



## Interaction genotypes x sowing periods in experimental $F_{9;2}$ soybean lines

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**ABSTRACT** - The magnitude of the interaction  $G \times S$  was measured by different biometric techniques to draw inferences on improvement strategies for soybean. Twenty-five highly homozygotic ( $F_{9;2}$ ) soybean lines were evaluated in three sowing periods. The trials were set up in randomized complete blocks with three replications. The controls IAC-100, OCEPAR-4, MTBR-45, and EMGOPA-313 were used. Number of days to flowering and to maturity, grain filling period, stained seeds, weight of a hundred seeds and the grain yield (GY) were evaluated. The complex part was predominant in the partition of this interaction. In relation to the selection gain for GY a mean reduction of 10% is expected in comparison to a selection realized in period 2 only with specific selections per period, admitting a selection intensity of 40%. A reduction of 28% is expected under a selection intensity of 20%. The selection of more generalist genotypes is possible, although it leads to losses in mean terms.

**Key words:** *Glycine max*, resistance to insects, grain yield, juvenile period.

### INTRODUCTION

Soybean (*Glycine max* (L.) Merrill) in Brazil is commonly exposed to countless environmental conditions in terms of locals as much as sowing periods and crop years. In this setting the interaction genotypes x environments ( $G \times E$ ) is expected to play a fundamental role in the phenotypic manifestation. It should therefore be estimated and considered in the recommendation of cultivars and in genetic improvement programs (Prado et al. 2001).

According to Cruz and Regazzi (1994) the evaluation of the interaction genotypes x environments is of great importance for improvement, since, when this interaction is present, the

best genotype in one environment is not necessarily the best in another. This fact influences the selection gain and makes the recommendation of genotypes with broad adaptability or for a specific period difficult.

There are various studies on the interaction genotypes x environments in soybean indicating that the quantitative traits are affected by sites and sowing periods (Oliveira et al. 2003, Morais et al. 2003).

An important point in the study of the interaction  $G \times E$  is its estimation which can be based on an analysis of variance. However, from the point of view of improvement, significance in the source of variation  $G \times E$  does not mean a lot isolatedly but calls for complementary analyses (Vencovsky and Barriga

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1992). One of the ways to understand the interaction G x E better is through the application of the partition of the variance due to the interaction in the independent and dependent parts of the Pearson correlation of the genotypes in the different pairs of environments, in other words, the partition of the mean square of the interaction G x E in the simple and complex components. Another quite useful method for the analysis of the interaction G x E is the calculation of the expected progress with specific selections for each period of interest and with direct selection in a certain period (most recommended). Based on these calculations comparisons can be realized to predict the gain achieved in each one of them.

This study aimed at a better understanding of the interaction G x E in the diverse studied traits and the verification of the maintenance of the lines performance regarding the traits evaluated throughout the sowing periods for selection.

## MATERIAL AND METHODS

The experimental material consisted in 25 F<sub>9,2</sub> soybean lines/entries, obtained in subsequent selections of 170 lines originates of partial diallels crosses (4 x 4) involving eight parents genotypes based on the reaction to pod-sucker and leaf-chewer insects, grain yield and juvenile period (Moura and Pinheiro 2002, Moura et al. 2003). The cultivars Crockett, Lamar, IAC-100 and the line D72-9601-1 were chosen as resistant parents. As productive and adapted parents (however susceptible) the cultivars BR-6 (Nova Bragg), IAS-5, Davis and OCEPAR-4 (Iguaçu) were selected. The crossings were realized among the resistant and susceptible genotypes, amounting to 16 biparents combinations.

The F<sub>9,2</sub> lines were evaluated in different sowing periods (10/21/1998, 09/11/98 and 11/12/98) on the experimental field of the Escola de Agronomia/UFG in Goiânia, state of Goiás, (16° 41' lat S and 49° 13' long W, altitude 730m asl). The experiment had a randomized complete blocks design, with three replications per period in which the experimental plot consisted in four rows of 4 x 0.5m and the useful plot in two rows of 4 x 0.5m. The cultivars IAC-100 and OCEPAR-4 (parents involved in the crossings), MTBR-45 (Paiaguás) and EMGOPA-313 (cultivars recommended for the region) were chosen as controls. These lines were evaluated for grain yield, juvenile period and resistance to insects. A high natural infestation with stink bugs was observed in the field in all experiments.

