ORIGINAL RESEARCH ARTICLE

Agrosystems

Heritability and the genotype × environment interaction in soybean

Mariane Cristina Bianchi[1] | **Adriano Teodoro Bruzi[1]** | **Igor Oliveri Soares[2]** |
Flaviane De Oliveira Ribeiro[3] | **Gabriel De Siqueira Gesteira[4]**

[1]Programa de Pós-Graduação em Agronomia/Fitotecnia, Departamento de Agricultura, Universidade Federal de Lavras (UFLA), Câmpus Universitário, Caixa Postal 3037, 37200-000 Lavras, Minas Gerais, Brasil

[2]TIMAC Agro Brasil, 1340 Carlos Gomes Av., 90480-001 Porto Alegre, Rio Grande do Sul, Brasil

[3]Programa de Pós-Graduação em Genética e Melhoramento de Plantas, Departamento de Biologia, Universidade Federal de Viçosa (UFV), Campus Universitário, s/n Peter Henry Rolfs Av., 36570–900 Viçosa, Minas Gerais, Brasil

[4]Programa de Pós-Graduação em Genética e Melhoramento de Plantas, Departamento de Biologia, Escola Superior de Agricultura Luiz de Queiroz (ESALQ), 11 Pádua Dias Av., 13418–900 Piracicaba, São Paulo, Brasil

Correspondence

Mariane Cristina Bianchi, Programa de Pós-Graduação em Agronomia/Fitotecnia, Departamento de Agricultura, Universidade Federal de Lavras (UFLA), Câmpus Universitário, Caixa Postal 3037, 37200-000, Lavras, Minas Gerais, Brasil
Email: maricbianchi@gmail.com

Abstract

The objectives of this study were to examine the implication of the genotype × environment interaction (G × E) in the identification of genetically superior soybean [*Glycine max* (L.) Merr.] progenies; to obtain estimates of genetic and phenotypic parameters for agronomic traits in soybean progenies; and to select genetically superior progenies to obtain lineages. Progenies $F_{3:4}$ were evaluated in the municipalities of Lavras-MG and Itutinga-MG, Brazil, in the agricultural year 2016–2017. Progenies $F_{3:5}$ were evaluated in the summer of 2017–2018 in the municipalities of Lavras-MG, Itutinga-MG, and Ijaci-MG. The traits of days to flowering, days to full maturity, plant height, bottom pod height, lodging, and grain yield were evaluated. The genetic and phenotypic parameters, expected gain from selection, genetic correlation, correlated response, achieved heritability, and frequency distribution of the adjusted means were estimated. The estimates of the components of variance showed the existence of variability among the progenies, enabling the selection of superior genotypes. There was an effect of the G × E interaction for all traits, and most of the interaction was due to complex interaction. From the analysis of genotypic correlation, significant estimates were observed between the traits. The G × E interaction affected the estimates of genetic and phenotypic parameters in the soybean, and the achieved heritability is a tool to study this interaction.

1 | INTRODUCTION

Obtaining superior genotypes each year can be considered one of the main challenges for soybean [*Glycine max* (L.) Merr.] breeders; thus, a few stages of the breeding program are key to achieving the ultimate goal. These key stages include the selection of parentals/progenitors to perform the hybridizations, identification of the best progenies to advance in the

program stages, evaluation of these progenies in different sites and agricultural years to mitigate the effect of the genotype × environment interaction (G × E), and, finally, selection of the best lineage to be launched in the agricultural market (Gesteira, Bruzi, Zito, Fronza, & Arantes, 2018).

Estimates of genetic and phenotypic parameters, such as genetic and phenotypic variances, heritability in the broad and restricted senses, achieved heritability, genetic and phenotypic correlations, and expected gains from selection, are essential for the success of breeding programs because they support decision making by the breeder. The authors emphasize the importance of obtaining the parameters from experimental data from more than one environment (year, site) because the parameters estimated from only one environment can be greatly influenced by the G × E interaction effect, which can lead to errors in decision making related to genotype selection (Soares et al., 2015).

The G × E interaction in the soybean crop has been studied, and reports were found in the literature mainly using methods to evaluate adaptability and stability (Gesteira et al., 2018; Silva et al., 2015; Soares et al., 2015). However, in the initial stages of the breeding programs, when segregating progenies are available, other tools may be employed to measure the implications of G × E to classify superior progenies. In this context, achieved heritability (h_R^2), in which the average performance of the superior progenies in different generations is evaluated, is an option.

Given the above, this study was conducted with the following aims: (i) to study the implications of the G × E interaction (crop years/generations and sites) to identify genetically superior progeny; (ii) to obtain estimates of genetic and phenotypic parameters for agronomic traits in soybean progenies; and (iii) to select genetically superior progenies to obtain lineages.

