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Genetic analysis of F₆ and F_{6:7} soybean generations

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ABSTRACT - For estimating genetic parameters and selecting superior lines for grain yield, forty-five soybean (Glycine max L.) crosses in F_6 and $F_{6:7}$ generations were evaluated. The soybean lines FT-Cristalina, EMGOPA-301, IAC-4, IAC-5, IAC-6, IAC-8, IAC-9, IAC-11, Santa Rosa, and OCEPAR-9-SS-1 were used in the crosses. The F_6 progenies of 44 crosses (except EMGOPA-301 x IAC-5) and the ten parents were evaluated as well as the $F_{6:7}$ progenies from all 45 crosses and the ten parents in the next crop. The number of days to maturity (NDM), plant height at maturity (PHM), agronomic value (AV) and grain yield (GY) were evaluated for both generations. There was some difficulty to select early top yield lines due to the high positive genotypic correlation between GY and NDM. The heritability estimates were high (> 0.70) and moderate (0.40 – 0.70) for NDM and PHM, respectively. The presence of transgressive segregates indicated the possibility of selecting lines with high grain yield.

Key words: Glycine max, heritability, genotypic correlation, augmented block design, grain yield.

INTRODUCTION

Research into genetics and improvement of soybean has offered a somewhat significant contribution to agriculture. The developed methodologies for the selection of parents and crosses with a high genetic potential to produce superior populations now allow a more precise choice of lines in relation to quantitative traits.

Results of genetic improvement of cultivated plants have become more predictable due to the awareness and understanding of genetic parameters. The estimate of the correlation coefficient is essential for selection, mainly if one of the desirable traits presents low heritability or problems with evaluation and identification (Cruz and Regazzi 1994). The magnitude of heritability helps predict selection gains and define the best strategy for an improvement program (Fehr 1987). For the selection of inbred lines, low heritability traits must be selected in more advanced generations (F_6 , F_7 , F_8 ...), since there is an increase in heritability in the course of inbreeding generations, owing to the increase of additive genetic variance and decrease of the dominance variance (Ramalho and Vencovsky 1978). Besides, there is the possibility to use a higher number of replications to reduce the experimental error.

The goal set for this study was the evaluation of 45 diallel soybean crosses in advanced generations, aiming to estimate genetic parameters of agronomic traits, which support the selection of superior seed yield lines.

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MATERIAL AND METHODS

The following plant material with a maturity cycle semi-late was used as parent in diallel crosses: FT-Cristalina, EMGOPA-301, IAC-4, IAC-5, IAC-6, IAC-8, IAC-9, IAC-11, Santa Rosa, and OCEPAR-9-SS-1. This population was selected because of its tolerance to photoperiodic variations, high yield, and high genetic divergence estimated by the coefficients of parentage (Vello et al. 1988). The selection was realized after field tests at three sites (ESALQ, Sertãozinho, and Anhembi) in Piracicaba, SP, Brasil, 1983/1984 and 1984/1985 (Vello 1992). The diallel system for the achievement of the first recombination generation followed Method 4, Griffing (1956) model I.

Generations F_1 and F_2 were conducted by Nass (1989), generation F_3 by Moreira (1992) and generations F_4 and F_5 by the Setor de Genética Aplicada às Espécies Autógamas do Departamento de Genética - ESALQ/USP. The SHDT (Single Hill Descent Thinned; Vello 1992) method was employed to advance the populations until obtaining F_6 generation seeds.

In generation F₆, 72 plants derived from each of the 44 crosses (with exception of cross EMGOPA-301 x IAC-5, due to the delay in the achievement of F₂ seeds) and the ten parents were evaluated. The trial was established in randomized block design with six replications, sown November 6, 1991, Piracicaba, SP (lat 22° 45' S, long 47° 38' W, altitude 540m asl). Every plot consisted of 12 individual hills spaced 0.5 x 0.6 m.

In generation $F_{6:7}$, 24 lines of each one of the 45 crosses (1080 lines), originated by one individual F_6 plant and the ten parents were evaluated in an augmented block design (Federer 1956) with 24 blocks. Each block consisted of 55 plots (one line of each cross and the ten parents), and every plot held a 2.0 m row spaced 0.5 m. In this generation, cross EMGOPA-301 x IAC-5, which had been advanced separately up to F_6 , was included by the SHDT method, too. The trial was sown December 4, 1992, in Piracicaba.