The following traits were evaluated: number of days to flowering (NDF), number of days to maturity (NDM), grain filling period (GFP), stained seeds (SS), 100-seed weight (HSW)

and grain yield (GY). The data of trait SS were transformed into  $\sqrt{x+0.5}$ , creating gerating the variable SST.

Individual variance analyses were realized for each period of generation F<sub>9,2</sub>, besides a joint analysis after the verification of the homogeneity of variances.

After the analysis of joint variance of the experiments, the interaction genotypes x sowing periods was decomposed for the environment pairs. The decomposition was based on the expression presented by Cockerham (1963) and applied by Santos (1981) to the mean squares as shown below for periods 1 and 2:

$$QM_{G \times E} = (1/2)(\sqrt{QM_{G1}} - \sqrt{QM_{G2}})^2 + (1-r_{12})\sqrt{QM_{G1} \cdot QM_{G2}}$$

where:

QM<sub>GxE</sub>: mean square of the interaction genotypes x sowing periods;

The same decomposition was realized for the period pairs 1 and 3 and 2 and 3, taking the mean squares and corresponding correlations into consideration, in other words:

QM<sub>G1</sub>, QM<sub>G2</sub>, QM<sub>G3</sub>: mean squares regarding the treatments (genotypes) in periods 1, 2 and 3, respectively;

r<sub>12</sub>, r<sub>13</sub>, r<sub>23</sub>: Pearson correlations among the genotype means of one environment (period) with the other.

The correlation coefficient of Spearman (r<sub>s</sub>) for all pairs of environments (periods) was calculated by the expression:

$$r_s = 1 - \frac{6 \times \sum d_i^2}{(n-1)n(n+1)},$$

and the significance of this estimate based on the following expression was verified:

$t = r_s \sqrt{(n-2)/(1-r_s^2)}$  with (n-2) degrees of freedom (Steel and Torrie 1960) and n numbers of lines.

Fisher's exact test was used as presented by Pimentel-Gomes (2000) to test the randomness of the coincidence of the lines selected in the sowing period pairs.

The expected gains with selection (selection intensity of 40% and of 20%) were also computed within each period separately (specific selection) and the expected progress in periods 1 and 3 based on the selections realized in period 2 (selection in period 2, the most recommended, and expected response in the other periods, in other words, generalist selection). The gains were calculated according to Vencovsky and Barriga (1992), who used the differential of selection (ds). Thus, the following expressions were used:

Expected progress in period *i* (specific selection):

$$\hat{ds}_i = \bar{Y}_{s(i)} - \bar{Y}_{(i)}, \text{ where:}$$

$\hat{ds}_i$ : differential of selection in period *i*;

$\bar{Y}_{s(i)}$ : mean of the lines selected in period *i*;

$\bar{Y}_{(i)}$ : mean of all lines in period *i*.

Periods 1, 2 and 3 were calculated taking the means of the lines of each site and the means of the lines selected in each specific period into account.

Based on the differential of selection computed for the specific period, the expected progress with the selection realized within each period separately (specific selection) were computed by the expression below:

$$\hat{G}s_{(i)} = \hat{d}s_i \cdot \hat{h}_{m(i)}^2, \text{ where:}$$

$\hat{G}s_{(i)}$ : differential of selection in period  $i$ ;

$\hat{h}_{m(i)}^2$ : heritability at the mean level for period  $i$ .

The percentual expected progress with selection was obtained by:

$$\hat{G}s_{(i)} \% = \hat{G}s_{(i)} / \bar{Y}_{(i)} \cdot 100, \text{ where:}$$

$\bar{Y}_{(i)}$ : mean of all lines in period  $i$ .