2 | MATERIALS AND METHODS

Segregant progenies $F_{3:4}$ and $F_{3:5}$ were from the cross P 98Y11 RR × BRS FAVORITA RR. The crossing was performed in a greenhouse during the 2013–2014 harvest. Manual hybridization followed a procedure similar to that described by Borém (2009). Subsequently, the seeds of the F_1 generation were multiplied in the 2014 winter season in a greenhouse, adopting two plants per pot. The population was transferred in bulk to F_3, selecting 200 plants per population in the 2015–2016 summer crop to evaluate the progenies. The plants were individually and manually threshed.

Progenies $F_{3:4}$ were evaluated in the 2016–2017 summer crop in the municipality of Lavras- MG at the Center for Scientific and Technological Development in Agriculture–Muquém Farm, located at latitude 21°14′ S, longitude 45°00′ W and altitude of 918 m in the municipality of Itutinga- MG, at Milanez Farm, latitude 21°17′52″ S, longi-

Core Ideas
- Estimates of genetic and phenotypic parameters are essential for breeding programs.
- One of the greatest challenges in plant breeding is the G × E interaction.
- Successful breeding programs require genetic variability.
- Achieved heritability is a tool to study the G × E interaction.

tude 44°39′28″ W and altitude of 969 m. Plots with a single row that was 2 m long were used with two replicates, adopting a simple lattice design 14 × 14 (194 progeny + 2 parental).

Progenies $F_{3:5}$ were evaluated in the 2017–2018 summer crop, in the previously described municipalities, Lavras-MG and Itutinga-MG, and in the municipality of Ijaci-MG, at the Center for the Development and Transfer of Technology in Agriculture of UFLA–Palmital Farm, located at 21°09′ S, 44°54′ W and altitude of 920 m. Experimental plots with 1 row that was 3 m long were adopted, using a triple lattice design of 10 × 10 (98 progeny + 2 parental).

In all evaluated environments, the no-tillage system was adopted, with sowing furrows spaced 0.50 m apart. Sowing was performed in the first half of November in all production environments. The fertilization consisted of 350 kg ha^{-1} of the formulation of N–P_2O_5–K_2O (2–30–20), applied in the furrow. Furrow inoculation was performed with the bacteria *Bradyrhizobium japonicum* after sowing at a dose of 18 ml commercial product kg^{-1} of seed-SEMIA strains 5079 and 5080, containing 10.8×10^6 colony-forming units (CFU) seed^{-1} of inoculant Nitragin Cell Tech HC (3×10^9 CFU ml^{-1}), using a four-spindle XR 11002 nozzle-coupled motorized spur, with a liquid volume of 150 L ha^{-1}.

Pest control in the crop was performed as needed using insecticides with the active ingredients tiametoxam (3-(2-chloro -1,3-thiazol-5-ylmethyl)-5-methyl-1,3,5-oxadiazinan-4-ylidene(nitro) amine), imidacloprid (1-(6-chloro-3-pyridylmethyl)-*N*-nitroimidazolidin-2-ylideneamine), and chlorpyrifos (*O,O*-diethyl *O*-3,5,6-trichloro-2-pyridyl phosphorothioate). Postemergence weed control was performed using glyphosate (*N*-(phosphonomethyl)glycine) at the dosage of 2 L ha^{-1}.

The following traits were evaluated:

- Days to flowering: 50% of the plants of the plot showing full flowering, stage R2 according to the scale by Fehr and Caviness (1977).
- Days to full maturity: 90% of the plants of the plot in stage R8 (absolute ripening) according to the scale of Fehr and Caviness (1977).

- Bottom pod height: distance from the plant root collar to the lowest node that had pods, in centimeters, of five plants taken at random;
- Plant height: distance from the plant's neck to the end of the main stem, in centimeters, measured in five plants taken at random;
- Lodging score: evaluated according to Bernard, Chamberlain, and Lawrence (1965) with the following scores: a score of 1 for all upright plants, 2 for some inclined or slightly lodged plants, 3 for all moderately inclined plants or 25–50% lodged, 4 for all plants severely inclined or 50–80% lodged, and 5 for more than 80% lodged plants;
- Grain yield: value in bags ha^{-1} after conversion to 13% moisture.

The data were analyzed using the R Development Core Team software (R Core Team, 2018) and a mixed-model approach (Bernardo, 2010). This type of approach has been developed for animal breeding but has been widely used in plant breeding (Piepho, Mohring, & Melchinger, 2008) because it is very advantageous when there are unbalanced data, resulting in more reliable predictions than those obtained by least squares, in addition to greater efficiency in the selection of superior genotypes.