In view of the soil analysis, the crop was fertilized with 25 g m⁻¹ in furrows (500 kg ha⁻¹) with the formula 4-20-20 of N-P₂O₅-K₂O, respectively. Seeds were inoculated with *Bradyrhizobium japonicum*, which was diluted in water (800 g 20 L⁻¹) and applied by a back sprayer minutes before sowing into the furrows. Initial additional irrigation helped guarantee the establishment of the crop. Weeds were controlled with two applications of postemergent herbicides and manual weeding. Insecticides were applied to control pests, mainly bugs. No diseases occurred which would have required control.

In both generations the following traits were evaluated: NDM - number of days to maturity, referring to the period between the sowing date and stage R8 of the Fehr and Caviness (1977) scale; PHM - plant height at maturity, measured in centimeters from the plant base to the plant tip of the main stem; AV - agronomic value, based on the evaluation realized at maturity, in a visual grading system from 1 to 5. Score 1 refers to a plant or row with no agronomic value, and score 5 to a plant or row with excellent agronomic traits (high number of full pods, height above 60 cm, vigorous, no bending, absence of green stems and leaf retention, without opening of pods or disease symptoms); and GY - grain

yield transformed in kg ha⁻¹, which corresponds to g plant⁻¹ or g 0.3 m⁻² in generation F_6 since the analyses were based on the mean of the 12 planting hills of individual plants of each plot; and corresponds to g m⁻² in $F_{6:7}$, as the analyses were based on the total plot yield.

Variance and covariance analyses in generation F_6 were based on plot means for each trait, with posterior inclusion of within variance and covariance, considering the fixed effect of treatments.

Data of generation $F_{6:7}$ were initially analyzed for intra-block variance, considering a fixed effect of parents and a random effect of lines. Since the intra-block error ($\hat{\sigma}_e^2$) from the referred analysis can only be used for comparisons among lines tested in the same block, a comparison among lines of a same cross, placed in different blocks must be carried out with the inter-block error ($\hat{\sigma}_e^2$), using the adjusted means of regular treatments. However, to avoid the use of two different errors, the mean effective error ($\hat{\sigma}_{ef}^2$) was estimated in analogy to the procedure of Cochran and Cox (1957) for the classic square lattice designs, whose mean square (MS) was given by the following expression, based on Vencovsky (1994)⁴:

MS of the effective error =
$$\left(\sum_{j=1}^{B} C_1 \hat{\boldsymbol{\sigma}}_e^2 + \sum_{j$$

where: B is the number of blocks; C_1 the number of line combinations in block j, considered in pairs; C_2 is the number of possible contrasts between the lines of any block j with the lines of another block j', considered in pairs; $\hat{\sigma}_e^2$ is the mean square of the intra-block error; $\hat{\sigma}_e^{2'} = [i + (i/c)]\hat{\sigma}_e^2$ and c is the number of common treatments according to Vizoni (1984).

Coefficients of genotypic correlation between the trait pairs were estimated by the variance and covariance estimates expressed by the equation (Vencovsky and Barriga 1992):

$$r_{G} = C\hat{O}V_{G}(X,Y) / \sqrt{\hat{V}_{G}(X)\hat{V}_{G}(Y)}$$

where $\hat{COV}_G(X,Y)$ is the genetic covariance between traits x and Y estimated according to the methodology of Kempthorne (1973); and $\hat{V}_G(X)$ and $\hat{V}_G(Y)$ are genetic variances of traits x and Y, respectively.

Broad-sense heritability was estimated in generation F_6 , according to Mahmud and Kramer (1951):

$$\begin{split} \mathbf{h}^{2} &= \left(\hat{\boldsymbol{\sigma}}_{F}^{2} - \hat{\boldsymbol{\sigma}}^{2}\right) / \hat{\boldsymbol{\sigma}}_{F}^{2} \end{split}$$
 where, $\hat{\boldsymbol{\sigma}}^{2} &= \sqrt{\hat{\boldsymbol{\sigma}}_{P1}^{2} \hat{\boldsymbol{\sigma}}_{P2}^{2}}$, so:
$$\mathbf{h}^{2} &= \left(\hat{\boldsymbol{\sigma}}_{F}^{2} - \sqrt{\hat{\boldsymbol{\sigma}}_{P1}^{2} \hat{\boldsymbol{\sigma}}_{P2}^{2}}\right) / \hat{\boldsymbol{\sigma}}_{F}^{2}$$

where $\hat{\sigma}_{F}^{2}$ is the phenotypic variance estimate among lines; $\hat{\sigma}^{2}$ the error variance, estimated on the base of the geometric mean of the environmental variances among hills of the two parents