For the calculation of the expected progress in the other periods based on the selection in a particular period (selection in period 2 and expected response in periods 1 and 3), the following

expression was used:

$$\hat{d}s_{(i')} = \bar{Y}_{s(i')} - \bar{Y}_{(i')}, \text{ where:}$$

$\hat{d}s_{(i')}$ : differential of selection in period  $i'$  being selected in period  $i$ ;

$\bar{Y}_{s(i')}$ : mean of the lines in period  $i'$  that were selected in period  $i$ ;

$\bar{Y}_{(i')}$ : mean of all lines in period  $i'$ .

$$\hat{G}s_{(i')} = \hat{d}s_{(i')} \cdot \hat{h}_{m(i')}^2, \text{ where:}$$

$\hat{G}s_{(i')}$ : expected progress of selection in period  $i'$  selected in period  $i$ ;

$\hat{h}_{m(i')}^2$ : heritability at the mean level in period  $i'$ .

$$\hat{G}s_{(i')} \% = \hat{G}s_{(i')} / \bar{Y}_{(i')} \cdot 100, \text{ where:}$$

$\hat{G}s_{(i')} \%$ : expected progress of selection in percent in period  $i'$  selected in period  $i$ ;

$\bar{Y}_{(i')}$ : mean of all lines in period  $i'$ .

The ten most productive lines were identified in the different sowing periods, identifying the number of the line and the periods in which it was selected for the diverse traits evaluated (Table 1).

**Table 1.** Identification of the ten most productive lines considering the three sowing periods (P1: 10/21, P2: 11/09 and P3: 12/11) in which they were selected for the diverse traits<sup>1</sup> evaluated. Soybean, generation F<sub>9,2</sub>

Lines	GY kg ha <sup>-1</sup>	GFP days	HSW g	SST <sup>2</sup> note	NDF days	NDM days
81-1-23	P1, P2, P3	P1, P2	P3	P1, P2, P3	P1, P2, P3	P2
81-1-24	P1, P2, P3	P1, P2	P1, P2, P3	P1, P2, P3	P1, P2, P3	P3
81-10-08	P1, P2, P3	P1, P2	P1, P2, P3	P1, P2	P1, P3	-
81-4-13	P1, P2, P3	-	P1	P1	P1, P2, P3	P1, P2, P3
81-7-01	P1, P2, P3	P2	P1, P2, P3	P1, P3	-	-
81-1-28	P1, P2, P3	P1, P2, P3	P1, P2, P3	P1, P2, P3	P1, P2, P3	-
81-10-09	P1, P2	P2	P1, P2, P3	P1	-	-
81-9-18	P1, P2	-	-	-	P1, P2, P3	P1, P2, P3
81-9-13	P1, P2	P2, P3	P1, P2	P1, P2	P1, P2, P3	P1, P2, P3
81-1-25	P1, P3	P1, P2	P2	P2	P1, P2	-

<sup>1</sup>GY: grain yield; GFP: grain filling period; HSW: 100-seed weight; SST: stained seeds with transformed data; NDF: number of days to flowering and NDM: number of days to maturity

<sup>2</sup>data of trait SS were transformed into  $\sqrt{x+0.5}$  (SST)

## RESULTS AND DISCUSSION

The joint analysis of variance of the experiments presented significance ( $P < 0.01$ ) of the source of variation lines x periods for all traits (Table 2).

The partition of the mean square of the interaction lines x sowing periods (G x S) for the different pairs of environments (periods) in the simple and complex parts (Table 3) for the grain yield (GY) showed that the complex part contributed with the highest mean square percentage to the interaction in all pairs of periods, despite the relatively high observed values of the Pearson correlations ( $r_{12} = 0.751$ ;  $r_{13} = 0.728$  and  $r_{23} = 0.635$ );

this can be explained by the similarity of the mean squares of genotypes in the different locals.

Spearman's correlation coefficients were estimated for all pairs of environments (periods) with the objective of testing the randomness of the coincidence of lines selected in the pairs of sowing periods using Fisher's exact test.

In relation to the correlation coefficients of Spearman for the diverse pairs of environments (Table 4) relatively high and significant values were verified. This fact can be explained by the presence of some genotypes in equal positions in the ranking realized in the different sowing periods. Nevertheless, Fisher's

exact test verified (Table 5) that only in the analysis involving periods 1 and 2 jointly significance ( $P < 0.05$ ) was obtained for the coincidence of the number of genotypes after selecting the ten best lines in these two periods. The partition of the mean square and Fisher's exact test indicate the difficulty of selecting promising lines for the yield, adapted to the pairs of sowing periods 1 x 3 and 2 x 3. Specific selection is in this case more promising.

