams, and the seed coat and hilum color were determined as well.

Evaluation of genotypes

The experiment was performed according to the augmented block design of Federer. The three parents (BRSMG 810C, BRSMG 790A, and BRSMG 800A) and the commercial cultivar TMG 7262 were used as controls. The adopted experimental design was chosen because the low number of seeds available from each progeny plant made it impossible to use statistical designs that required replicates. Each plot consisted of 5 m-long rows with 0.5 m distances between rows, and the density was 12 to 15 plants per meter.

In 2015/16, 386 F3:4 progenies were selected, based primarily on the market attributes for food and agronomic traits. Then, 80 F3:4 families (40 for each crossing) with superior yield were selected, and from each family, 3 individual plants with the highest grain yield per plant (among the 6 plants evaluated in each plot) were selected, totaling 240 selected plants with 120 from each family.
Subsequently, in the 2016/17 agricultural year, 240 progeny \(F_{4.5}\) plants were sown and evaluated for the same traits described above.

**Statistical analysis**

The experiments were analyzed by mixed linear models (REML/BLUP procedure) using the statistical software Selegen (Resende, 2007).

Because the augmented design is unbalanced and nonorthogonal by design, we also performed an analysis of deviance (ANADEV) or the likelihood ratio test (LRT). According to Resende (2007), this analysis is preferred to replace the ANOVA F-test when using mixed model analysis with unbalanced data, so that the significance was tested by the chi-square test at 5 and 1%. In the Selegen software, the deviances can be obtained using the model with or without the effects to be tested by zeroing the corresponding determination coefficients.

The \(F_{3.4}\) and \(F_{4.5}\) progeny were analyzed according to the plot mean data using Selegen model 17:

\[
y = Xf + Zg + Wb + e
\]

where: \(y\) = data, \(f\) = fixed effect, \(g\) = individual genotypic effects (assumed to be random), \(b\) = block environmental effects (assumed to be random), and \(e\) = error or residual (random) vectors.

The uppercase letters indicate the incidence matrix for the analyzed effects.

**Results and discussion**

The results of the analysis of deviance indicated a significant effect of genotype (\(p < 0.01\)) on all traits evaluated in the \(F_{3.4}\) progeny (Table 1), except for the VA trait.

**Table 1.** Analysis of deviance (ANADEV) of the agronomic traits evaluated in soybean progeny in generation \(F_{3.4}\) grown in Jaboticabal, São Paulo State, Brazil, during the 2015/2016 agricultural year.

| Population A - BRSMG 790A x BRSMG 810C | PG | APM |
|----------------------------------------|----|-----|
| **Effect**                             | Deviance | LRT | **Effect** | Deviance | LRT |
| Genotype Model                         | 1659,0   | 25,4** | Genotype Model | 1371,7   | 2,6** |
| PCS                                    | 642,0    | 40,1** | Genotype Model | 967,5    | 35,0** |
| NV                                     | 2148,0   | 14,1** | Genotype Model | -200,1   | 3,6** |
| NN                                     | 656,7    | 10,4** | Genotype Model | -206,2   | 6,9** |
| NR                                     | 478,9    | 13,1** | Genotype Model | 641,8    | 311,5** |

| Population A - BRSMG 810C | PG | APM |
|---------------------------|----|-----|
| **Effect**                             | Deviance | LRT | **Effect** | Deviance | LRT |
| Genotype Model                         | 1577,5   | 15,7** | Genotype Model | 1386,5   | 4,3* |
| PCS                                    | 652,0    | 40,0** | Genotype Model | 630,6    | 42,2** |
| NV                                     | 2202,7   | 20,1** | Genotype Model | 494,2    | 101,9** |
| NN                                     | 651,3    | 22,6** | Genotype Model | -286,0   | 27,5** |
| NR                                     | 386,7    | 47,7** | Genotype Model | 513,4    | 401,4** |

NDM: number of days to maturity; APM: plant height at maturity (cm); AIV: insertion height of the first pod (cm); AC: lodging (score); VA: agronomic value (score); NR: number of branches (count); NN: number of nodes (count); NV: number of pods (count); PCS: 100-seed weight; PG: grain yield (grams per plant). *, **: significance at 5% and 1% according to the Chi-square test (5% = 3.84; 1% = 6.63). ns: non-significant at 5%.
The results for the F4:5 progeny (Table 2) show a significant effect of genotype on all traits in both populations, except for the AC characteristic in population A. These results indicate the presence of genetic variability in these traits, thus making it possible to select genotypes corresponding to the studied traits.