⁴ Vencovsky R (1994) Personal comunication.

involved in the cross; $\hat{\sigma}_{P1}^2$ and $\hat{\sigma}_{P2}^2$ are environmental variances estimates among hills of parents 1 and 2. In generation $F_{6:7}$, the heritability was estimated according to the following equation:

$$h^2 = (\hat{\boldsymbol{\sigma}}_F^2 - \hat{\boldsymbol{\sigma}}_{ef}^2) / \hat{\boldsymbol{\sigma}}_F^2$$

where $\hat{\sigma}_F^2$ is the phenotypic variance estimated among lines of one cross; $\hat{\sigma}_{ef}^2$ is the estimate of the mean effective error, according to the augmented block design.

For the grain yield (GY) in generation $F_{6:7}$ the percentage of lines with a superior mean to the parent mean for each cross (observed positive selection gain) was calculated and the proportional selection gain (Gs %) of the best line in relation to the mean of the parents involved in the cross, by the following expression:

Gs % = [(best line yield – parent mean)/parent mean] x 100

RESULTS AND DISCUSSION

In the variance analyses of generation F_6 , significant effects of parents and crosses in all traits were observed (Table 1). The contrast parents *vs* crosses was significant for NDM and AV. Among the lines within the 45 crosses in generation $F_{6:7}$, there was a significant difference for NDM and PHM in 41 and 37 crosses, respectively (Table 2). In relation to the traits AV and GY, only 22 and 10 crosses, respectively, presented significant differences among their lines. This indicates a lower variability for AV and GY, and therefore, a greater difficulty to improve these traits. The estimated variation coefficients (VC) in both generations showed that NDM and AV presented the best experimental precision; PHM attained intermediate values; and GY presented the highest VC. The VC value in the planting hills trial was superior for GY. Garland and Fehr (1981) found similar results. Regarding the general means, the populations were earlier, higher, and had a higher agronomic value and yield in generation F_{6:7}. All parents and crosses proved to be earlier in generation $F_{6:7}$, due to the effect of the sowing periods (06/11/91 vs 04/12/92) in a photoperiodsensitive species like soybean. In the population sown in November as well as the one sown in December, flower induction occurred in the time of reduced photoperiod, in other words, after the 23rd of December (southern hemisphere), except for those genotypes that own genes for a long juvenile period. Garland and Fehr (1981) also observed an earlier cycle in inbred lines of row plots, compared to the planting hills. In generation F₆, parents and crosses had shorter plants than in F_{6:7}. The reduction in PHM was associated to a greater amount of branches, on account of the lower competition degree in the planting hill system, where the 50 cm spacing between the plant hills in a row was considerably greater than the spacing in rows, where plants grew approximately 5 cm apart. As expected, the grain yield in parents and lines per area unit was lower in planting hills (F₆), owing to the lower plant density in the plots; similar observations were made by Garland and Fehr (1981).

The estimates of the genotypic correlation coefficients (r_G) were similar between generations F_6 and $F_{6:7}$, based on parents and crosses (Table 3). On the other hand, the estimated correlations based on the $F_{6:7}$ lines were different, most likely due to the absence of replications in the evaluation of the lines.

Correlations between GY and NDM were positive, with a high magnitude (> 0.70) in the parent and crosses groups, in both studied crops. These results agree with those observed by Johnson et al. (1955), Shimoya (1990), and Santos et al. (1995). One of the crucial traits for the improvement of grain size and yield in soybean, for Saka et al. (1996), is the NDM. The strong association between GY and NDM

a	10	Mean squares							
Sources	df	NDM	РНМ	AV^1	GY				
		days	cm	score	kg ha ⁻¹				
Blocks	5	66.240	574.292	0.108	31885.100				
Genotypes	53	226.638**	228.201**	0.037**	7769.600**				
Parents (P)	9	445.482**	404.296**	0.079**	15376.433**				
Crosses (C)	43	183.971**	196.637**	0.026**	6204.200**				
P vs C	1	91.738**	0.616	0.129**	6621.467				
Error	265	10.964	25.765	0.009	2055.600				
General mean		154.016	56.232	1.611	829.300				
Parent mean		152.900	56.140	2.270	884.000				
Line mean		154.270	56.250	2.11	817.000				
VC (%)		2.150	9.030	6.000	31.560				

Table 1. Mean squares for number of days to maturity (NDM), plant height at maturity (PHM), agronomic value (AV) and grain yield (GY), evaluated in semi-late soybean generation F_6

¹ Data transformed to $\sqrt{x + 0.5}$. ** P < 0.01 by test F.