Once calculated the expected progress with selection realized within each period (specific selection) and the expected progress in periods 1 and 3 based on the selection realized in period 2 (generalist selection) with selection intensities of 40% and 20% (Tables 6 and 7) was computed, a loss in kg ha<sup>-1</sup> was observed when using generalist selection. Although this loss is present, its magnitude is also related to the selection intensity, in other words, in the generalist selection where a greater selection intensity (40%) was used there were no great losses while with a lower selection intensity (20%) this loss became considerable.

Breeders should be aware of these results when choosing generalist or specific selection, not only taking the availability of time and resources into consideration, but also the methodology to be used in the decision on the selection type.

An analysis of the partition of the interaction G x E in the simple and complex parts is of great usefulness for studies into the interaction G x E, however the mean squares of genotypes at each local must be observed. The reason is that if the mean squares of the genotypes are similar there is an overestimation of the complex part of the interaction. Another point to be observed is the use of Fisher's exact test in the verification of the coincidence of the lines selected in the diverse period pairs. This test can be quite useful, however as it is a non-parametric test it does not consider the mean values and only evaluates whether the genotype positions are close or not. In this case, Fisher's test was very strict, since the significance of the coincidence was only manifested when a minimum of eight lines coincided from one period to another (Table 5). Therefore, this test is only recommended in the absence of another more appropriate one.

In relation to the traits of resistance against the stink bugs (GFP and HSW) a greater contribution of the complex part to the mean square of the interaction G x E in the different period pairs was also observed due to the similarity of the mean squares of genotypes at the different sites. For SST however, variation was observed in the contribution of the complex part. The contribution was greatest in the pair of environments 2 x 3, followed by the pairs 1 x 2 and 1 x 3 (Table 3). An analysis of Spearman's correlation coefficients (Table 4) verified significance for HSW ( $P < 0.05$ ) in the different environment pairs and for GFP only for pair 1 x 3. This result was confirmed by Fisher's

exact test (Table 5) which also revealed significance for HSW only in all environment pairs. The conclusion can therefore be drawn that selecting more promising generalist genotypes in the different sowing periods would only be feasible for HSW.

Likewise, the greatest contribution of the complex part in all environment pairs was observed for the traits related to a long juvenile period (NDF and NDM), (Table 3). However, significant and relatively high values were observed for all environment pairs when analyzing the Spearman correlation coefficients (Table 4). Despite the high and significant coefficients significance was only observed for the values of coincidence in the selection for NDF by Fisher's test (Table 5). The insignificant differences of the values of coincidence in the selection for the trait NDM in the diverse environment pairs may have been influenced by the GFP trait, since a difficulty of selecting promising genotypes in the different sowing periods was verified for this trait. Selection would therefore be more effective if realized specifically for each sowing period for NDM.

Ramalho et al. (1993) state that when a higher number of environments and cultivars is considered the presence of complex interaction nearly always indicates the existence of cultivars specifically adapted to a particular environment, as well as others with a broader adaptability, though not throughout with a high yield potential. This impedes the recommendation of cultivars in a generalized manner, increasing the difficulties and requiring the adoption of measures that control or minimize the effects of this interaction to proceed to a safer recommendation. Summing up, the interaction does not only interfere in the recommendation of cultivars, but also in the achievement of the estimate values of the genetic variance components which can result in a biased estimate of the expected gain with selection. Besides, the occurrence of complex interaction between genotypes will diminish the efficiency of the improvement program, since selection is normally realized in the mean of the various environments, which does not guarantee the selection of the best progenies for each environment in particular.

In an improvement program the selection of generalist genotypes may be an advantage if the objective is the identification of cultivars that respond positively to the fluctuation of the sowing period caused by climatic or other factors. According to Marchiori et al. (1999) and Peixoto et al. (2000) there is the possibility of selecting genotypes that stand out in sowing conditions different from the period recommended for the crop, thus revealing cultivars that respond positively to sowing in a more extensive time period, as long as they present traits such as a long juvenile period.