**Table 2.** Analysis of deviance (ANADEV) of the agronomic traits evaluated in soybean progeny in generation F4:5 grown in Jaboticabal, São Paulo State, Brazil, during the 2015/2016 agricultural year.

| Population A - BRSMG 790A x BRSMG 810C | Population B - BRSMG 800A x BRSMG 810C |
|----------------------------------------|----------------------------------------|
| **PG** | **APM** |
| **Effect** | **Deviance** | **LRT** | **Effect** | **Deviance** | **LRT** |
| Genotype | 1346.9 | 54.8** | Genotype | 1282.13 | 120.1** |
| Model | 1401.7 | | Model | 1402.19 | |
| PCS | 520.45 | 45.7** | AIV | 792.69 | 18.5** |
| Model | 364.1 | | Model | 811.21 | |
| NV | | | | | |
| Genotype | 1792.29 | 49.3** | Genotype | -53.39 | 115.5** |
| Model | 1841.58 | | Model | 80.1 | |
| Genotype | 532.14 | 15.3** | Genotype | -132.3 | 0.0** |
| Model | 547.47 | | Model | -132.3 | |
| NV | | | NDM | 745.3 | 281.5** |
| Genotype | 389.91 | 37.6** | Model | 1026.8 | |
| Model | 427.46 | | |
| **Effect** | **Deviance** | **LRT** | **Effect** | **Deviance** | **LRT** |
| Genotype | 1520 | 38.4** | Genotype | 1475.5 | 90.4** |
| Model | 1559 | | Model | 1565.9 | |
| PCS | 365.1 | 41.7** | AIV | 914.6 | 17.6** |
| Model | 406.8 | | Model | 932.1 | |
| NV | | | VA | -6.3 | 106.0** |
| Genotype | 2045.6 | 56.6** | Genotype | -163.7 | 4.0* |
| Model | 2100.2 | | Model | -159.7 | |
| NN | | | | | |
| Genotype | 655.9 | 19.2** | NDM | | |
| Model | 675.2 | | |
| NR | | | | | |
| Genotype | 442.7 | 21.0** | Genotype | 837.0 | 505.5** |
| Model | 465.7 | | Model | 1142.5 | |

NDM: number of days to maturity; APM: plant height at maturity (cm); AIV: insertion height of the first pod (cm); AC: lodging (score); VA: agronomic value (score); NR: number of branches (count); NN: number of nodes (count); NV: number of pods (count); PCS: 100-seed weight; PG: grain yield (grams per plant). *, **: significance at 5% and 1% by the Chi-square test (5% = 3.84; 1% = 6.63). ns: non-significant at 5%.

The coefficients of environmental variation (CVE) for the F3:4 progeny (Table 3) varied between 1.04% (NDM) and 35.00% (NV) in population A and between 0.85% (NDM) and 49.58% (NR) in population B. For the F4:5 progeny (Table 4), the CVE varied between 1.87% (NDM) and 31.13% (AC) for population A and between 1.83% (NDM) and 33.44% (AC) for population B.

Storck, Cargnelutti Filho, Lúcio, Missio, and Rubin, (2010) conducted several competition trials with soybean cultivars and reported that the average coefficient of variation was 13.3% for grain yield, and 3.5 and 33.9% were the minimum and maximum values, respectively.

Pinheiro et al. (2013) reported CVE values of 27.8% and 20.0% for grain yield for the F4:6 and F4:7 progenies, respectively. Furthermore, Bhat, Basavaraja, and Salimath (2012) reported a CVE value of 50.41% for grain yield for the F2:3 progeny, which was higher than the values obtained in this experiment. Regarding the other traits, the obtained coefficients of variation were similar to those reported by Andrade, da Silva, Ferrau, Unêda-Trevisoli, and Di Mauro (2016) and Bhat et al. (2012).

The average heritability of grain yield (Table 4) was 0.77 and 0.75 for populations A and B, respectively. However, PCS, NR, AC, and APM (Table 3) had low heritability values. It is noteworthy that the VA trait had very different heritability values among the F3:4 populations, ranging from 0.14 for the A population to 0.97 for the B population, respectively. This result can be explained by the differences in the genetic variance for this trait among these populations, which was very low for the A population and very high for the B population. Similarly, the coefficient of genotype variation was 4.57 and 64.99% for populations A and B, respectively.
Table 3. Estimated genetic parameters for the agronomic traits evaluated in soybean F4× progeny grown in Jaboticabal, São Paulo State, Brazil, in the 2015/2016 agricultural year.