Table 2. Mean squares (analysis in augmented blocks), using the effective error, with a partition of the sum of squares of $F_{6:7}$ lines under the effect of crosses, and $F_{6:7}$ progenies/crosses, for number of days to maturity (NDM, in days), plant height at maturity (PHM, in cm), agronomic value (AV, score) and grain yield (GY, in kg ha⁻¹), in semi-late soybean

	Mean squares							
Sources	df	NDM	PHM	\mathbf{AV}^{1}	GY			
Progenies $F_{6.7}$	1012	73.139**	313.460**	0.033**	96470.60**			
Crosses (C)	44	486.325**	1436.460**	0.146**	475157.20**			
Progenies (P) /C	968	54.358**	262.420**	0.028**	79257.50**			
P / Cristalina x EMGOPA-301	22	59.856**	90.476	0.011	74988.80			
P / Cristalina x IAC-4	22	90.833**	298.975**	0.026*	108675.40*			
P / Cristalina x IAC-5	23	68.663**	403.332**	0.029**	119842.50**			
P / Cristalina x IAC-6	22	46.135**	177.737*	0.031**	95262.20*			
P / Cristalina x IAC-8	22	56.460**	265.192**	0.034**	91510.30			
P / Cristalina x IAC-9	23	40.017**	267.197**	0.021	137182.60**			
P / Cristalina x IAC-11	21	45.695**	309.980**	0.039**	91534.90			
P / Cristalina x Santa Rosa	22	64.136**	198.975*	0.017	71470.90			
P / Cristalina x OCEPAR9-SS-1	23	129.000**	374.805**	0.061**	72317.60			
P / EMGOPA-301 x IAC-4	23	92.334**	205.957**	0.015	82816.90			
P / EMGOPA-301 x IAC-5	21	12.518	126.428	0.036**	47112.10			
P / EMGOPA-301 x IAC-6	21	86.065*	200.669*	0.014	72426.80			
P / EMGOPA-301 x IAC-8	23	52.922*	248.010**	0.022	92123.60*			
P / EMGOPA-301 x IAC-9	23	40.665*	115.627	0.011	73074.50			
P / EMGOPA-301 x IAC-11	22	54.449*	288.681**	0.013	39442.40			
P / EMGOPA-301 x Santa Rosa	22	59.417*	302.151**	0.020	110035.50**			
P / EMGOPA-301 x OCEPAR-9-SS-1	19	83.248*	311.198**	0.012	77007.10			
P / IAC-4 x IAC-5	23	29.035*	209.545**	0.022	50034.20			
P / IAC-4 x IAC-6	22	11.063	230.868**	0.010	41547.00			
P / IAC-4 x IAC-8	21	48.952**	221.681**	0.049**	121359.50**			
P / IAC-4 x IAC-9	23	41.946**	280.908**	0.028**	47842.20			
P / IAC-4 x IAC-11	23	56.443**	211.860**	0.042**	89810.50			
P / IAC-4 x Santa Rosa	22	13.156	106.033	0.015	74636.70			
P / IAC-4 x OCEPAR-9-SS-1	19	72.718**	249.181**	0.051**	89581.10			
P / IAC-5 x IAC-6	23	83.505**	410.423**	0.018	75049.10			
P / IAC-5 x IAC-8	23	59.408**	526.564**	0.042**	56863.90			
P / IAC-5 x IAC-9	20	40.480**	338.781**	0.021	54380.00			
P / IAC-5 x IAC-11	21	30.486**	510.429**	0.032**	72057.00			
P / IAC-5 x Santa Rosa	22	4.070	117.108	0.017	63571.20			
P / IAC-5 x OCEPAR-9-SS-1	19	69.148**	353.332**	0.023	89639.20			
P / IAC-6 x IAC-8	22	41.142**	286.215**	0.030**	56980.20			
P / IAC-6 x IAC-9	21	39.459**	222.879**	0.023	59667.20			
P/IAC-6 x IAC-11	23	35.476**	181.177*	0.017	58698.20			
P / IAC-6 x Santa Rosa	22	74.220**	214.115**	0.039**	72635.70			
P / IAC-6 x OCEPAR-9-SS-1	23	20.343*	102.179	0.026*	72287.50			
P/IAC-8 x IAC-9	23	47.602**	434.018**	0.020	48884.40			
P/IAC-8 x IAC-11	20	70.112**	284.924**	0.040**	87628.80			
P / IAC-8 x Santa Rosa	20	29.711**	377.046**	0.023	89248.90			
P / IAC-8 x OCEPAR-9-SS-1	20	26.194**	330.408**	0.046**	85778.60			
P/IAC-9 x IAC-11	21	22.907**	209.164**	0.023	61827.50			
P / IAC-9 x Santa Rosa	21	57.244**	204.784*	0.025*	81700.50			
P / IAC-9 x OCEPAR-9-SS-1	16	29.141**	172.077	0.025	73467.80			
P / IAC-11 x Santa Rosa	21	54.639**	239.150*	0.038**	123170.30**			
P / IAC-11 x OCEPAR-9-SS-1	20	59.436**	153.066	0.025*	97020.20*			
P / Santa Rosa x OCEPAR-9-SS-1	20	200.559**	452.207**	0.093**	123235.40**			
Mean effective error	207	11.282	111.637	0.015	59332.76			
General mean		143.952	84.995	1.956	3077.16			
VC (%)		2.300	12.400	6.300	25.00			