Likewise, the study of the sowing period is highly important for the analysis of stability and phenotypic adaptability since it allows the identification of periods in which the genotypes have little sensitivity, causing a small fluctuation

in the yield, which allows the sowing of the genotypes beyond the recommended periods. According to Morais et al. (2003) the search for specific adaptations may lead to conclusions on recommendations of more productive sowing periods for a specific cultivar. The authors state that specific sowing periods must be adopted for the cultivars IAC-100 and OCEPAR-04.

Despite the difficulty in selecting promising lines adapted simultaneously to the different sowing periods for the diverse traits, according to the partition of the interaction G x S except

for HSW and NDF, another alternative would be the observation and selection of superior lines in all sowing periods, which would surely present a broader adaptation. This alternative was verified by Moura and Pinheiro (2002) who selected ten promising lines for GY based on the superiority throughout three generations and as a result observed that these were superior for GY and for the diverse traits of resistance to insects as well as for the long juvenile period.

**Table 2.** Summary of the joint analysis of variance with the values and significance of the mean squares of five traits<sup>1</sup>. Soybean, generation F<sub>9,2</sub>

Sources of variation	df	NDF days	NDM days	GFP days	SST <sup>2</sup> note	HSW g	GY kg ha <sup>-1</sup>
Sowing	2	136.2**	3.194.7**	228.7**	36.9**	37.0**	23874750.9**
Blocks/Sowing	6	3.2	25.7	1.6	1.4	1.4	102097.7
Treatments	28	254.9**	674.5**	98.6**	64.4**	64.4**	3287812.2*
Lines	24	124.3**	253.1**	49.8**	64.6**	64.6**	3459188.2**
Checks	3	837.0**	3040.2**	422.3**	73.2**	73.2**	2769699.1**
Lines vs Checks	1	1642.3**	3691.7**	638.3**	33.2	33.2	729126.5
Treatments x Sowing	56	4.9**	67.7**	38.8**	3.3**	3.3**	453543.1**
Lines x Sowing	48	5.1**	43.5**	17.8**	3.5**	3.5**	357551.4**
Checks x Sowing	6	4.4**	204.2**	114.9**	1.8	1.8	1071799.8**
Lines vs Checks x Sowing	2	1.7	240.2**	314.2**	2.6	2.6	902574.7
Error	168	1.6	17.1	7.7	1.0	1.0	195126.0
Total	260						
General mean		42.8	120.5	37.0	1.9	15.6	2088.7
Line mean		41.8	119.0	36.5	1.9	15.5	2067.6
Check mean		49.1	130.0	39.6	2.1	16.5	2220.8
CV %		3.0	3.4	7.5	29.6	6.3	21.1

<sup>1</sup>NDF: number of days to flowering; NDM: number of days to maturity; GFP: grain-filling period; SMT: stained seeds with data transformation; HSW: 100-seed weight and GY: grain yield

<sup>2</sup>data of trait SS were transformed into  $\sqrt{x+0.5}$  (SST)

\*and\*\*: Significant at 5% and 1% by the F test, respectively

**Table 3.** Partition of the interaction Lines x Sowing periods in the parts simple (S) and complex (C) in percentage for the period pairs (P1 x P2, P1 x P3 and P2 x P3). Soybean, generation F<sub>9,2</sub>

Trait interactions <sup>1</sup>	Ep1 x Ep2		Ep1 x Ep3		Ep2 x Ep3	
	S	C	S	C	S	C
GY	7.85	92.15	26.95	73.05	10.90	89.10
GFP	3.32	96.68	13.23	86.75	1.91	98.09
HSW	28.42	71.58	31.35	68.65	1.34	98.66
SST	45.29	54.71	66.86	33.14	26.75	73.25
NDF	5.95	94.05	8.11	91.89	0.03	99.97
NDM	4.80	95.20	1.00	99.00	28.12	71.88

<sup>1</sup>GY: grain yield; GFP: grain filling period; HSW: 100-seed weight; SST: stained seeds with data transformation; NDF: number of days to flowering and NDM: number of days to maturity

**Table 4.** Correlation coefficients of Spearman (r<sub>s</sub>) and their significances. Soybean, generation F<sub>9,2</sub>

