Acta Scientiarum
http://periodicos.uem.br/ojs
ISSN on-line: 1807-8621
Doi: 10.4025/actasciagron.v43i1.46968

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

Cleber Vinicius Giaretta Azevedo[1*], Bruno Henrique Pedroso Val[1], Lilian Cristina Andrade de Araújo[1], Ana Cristina Pinto Juhász[2], Antonio Orlando Di Mauro[1] and Sandra Helena Unêda-Trevisoli[1]

[1]Faculdade 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. [2]Departamento de Genética e Melhoramento, Empresa de Pesquisa Agropecuária de Minas Gerais, Uberaba, Minas Gerais, Brazil. *Author 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 $F_{3:4}$ and $F_{4:5}$ 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.

Received on March 13, 2019.
Accepted on December 11, 2019.

Introduction

Conventional breeding is the most widely used method for selecting genotypes with specific combinations of desirable agronomic and commercial traits (Jaureguy, 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 (F_2 to F_5), 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 lipoxygenase 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 $F_{3:4}$ progenies were selected, based primarily on the market attributes for food and agronomic traits. Then, 80 $F_{3:4}$ 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	1659,0	25,4**	Genotype	1371,7	2,6**
Model	1684,4		Model	1374,3	
	PCS			AIV	
Genotype	642,0	40,1**	Genotype	967,5	35,0**
Model	682,1		Model	1002,5	
	NV			VA	
Genotype	2148,0	14,1**	Genotype	-200,1	3,6^{ns}
Model	2162,1		Model	-196,5	
	NN			AC	
Genotype	656,7	10,4**	Genotype	-206,2	6,9**
Model	667,1		Model	-199,3	
	NR			NDM	
Genotype	478,9	13,1**	Genotype	641,8	311,3**
Model	492,0		Model	953,1	
Population B - BRSMG 800A x BRSMG 810C					
	PG			APM	
Effect	Deviance	LRT	Effect	Deviance	LRT
Genotype	1577,5	15,7**	Genotype	1386,5	4,3*
Model	1593,2		Model	1390,8	
	PCS			AIV	
Genotype	652,0	40,0**	Genotype	630,6	42,2**
Model	692,0		Model	672,8	
	NV			VA	
Genotype	2202,7	20,1**	Genotype	494,2	101,9**
Model	2222,8		Model	596,1	
	NN			AC	
Genotype	651,3	22,6**	Genotype	-286,0	27,3**
Model	673,9		Model	-258,7	
	NR			NDM	
Genotype	386,7	47,7**	Genotype	513,4	401,4**
Model	434,4		Model	914,8	

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 F$_{4:5}$ 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	1346,9	54,8**	Genotype	1282,13	120,1**
Model	1401,7		Model	1402,19	
	PCS			AIV	
Genotype	320,43	43,7**	Genotype	792,69	18,5**
Model	364,1		Model	811,21	
	NV			VA	
Genotype	1792,29	49,3**	Genotype	-33,39	113,5**
Model	1841,58		Model	80,1	
	NN			AC	
Genotype	532,14	15,3**	Genotype	-132,3	0,0^{ns}
Model	547,47		Model	-132,3	
	NR			NDM	
Genotype	389,91	37,6**	Genotype	745,3	281,5**
Model	427,46		Model	1026,8	
Population B - BRSMG 800A x BRSMG 810C					
	PG			APM	
Effect	Deviance	LRT	Effect	Deviance	LRT
Genotype	1520	38,4**	Genotype	1475,5	90,4**
Model	1559		Model	1565,9	
	PCS			AIV	
Genotype	365,1	41,7**	Genotype	914,6	17,6**
Model	406,8		Model	932,1	
	NV			VA	
Genotype	2043,6	56,6**	Genotype	-6,3	106,0**
Model	2100,2		Model	99,7	
	NN			AC	
Genotype	655,9	19,2**	Genotype	-163,7	4,0*
Model	675,2		Model	-159,7	
	NR			NDM	
Genotype	442,7	21,0**	Genotype	837,0	305,3**
Model	463,7		Model	1142,3	

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, Ferraudo, 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 $F_{3:4}$ progeny grown in Jaboticabal, São Paulo State, Brazil, in the 2015/2016 agricultural year.