¹ Data transformed to $\sqrt{x + 0.5}$. ** P < 0.01 by test F.

complicates the achievement of productive and early inbred lines. This relation underpins the theory of Johnson and Bernard (1963), which claim that many of the high and most consistent associations must have surged because the traits are affected by the same fundamental physiological plant processes. Shukla and Pushpendra (1998), on the other hand, estimated a positive correlation of low magnitude ($r_G = 0.03$) among these traits.

Table 3. Estimates of the genotypic correlation coefficients (r_{c}) between number of days to maturity (NDM), plant height at maturity (PHM), agronomic value (AV), and grain yield (GY), based on the parents, diallel crosses, and progenies F_{6} and $F_{6:7}$ in semi-late soybean

Genotypes	Traits	PH	łM	Α	V	GY	
		F ₆	F _{6:7}	F ₆	F 6:7	\mathbf{F}_{6}	F _{6:7}
	NDM (days)	cm		score		kg ha ⁻¹	
Parents		0.458	0.516	0.900	0.850	0.863	0.912
Crosses		0.591	0.581	0.755	0.686	0.768	0.688
Progenies			0.368		0.002		0.453
	PHM (cm)						
Parents				0.671	0.823	0.452	0.403
Crosses				0.761	0.853	0.543	0.451
Progenies					0.787		-0.080
	AV (score)						
Parents						0.929	0.859
Crosses						0.883	0.774
Progenies							-0.180

As expected, correlations between GY and AV were positive and high (r_G of 0.77 to 0.92), in parents as well as in the F_6 and $F_{6:7}$ crosses. These associations show that the AV, although a complex trait for the evaluation in a grading system with visual scores, might be useful for the process of grain yield evaluation. Similar results were obtained by Yokomizo et al. (2000) and Pandini et al. (2001). Lopes et al. (2002) estimated positive and high genotypic correlations in generation F_2 as well as in the parents. Freire Filho (1988) obtained positive correlations in the parents groups and generation F_2 , however of small magnitude in the parents, and suggested the use of more than one evaluator to increase the efficiency of AV. The positive and moderate association between GY, NDM, and PHM in soybean complicates the achievement of early high yield inbred lines of mean plant height.

As expected, heritability coefficient estimates (h^2) presented a broad variation in all traits and different crosses (Table 4), since heritability varies on account of the employed population, mainly due to the genetic diversity among parents and the higher or lower sensitivity of the parents to environmental variations (Vello et al. 1988). Some heritability estimates with value zero were observed for GY in both generations, and for NDM, PHM, and AV in generation F_{6:7}. These estimates gave rise to negative values of genetic variance estimates, which can be explained by the small number of plants in some crosses. For Dudley and Moll (1969), such results have no other explanation than a sampling error.

The h² estimates for NDM varied from 0.37 to 0.99 among crosses, with a mean of 0.92 in generation F_6 , and from 0 to 0.93 among crosses, with a mean of 0.74 in generation $F_{6:7}$. Most crosses presented a high h² estimate (> 0.70) in both generations, indicating the importance of genetic causes in the phenotypic variation of trait NDM. Similar coefficients of heritability were observed by several authors: Shimoya (1990) found values that vary from 0.92 to 0.98 in F_9 inbred lines; and Prado (1994), whose estimates oscillated from 0.47 to 0.84 in F_8 lines. Santos et al. (1995) and Hamawaki et al. (2000) reported h^2 estimates of small magnitude for NDM.