Traits <sup>1</sup>	r <sub>s</sub>		
	P1 x P2	P1 x P3	P2 x P3
GY	0.834**	0.645**	0.608**
GFP	0.055	0.498*	0.336
HSW	0.801**	0.898**	0.840**
SST	0.377	0.274	0.347
NDF	0.818**	0.908**	0.892**
NDM	0.452*	0.595**	0.805**

<sup>1</sup>GY: grain yield; GFP: grain filling period; HSW: 100-seed weight; SST: stained seeds with data transformation; NDF: number of days to flowering and NDM: number of days to maturity

\*, \*\*: Significant at 5%, 1% by the t test, respectively

**Table 5.** Number of common lines (n) and probabilities (P, in %) of random occurrence with a truncation selection of 10 lines for each experiment in each period. Soybean, generation F<sub>9,2</sub>

Traits <sup>1</sup>	Period 1 x Period 2		Period 1 x Period 3		Period 2 x Period 3	
	n	P	n	P	n	P
GY	9	2.86*	6	32.81	7	18.49
GFP	4	32.81	7	18.49	4	32.81
HSW	8	1.74*	8	1.74*	8	1.74*
SST	6	32.81	5	50.00	5	50.00
NDF	8	1.74*	9	2.86*	8	1.74*
NDM	6	32.81	6	32.81	7	18.49

<sup>1</sup>GY: grain yield; GFP: grain filling period; HSW: 100-seed weight; SST: stained seeds with data transformation; NDF: number of days to flowering and NDM: number of days to maturity \* : Significant at 5% by the t test

**Table 6.** Expected progress with selection within each period (specific selection) and expected progress in periods 1 and 3 based on the selection realized in period 2 (generalist selection). Selection intensity of 40%. Grain yield in soybean, generation F<sub>9,2</sub>

Selection in period	Expected progress with selection (in kg)		
	Period 1	Period 2	Period 3
1	707.1		
2	644.5	426.7	266.6
3			351.7
Difference	62.6		85.1

**Table 7.** Expected progress with selection within each period (specific selection) and expected progress in periods 1 and 3 based on the selection realized in period 2 (generalist selection). Selection intensity of 20%. Grain yield in soybean, generation F<sub>9,2</sub>

Selection in period	Expected progress with selection (in kg)		
	Period 1	Period 2	Period 3
1	883.6		
2	593.0	526.7	240.7
3			493.7
Difference	290.6		253.0

**CONCLUSIONS**

1. The importance of the interaction genotypes x sowing periods in the evaluation of the soybean lines was confirmed;
2. The selection of more generalist lines in relation to the periods is possible, though this strategy would lead to mean yield losses;

3. It is up to the breeder to decide about the grade of specificity of his selections regarding the sowing periods;
4. The biometric methods used to study the interaction differed in the level of rigor and sensibility. Parameters that take correlations as well as expected progress in the direct and indirect selection into account should be preferred.

# Interação genótipos x épocas de semeadura em linhagens experimentais $F_{9:2}$ de soja

**RESUMO:** Objetivou-se mensurar a grandeza da interação  $G \times E$  usando diferentes técnicas biométricas e fazer inferências sobre estratégias de melhoramento para a soja. Avaliaram-se 25 linhagens altamente homozigóticas ( $F_{9:2}$ ) em três épocas de semeadura. Os ensaios foram em blocos casualizados com três repetições. Incluíram-se as testemunhas IAC-100, OCEPAR-4, MTBR-45 e EMGOPA-313. Os caracteres avaliados foram número de dias para o florescimento e para a maturidade, período de granação, sementes manchadas, peso de 100 sementes e a produtividade de grãos (PG). No desdobramento desta interação houve predomínio da parte complexa. Em relação ao progresso na seleção para PG espera-se uma redução média de 10%, ao confrontar uma seleção efetuada somente na época 2 com seleções específicas por época, admitindo intensidade de seleção de 40%. Com intensidade de seleção de 20% espera-se redução de 28%. A seleção de genótipos mais generalistas é possível, mas levará à perdas em termos médios.

**Palavras-chave:** *Glycine max*, resistência a insetos, produtividade de grãos, período juvenil.

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