Population A - BRSMG 790A x BRSMG 810C										
Parameter	PG	PCS	NV	NN	NR	VA	AC	APM	AIV	NDM
	g plant^{-1}	grams	------- count -------			score		----- cm ------		days
σ^2_g	315.89	1.72	1735.46	3.13	0.63	0.02	0.05	21.11	22.32	4.99
σ^2_b	6.09	0.00	89.31	0.01	0.09	0.00	0.01	0.04	0.01	0.12
σ^2_e	128.09	3.79	1415.00	3.06	2.05	0.14	0.10	92.84	4.88	1.51
σ^2_f	450.07	5.52	3240.15	6.20	2.77	0.16	0.16	113.98	27.21	6.62
h^2	0.70	0.31	0.54	0.50	0.23	0.14	0.31	0.19	0.82	0.75
Acclon	0.84	0.56	0.74	0.71	0.48	0.38	0.56	0.43	0.91	0.88
CVg$_{\%}$	46.93	8.04	38.75	12.12	18.63	4.57	17.95	5.82	35.56	1.89
CVe$_{\%}$	29.88	11.93	35.00	11.98	33.74	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
Population B - BRSMG 790A x BRSMG 810C										
Parameter	PG	PCS	NV	NN	NR	VA	AC	APM	AIV	NDM
	g plant^{-1}	grams	------- count-------			score		----- cm ------		days
σ^2_g	167.92	1.86	2916.17	3.09	0.76	5.14	0.03	31.43	1.79	2.59
σ^2_b	0.23	0.00	5.31	0.11	0.00	0.00	0.01	0.05	0.25	0.10
σ^2_e	130.05	3.90	1382.22	2.87	1.23	0.14	0.08	91.39	3.34	1.04
σ^2_f	298.21	5.77	4303.71	6.09	2.00	5.29	0.11	122.88	5.38	3.74
h^2	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	43.32	11.48	39.02	64.99	12.00	7.38	13.79	1.34
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	0.63	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

σ^2_g: genetic variance; σ^2_e: environmental variance between blocks; σ^2_e: environmental variance; σ^2_f: phenotypic variance; h^2: broad heritability of individual plots; H^2m: 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); NN: number of nodes (count); NV: number of pods (count); PCS: 100-seed weight; PG: grain yield (grams per plant).

Table 4. Estimated genetic parameters for the agronomic traits evaluated in soybean $F_{4:5}$ progeny grown in Jaboticabal, São Paulo State, Brazil, in the 2015/2016 agricultural year.