| Parameter | PG g plant⁻¹ | PCS grams | NV count | NN score | NR score | VA score | AC score | APM score | AIV score | NDM days |
|-----------|---------------|-----------|----------|----------|----------|----------|----------|-----------|-----------|-----------|
| σ²g        | 315.89        | 1.72      | 1755.46  | 3.13     | 0.63     | 0.02     | 0.05     | 21.11     | 22.32     | 4.99      |
| σ²h        | 6.09          | 0.00      | 89.51    | 0.01     | 0.09     | 0.00     | 0.01     | 0.04      | 0.01      | 0.12      |
| σ²g        | 128.09        | 3.79      | 1415.00  | 3.06     | 2.05     | 0.14     | 0.10     | 92.84     | 4.88      | 1.51      |
| σ²h        | 450.07        | 5.52      | 3240.60  | 6.20     | 2.77     | 0.16     | 0.16     | 115.98    | 27.21     | 6.62      |
| h²         | 0.70          | 0.31      | 0.54     | 0.50     | 0.23     | 0.14     | 0.51     | 0.19      | 0.82      | 0.75      |
| Acclon     | 0.84          | 0.56      | 0.74     | 0.71     | 0.48     | 0.38     | 0.56     | 0.45      | 0.91      | 0.88      |
| CVg        | 46.95         | 8.04      | 38.75    | 12.12    | 16.83    | 4.57     | 17.95    | 5.82      | 35.56     | 1.89      |
| CVE        | 29.88         | 11.95     | 35.00    | 11.98    | 35.74    | 11.26    | 26.41    | 12.21     | 16.63     | 1.04      |
| CVg/CVe    | 1.57          | 0.67      | 1.11     | 1.01     | 0.55     | 0.41     | 0.68     | 0.48      | 2.14      | 1.82      |
| Mean       | 37.87         | 16.31     | 107.48   | 14.60    | 4.24     | 3.27     | 1.23     | 78.87     | 13.29     | 118.16    |

Table 4. Estimated genetic parameters for the agronomic traits evaluated in soybean F4× progeny grown in Jaboticabal, São Paulo State, Brazil, in the 2015/2016 agricultural year.

| Parameter | PG g plant⁻¹ | PCS grams | NV count | NN score | NR score | VA score | AC score | APM score | AIV score | NDM days |
|-----------|---------------|-----------|----------|----------|----------|----------|----------|-----------|-----------|-----------|
| σ²g        | 167.92        | 1.86      | 2916.17  | 3.09     | 0.76     | 5.14     | 0.03     | 31.43     | 1.79      | 2.59      |
| σ²h        | 0.23          | 0.00      | 5.31     | 0.11     | 0.00     | 0.00     | 0.01     | 0.05      | 0.25      | 0.10      |
| σ²g        | 130.05        | 3.90      | 1382.22  | 2.87     | 1.23     | 0.14     | 0.08     | 91.39     | 3.34      | 1.04      |
| σ²h        | 298.21        | 5.77      | 4503.71  | 6.09     | 2.00     | 5.29     | 0.11     | 122.88    | 5.38      | 3.74      |
| h²         | 0.56          | 0.32      | 0.68     | 0.51     | 0.38     | 0.97     | 0.26     | 0.26      | 0.33      | 0.69      |
| Acclon     | 0.75          | 0.57      | 0.82     | 0.72     | 0.62     | 0.99     | 0.53     | 0.51      | 0.59      | 0.84      |
| CVg        | 32.66         | 7.75      | 45.32    | 11.48    | 39.02    | 64.99    | 12.00    | 7.38      | 15.79     | 1.54      |
| CVE        | 28.74         | 11.21     | 29.82    | 11.07    | 49.58    | 10.91    | 19.17    | 12.58     | 18.79     | 0.85      |
| CVg/CVe    | 1.14          | 0.69      | 1.45     | 1.04     | 0.79     | 5.96     | 0.65     | 0.59      | 0.73      | 1.58      |
| Mean       | 39.67         | 17.60     | 124.63   | 15.32    | 2.23     | 3.49     | 1.45     | 75.24     | 9.72      | 119.92    |

σ²g: genetic variance; σ²h: environmental variance between blocks; σ²e: environmental variance; σ²f: phenotypic variance; h²: broad heritability of individual plots; Hf: adjusted heritability according to the mean of the progeny assuming complete survival; Ac: genotype selection accuracy assuming complete survival; CVg: coefficient of genetic variation; CVE: coefficient of environmental variation; CVg/CVe: ratio of the coefficients of genetic and environmental variation. NDM: number of days to maturity; APM: plant height at maturity (cm); AIV: insertion height of the first pod (cm); AC: lodging (score); VA: agronomic value (score); NR: number of branches (count); NV: number of nodes (count); NV: number of pods (count); PCS: 100-seed weight; PG: grain yield (grams per plant).
According to Brogin, Arias, and de Toledo (2003), the broad heritability values are considered low when they are lower than 0.30, intermediate when they are between 0.30 and 0.60, and high when they are higher than 0.60. These authors also mention that a heritability greater than 30% allows genetic gains through selection in early generations of inbreeding, as in the F3 or F4 progenies. It is also shown that the heritability estimate refers to a population trait that is specific to the environment in which the genotypes were evaluated (Borém et al., 2017).