For PHM, the h^2 estimates varied from 0.37 to 0.85 among crosses, with a mean of 0.65 in generation $F_{6.}$ In $F_{6:7}$, the mean was 0.50, and estimates within the crosses oscillated from zero to 0.77. In both generations, most crosses presented estimates considered moderate (0.4 < h^2 < 0.7), suggesting that the trait is slightly affected by the environment. Highest values were found by Shimoya (1990), who obtained h^2 varying from 0.60 to 0.97, in generation $F_{9.}$ and by Santos et al. (1995), who discovered a h^2 estimate of 0.98, using F_6 inbred lines.

The heritability estimate for AV in F_6 presented a mean of 0.69, with a spread of 0.45 to 0.84 between crosses, and a mean of 0.37 in $F_{6:7}$, with a spread of zero to 0.90. Hamawaki et al. (2000) obtained lower h^2 values, in a range of zero to 0.61 and a mean of 0.51 in $F_{4:3}$ lines of octuple soybean crosses.

For GY, the mean heritability estimates were 0.62 (F₆) and 0.29 ($F_{6:7}$), and the values for the crosses varied from zero to 0.85 in F_6 , and from zero to 0.58 in $F_{6;7}$. These values were compared to those reported in other studies: 0.22 to 0.86 for F₉ inbred lines (Shimoya 1990); 0.48 to 0.61 for F₈ inbred lines (Prado 1994); and zero to 0.61 for $F_{4,3}$ lines (Hamawaki et al. 2000). Inconsistent results between the two generations were not foreseen, as we are dealing with advanced generations of inbreeding. Nevertheless, as the trait GY is strongly influenced by environmental factors, some causes can be cited which possibly contributed to these results. One was the method applied to estimate the experimental variance. In F_6 the geometric mean of environmental variances among hills of both parents involved in the cross was employed; and in F_{6:7} the mean effective error, obtained by the variance analysis, according to the design in augmented blocks. Furthermore, the sowing time and kind of plot also varied from one

generation to the next. According to Johnson et al. (1955), variance component estimates are subjected to errors, mainly in the presence of interactions, and these affect the obtained parameters based on these estimates, such as heritability. The estimate of h², ratio between the genotypic and phenotypic variance, can vary considerably on account of the selection unit, or the interaction genotypes by environments; in conclusion, any significant comparison of estimates obtained in different experimental situations must provide a careful evaluation of the employed material and methods.

The percentage of $F_{6:7}$ inbred lines with an observed positive progress oscillated from 27.78% (IAC-9 x OCEPAR-9-SS-1) to 59.09% (IAC-4 x IAC-9), and the following crosses presented a percentage of over 50%: IAC-4 x IAC-9, IAC-6 x OCEPAR-9-SS-1, EMGOPA-301 x IAC-11, IAC-4 x IAC-5, FT-Cristalina x Santa Rosa, EMGOPA-301 x IAC-9 (Table 5). In relation to the parents involved in the crosses, the proportional line mean with an observed positive gain varied from 37.68% (IAC-11) to 45.67% (IAC-6). The gain observed in the selection for the best inbred line of each cross

Table 4. Estimate of the heritability coefficients (h^2) which refer to the traits: number of days to maturity (NDM), plant height at maturity (PHM), agronomic value (AV), and grain yield (GY) for the lines F_6 and $F_{6:7}$, in semi-late soybean