Population A - BRSMG 790A x BRSMG 810C										
Parameter	PG	PCS	NV	NN	NR	VA	AC	APM	AIV	NDM
	g plant^{-1}	grams	------- count -------			score		----- cm ------		days
σ^2_g	150.58	0.40	1138.36	1.76	1.92	0.20	0.01	79.70	8.74	6.16
σ^2_b	0.10	0.05	2.09	0.01	0.01	0.00	0.00	1.02	0.01	0.05
σ^2_e	49.09	1.14	340.44	2.51	0.95	0.16	0.19	52.30	6.11	5.43
σ^2_f	199.76	1.58	1480.89	4.27	2.88	0.36	0.20	133.02	14.86	11.65
h^2g	0.75	0.25	0.77	0.41	0.67	0.55	0.02	0.60	0.59	0.53
Acclon	0.87	0.51	0.88	0.64	0.82	0.74	0,15	0.78	0.77	0.73
CVg$_{\%}$	31.66	4.15	33.84	8.42	39.09	14.78	4.64	9.27	23.99	1.99
CVe$_{\%}$	18.09	7.02	18.51	10.04	27.53	13.35	31.13	7.51	20.06	1.87
CVg/CVe	1.75	0.59	1.83	0.84	1.42	1.11	0.15	1.23	1.20	1.06
Mean	38.76	15.19	99.70	15.76	3.55	3.03	1.41	96.28	12.32	124.99
Population B - BRSMG 790A x BRSMG 810C										
Parameter	PG	PCS	NV	NN	NR	VA	AC	APM	AIV	NDM
	g plant^{-1}	grams	------- count -------			score		----- cm ------		days
σ^2_g	133.87	0.37	1175.83	2.96	1.91	0.24	0.42	85.91	9.53	5.81
σ^2_b	2.18	0.00	27.68	0.00	0.01	0.00	0.00	0.41	0.01	0.02
σ^2_e	48.08	1.20	311.32	2.51	0.98	0.17	0.15	55.91	6.12	5.26
σ^2_f	184.13	1.57	1514.83	5.47	2.91	0.41	0.20	142.23	15.66	11.08
h^2g	0.73	0.23	0.78	0.54	0.66	0.58	0.22	0.60	0.61	0.52
Acclon	0.86	0.48	0.89	0.74	0.81	0.76	0.47	0.78	0.78	0.72
CVg$_{\%}$	32.98	3.79	33.50	11.59	46.70	15.94	13.56	9.22	23.99	1.93
CVe$_{\%}$	19.77	6.85	17.23	10.68	33.44	13.59	25.56	7.44	19.22	1.83
CVg/CVe	1.67	0.55	1.94	1.09	1.40	1.17	0.53	1.24	1.25	1.05
Mean	35.08	16.01	102.36	14.84	2.96	3.05	1.52	100.45	12.86	123.97

σ^2_g: genetic variance; σ^2_e: environmental variance between blocks; σ^2_e: environmental variance; σ^2_f: phenotypic variance; h^2: broad heritability of individual plots; H^2m: adjusted heritability according to the progeny mean 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); NN: 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 3), 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, and the selective accuracy of the genotypes was 0.84 and 0.75 in populations A and B, respectively. Likewise, Bhat et al. (2012) evaluated two populations within the F3:4 progeny and reported broad heritability values of 67.95 and 84.04% for grain yield per plant, values of 79.54 and 91.25% for PCS, and 94.18 and 92.97% for the number of pods per plant.

The CVg/CVe ratio or relative coefficient of variation is favorable to selection when it is higher than 1.0. For the F3:4 progeny, the value was above 1.0 only for the APM trait in both populations and the VA trait in the A population.

For the F3:4 progeny, the relative coefficients of variation were higher than 1 for the PG, NV, NN, and NDM traits in both populations, 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 $F_{3:4}$ soybean populations in terms of grain yield per plant in grams.

Rank	Population A				Population B			
	Family	a	u + a	GA (%)	Family	a	u + a	GA (%)
1	120	8.09	45.96	21.37	32	9.27	48.94	24.48
2	228	6.88	44.75	19.77	39	8.23	47.90	23.10
3	13	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	130	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	5.35	43.22	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				39.67	

[1]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.

Table 6. Average genetic effect (a), genetic value (u + a), and accumulated genetic gain (GA) predicted for families in the $F_{4:5}$ soybean populations in terms of grain yield per plant in grams.

Rank	Population A				Population B			
	Progeny	a	u + a	GA (%)	Progeny	a	u + a	GA (%)
1	67	10.19	48.95	26.30	57	8.94	44.02	25.48
2	20	8.71	47.47	24.38	89	8.21	43.29	24.44
3	133	7.34	46.10	22.56	188	7.86	42.94	23.76
4	123	6.95	45.71	21.41	18	7.75	42.83	23.34
5	147	6.20	44.96	20.32	140	6.92	42.00	22.62
6	101	5.77	44.53	19.42	39	6.67	41.75	22.02
7	11	5.25	44.01	18.58	75	6.05	41.13	21.33
8	50	4.26	43.02	17.63	23	5.65	40.73	20.68
9	77	4.10	42.86	16.84	86	5.32	40.40	20.07
10	6	3.78	42.54	16.14	50	4.79	39.87	19.43
PS[1]		0.65	39.41	8.76		1.07	36.15	11.31
Mean			38.76				35.08	

[1] Selected progeny.

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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