The accuracy of progeny selection indicates the quality of the information and the methods used to predict the genetic values. In general, the observed accuracy values were high and ranged from 0.77 to 0.94, except for the accuracy value of 0.62 for the AC trait in population 2. Pimentel et al. (2014) indicated that this measurement is associated with the precision of selection and refers to the correlation between the predicted and true genetic values.

The coefficient of genetic variation (CVg) indicates the existing proportion of variation, and thus, high values are desired. For the F3:4 progeny (Table 5), the plot heritability and genotype mean values showed high variation within and between populations.

The average heritability of the genotypes for grain yield was 0.71 and 0.56 for the A and B populations, respectively, indicating good precision in selecting these genotypes, for the AIV trait in population A, and the VA trait in population B, indicating the possibility of successful selection among the progenies.

Regarding the F4:5 progeny (Table 5), high values of average heritability of the plot (> 0.60) were observed for the traits PG, NV, NR, and APM in both populations and AIV in the B population. These values indicate good precision for the selection, as confirmed by the values of the selective accuracy of these traits, which ranged from 0.78 to 0.89. The relative coefficient of variation values were all above 1, confirming the favorable selection of these traits.

**Table 5.** Average genetic effect (a), genetic value (u + a), and accumulated genetic gain (GA) predicted for families among the F3:4 soybean populations in terms of grain yield per plant in grams.

| Rank | Family | Population A | | Population B | |
|------|--------|-------------|---|-------------|---|
|      |        | a           | u + a | GA (%)   | a | u + a | GA (%)   |
| 1    | 120    | 8.09        | 45.96 | 21.37 | 52 | 9.27  | 48.94 | 24.48 |
| 2    | 228    | 6.88        | 44.75 | 19.77 | 59 | 8.23  | 47.90 | 23.10 |
| 3    | 135    | 6.67        | 44.54 | 19.05 | 179| 8.00  | 47.67 | 22.44 |
| 4    | 144    | 6.20        | 44.07 | 18.38 | 79 | 7.23  | 46.90 | 21.61 |
| 5    | 150    | 6.01        | 43.88 | 17.87 | 54 | 6.61  | 46.28 | 20.78 |
| 6    | 100    | 5.98        | 43.85 | 17.53 | 185| 6.29  | 45.96 | 20.08 |
| 7    | 175    | 5.55        | 45.22 | 17.04 | 85 | 6.05  | 45.72 | 19.49 |
| 8    | 57     | 5.18        | 43.05 | 16.62 | 121| 5.95  | 45.62 | 19.02 |
| 9    | 138    | 5.09        | 42.96 | 16.27 | 49 | 5.76  | 45.43 | 18.60 |
| 10   | 108    | 5.02        | 42.89 | 15.97 | 191| 5.53  | 45.20 | 18.20 |
| PS^1 | 1.21   | 39.08       | 10.09 | 1.97  | 41.64 | 11.06 |
| Mean | 37.87  | 59.67       |   |   |   |   |   |

^Selected progenies

Resende (2004) affirmed that when considering the effect of treatments as random during analysis, the multiple comparison tests should not be used to compare the averages, since these tests assume the fixed effects of the treatments, producing inferences that affect the phenotypic and non-genotypic means. The analysis of the mixed models was used to estimate the genetic values, which corrected and penalized the environmental effects; according to these values, the genotypes were sorted in descending order.

Among the F3:4 progeny (Table 5), the accumulated selection gain for all selected progenies (PS) was 10.09% in population A and 11.06% in population B. Moreover, for the F4:5 progeny (Table 6), the predicted selection gain was 8.76% and 11.31% for the A and B populations, respectively.
Likewise, Costa et al. (2004) reported gains between 9.81 and 15.50%, which were lower than the estimates of 16.20 and 18.60% obtained by the REML/BLUP method used by Pinheiro et al. (2013), who compared the least-square and REML/BLUP methods and concluded that the REML/BLUP method predicted the highest gains.

**Conclusion**

The obtained estimates indicate high genetic variance for the traits PG, NV, NR, and VA in the evaluated populations.

The average heritabilities of the progenies were high for most of the evaluated traits, indicating that most of the phenotypic variance was due to genotypic effects, constituting a good condition for the selection of superior progeny.

The observed accuracies allow for efficient gain from selection.

**Acknowledgements**

We thank the financial support grant #2015/00407-9, São Paulo Research Foundation (FAPESP).

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