~	NDM		PHM		AV		GY	
Crosses	\mathbf{F}_{6}	F _{6:7}	\mathbf{F}_{6}	F _{6:7}	F ₆	F _{6:7}	\mathbf{F}_{6}	F _{6:7}
	days		cm		score		kg ha ⁻¹	
FT-Cristalina x EMGOPA-301	0.96	0.85	0.71	0.64	0.47	0.55	0.78	0.38
FT-Cristalina x IAC-4	0.97	0.98	0.71	0.92	0.60	0.90	0.58	0.88
FT-Cristalina x IAC-5	0.96	0.79	0.72	0.57	0.67	0.46	0.60	0.25
FT-Cristalina x IAC-6	0.79	0.81	0.58	0.00	0.51	0.00	0.36	0.21
FT-Cristalina x IAC-8	0.95	0.88	0.50	0.63	0.74	0.42	0.60	0.45
FT-Cristalina x IAC-9	0.85	0.84	0.57	0.72	0.56	0.48	0.59	0.50
FT-Cristalina x IAC-11	0.87	0.76	0.52	0.37	0.52	0.52	0.62	0.38
FT-Cristalina x Santa Rosa	0.97	0.80	0.68	0.58	0.70	0.56	0.60	0.35
FT-Cristalina x OCEPAR9-SS-1	0.99	0.72	0.71	0.58	0.72	0.29	0.68	0.57
EMGOPA-301 x IAC-4	0.97	0.75	0.42	0.64	0.71	0.62	0.73	0.35
EMGOPA-301 x IAC-6	0.96	0.82	0.67	0.44	0.68	0.12	0.78	0.17
EMGOPA-301 x IAC-8	0.94	0.91	0.57	0.70	0.66	0.75	0.81	0.18
EMGOPA-301 x IAC-9	0.93	0.88	0.72	0.46	0.70	0.00	0.61	0.28
EMGOPA-301 x IAC-11	0.97	0.10	0.38	0.12	0.67	0.58	0.32	0.00
EMGOPA-301 x Santa Rosa	0.96	0.87	0.71	0.44	0.60	0.00	0.80	0.18
EMGOPA-301 x OCEPAR-9-SS-1	0.99	0.79	0.73	0.55	0.73	0.32	0.81	0.36
IAC-4 x IAC-5	0.94	0.72	0.80	0.03	0.79	0.00	0.49	0.19
IAC-4 x IAC-6	0.89	0.79	0.67	0.61	0.78	0.00	0.72	0.00
IAC-4 x IAC-8	0.96	0.81	0.62	0.63	0.63	0.25	0.60	0.46
IAC-4 x IAC-9	0.95	0.86	0.65	0.64	0.76	0.00	0.80	0.23
IAC-4 x IAC-11	0.97	0.61	0.71	0.47	0.70	0.32	0.29	0.00
IAC-4 x Santa Rosa	0.88	0.00	0.62	0.52	0.52	0.00	0.68	0.00
IAC-4 x OCEPAR-9-SS-1	0.96	0.77	0.75	0.50	0.76	0.69	0.65	0.51
IAC-5 x IAC-6	0.94	0.73	0.81	0.60	0.74	0.46	0.43	0.00
IAC-5 x IAC-8	0.97	0.80	0.85	0.47	0.66	0.64	0.57	0.34
IAC-5 x IAC-9	0.92	0.14	0.83	0.00	0.69	0.00	0.54	0.21
IAC-5 x IAC-11	0.96	0.84	0.83	0.55	0.78	0.71	0.61	0.34
IAC-5 x Santa Rosa	0.69	0.86	0.43	0.73	0.58	0.17	0.00	0.21
IAC-5 x OCEPAR-9-SS-1	0.98	0.81	0.81	0.79	0.78	0.64	0.66	0.00
IAC-6 x IAC-8	0.93	0.72	0.65	0.67	0.81	0.29	0.78	0.00
IAC-6 x IAC-9	0.69	0.63	0.69	0.78	0.73	0.53	0.69	0.18
IAC-6 x IAC-11	0.71	0.00	0.45	0.05	0.75	0.12	0.38	0.07
IAC-6 x Santa Rosa	0.94	0.84	0.74	0.68	0.83	0.35	0.73	0.34
IAC-6 x OCEPAR-9-SS-1	0.37	0.73	0.43	0.61	0.79	0.50	0.46	0.00
IAC-8 x IAC-9	0.96	0.71	0.79	0.50	0.82	0.35	0.73	0.01
IAC-8 x IAC-11	0.96	0.68	0.64	0.38	0.65	0.12	0.65	0.00
IAC-8 x Santa Rosa	0.96	0.85	0.37	0.48	0.45	0.62	0.55	0.18
IAC-8 x OCEPAR-9-SS-1	0.97	0.45	0.75	0.00	0.76	0.42	0.67	0.18
IAC-9 x IAC-11	0.94	0.76	0.60	0.74	0.67	0.25	0.32	0.00
IAC-9 x Santa Rosa	0.98	0.84	0.66	0.61	0.75	0.63	0.69	0.32
IAC-9 x OCEPAR-9-SS-1	0.99	0.62	0.77	0.70	0.84	0.35	0.84	0.34
IAC-11 x Santa Rosa	0.94	0.57	0.57	0.66	0.76	0.67	0.38	0.31
IAC-11 x OCEPAR-9-SS-1	0.97	0.51	0.46	0.47	0.77	0.35	0.00	0.04
Santa Rosa x OCEPAR-9-SS-1	0.98	0.80	0.62	0.45	0.74	0.40	0.85	0.27
General mean	0.92	0.70	0.65	0.50	0.69	0.37	0.58	0.21

Parents	EMGOPA-301	IAC-4	IAC-5	IAC-6	IAC-8	IAC-9	IAC-11	Santa Rosa	OCEPAR-9-SS-1	Mean
FT-Cristalina	(1) 39.02(2) 53.75	33.33 136.81	41.86 132.07	40.48 83.01	39.53 62.30	50.00 118.44	35.71 76.81	51.16 95.15	35.71 54.31	40.76
EMGOPA-301		43.18 87.74	42.10 71.02	45.24 78.33	48.84 115.28	51.16 94.99	52.38 82.02	44.19 99.82	41.03 87.13	45.24
IAC-4			52.27 161.25	48.78 79.54	43.59 145.13	59.09 90.40	34.09 90.77	37.21 116.16	35.00 102.48	42.95
IAC-5				45.45 124.67	40.48 82.93	36.58 61.41	36.59 68.82	30.23 80.75	50.00 162.08	41.73
IAC-6					35.71 56.98	45.24 88.82	43.18 70.79	48.84 97.58	58.14 128.39	45.67
IAC-8						44.19 88.90	30.77 79.01	41.46 133.79	45.00 134.77	41.06
IAC-9							38.10 63.47	46.34 126.04	27.78 60.63	44.28
IAC-11								34.15 86.07	34.15 98.70	37.68
Santa Rosa									37.50 112.30	41.23
OCEPAR-9-SS-1										40.48

Table 5. Percentage of $F_{6:7}$ progenies obtained from 45 diallel crosses, with an observed positive select gain (1) and select gain of the best line in relation to the parents (2) involved in the cross, in relation to grain yield (kg ha⁻¹), in semi-late soybean

varied from 53.75% (FT-Cristalina x EMGOPA-301) to 162.08% (IAC-5 x OCEPAR-9-SS-1). The observed gain was over 100% in 15 crosses, between 75% and 100% in 20 crosses, and within a spread of 50% to 75% in 10 crosses. In all crosses, transgressive segregates indicate the possibility of high yield line selection, although the best performance was observed in the populations IAC-5 x OCEPAR-9-SS-1, IAC-4 x IAC-5,

IAC-4 x IAC-8, FT-Cristalina x IAC-4, IAC-8 x OCEPAR-9-SS-1, IAC-8 x Santa Rosa, FT-Cristalina x IAC-5, IAC-6 x OCEPAR-9-SS-1, IAC-9 x Santa Rosa, IAC-5 x IAC-6, FT-Cristalina x IAC-9, IAC-4 x Santa Rosa, EMGOPA-301 x IAC-8, Santa Rosa x OCEPAR-9-SS-1, and IAC-4 x OCEPAR-9-SS-1, IAC-4 x IAC-9, EMGOPA-301 x IAC-11, FT-Cristalina x Santa Rosa, and EMGOPA-301 x IAC-9.

Análise genética em gerações F₆ e F_{6:7} de soja

RESUMO - Avaliaram-se 45 cruzamentos de soja (Glycine max L.), nas gerações $F_6 e F_{6:7}$, visando estimar parâmetros genéticos e selecionar linhagens superiores em produtividade de grãos. Os genótipos parentais, de ciclo semi-tardio, utilizados nos cruzamentos foram FT-Cristalina, EMGOPA-301, IAC-4, IAC-5, IAC-6, IAC-8, IAC-9, IAC-11, Santa Rosa e OCEPAR-9-SS-1. As progênies F_6 de 44 cruzamentos (exceto EMGOPA-301 x IAC-5) e os dez parentais foram avaliadas em uma safra, enquanto na safra seguinte avaliaram-se as progênies $F_{6:7}$ dos 45 cruzamentos e os dez parentais. Nas duas gerações foram avaliados o número de dias para maturidade (NDM), a altura da planta na maturidade (PHM), o valor agronômico (VA) e a produtividade de grãos (GY). A obtenção de linhagens produtivas e precoces é dificultada pela alta correlação genotípica positiva entre GY e NDM. As herdabilidades foram altas (> 0,70) para NDM e moderadas (0,40 – 0,70) para PHM. A ocorrência de segregantes transgressivos, evidencia a possibilidade de seleção de linhagens com alta produtividade.

Palavras-chave: Glycine max, herdabilidade, correlação genotípica, blocos aumentados, produtividade de grãos.

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