The joint analysis was performed considering the model:

$$y_{ijkl} = \mu + p_i + r_{j(l)} + b_{k(jl)} + a_l + (ta)_{il} + e_{ijkl}$$

where

y_{ijkl} = observation concerning progeny i in replicate j in block k in environment l;
μ = general constant associated with all observations;
p_i = random effect of progeny i;
$r_{j(l)}$ = random effect of the replicate j within the environment l;
$b_{k(jl)}$ = random effect block k within the replicate j in the environment l;
a_l = fixed effect of the environment l;
$(ta)_{il}$ = random effect of interaction progenies × environments;
e_{ijkl} = random experimental error associated with observation y_{ijkl}.

The components of the variance were estimated using the residual maximum likelihood (REML) method. Spearman rank correlations among BLUP averages were estimated to decompose the variance of the genotype × environment interaction into simple and complex parts.

To evaluate the experimental quality, the coefficient of variation and selective accuracy were estimated (Resende & Duarte, 2007). To obtain estimates of the association between the traits analyzed, genotype correlations were analyzed according to Ramalho, Santos, Abreu, and Nunes (2012). Cor-

relation analyses were performed using the R Development Core Team software (R Core Team, 2018). Significance was verified by the Mantel test. Heritabilities (h^2) at the progeny level were obtained according to the estimator proposed by Piepho and Mohring (2007):

$$h^2 = \frac{\sigma_G^2}{\sigma_G^2 + \sigma_{GA}^2/n + \sigma_E^2/nr}$$

where

σ_G^2 = genotypic variance;
σ_{GA}^2 = variance of the genotype × environment interactions;
σ_E^2 = environmental variance;
n = number of environments;
r = harmonic mean for the number of repetitions.

The expected genetic gain from selection (GS) was estimated for all traits from the deviation of the genotypic values of the progenies at seven selection intensities (1, 5, 10, 15, 20, 25, and 30%) (Ramalho et al., 2012). Aiming to quantify the interaction effect of progenies × sites and progenies × agricultural years, as well as the influence of the interaction progenies × environments, estimates of heritability were obtained (h_R^2) at seven selection intensities (1, 5, 10, 15, 20, 25, and 30%), considering the following estimator:

$$h_R^2 = \frac{GS/mj}{ds/mi}$$

where

h_R^2 = heritability;
GS = gain from selection;
ds = selection differential;
mi = mean for progenies in F_i;
mj = mean for progenies in F_j.

In turn, the correlated response estimates (CR%) were used as the estimator:

$$CR_{y/y'}(\%) = \frac{\overline{BLUP_{y/y'}}}{\bar{y}} \times 100$$

where

$\overline{BLUP_{y/y'}}$ = BLUP means of the genotypes for trait y, after selection for trait y';
$\bar{y}$ = general mean of the genotypes for trait y'.

3 | RESULTS

The variance in the G × E interaction was significant for all evaluated traits; for the trait grain yield, most of the interaction

TABLE 1 Estimates of genetic and phenotypic parameters for trait grain yield (Yield), days to full maturity (DFM), days to flowering (DTF), plant height (PH), bottom pod height (BPH), and lodging (Lodg.). The data refer to progenies $F_{3:4}$ and $F_{3:5}$ in the agricultural years 2016–2017 and 2017–2018, respectively

| Source variation | Yield | DFM | DTF | PH | BPH | |
	bags ha^{-1}	——————days——————		——————cm——————		Lodg.
Genetic variance	13.09*	28.85*	23.00*	45.72*	2.64*	0.23*
Variance in the G × E interaction	83.28*	3.96*	1.85*	16.06*	4.78*	0.15*
Simple	(9.50)	–	–	–	–	–
Complex	(73.78)	–	–	–	–	–
Environmental variance	125.44	10.95	13.15	50.43	7.64	0.57
h^2	0.33	0.94	0.94	0.86	0.62	0.75
$r_{\hat{g}g}$%	48.43	94.55	94.19	87.52	70.53	79.51
CV%	17.36	2.24	5.28	7.74	15.30	36.25

Note. h^2, heritability; $r_{\hat{g}g}$%, accuracy; CV%, coefficient of variation.
*Significant at 5% probability by the maximum likelihood ratio test.

TABLE 2 Identification of the experimental sites, agricultural years, corresponding environments, and prediction of the effect of each environment on grain yield (bags ha^{-1})

Agricultural years	Local	Environments	Prediction of the effect bags ha^{-1}
2017–2018	Lavras	1	−5.07
2017–2018	Ijaci	2	−19.57
2017–2018	Itutinga	3	5.62
2016–2017	Lavras	4	13.36
2016–2017	Itutinga	5	5.66

is explained by the complex interaction (Table 1). This finding suggests that the progeny behavior was not similar in the evaluated environments for the different traits. It is also possible to infer that there is a significant difference between the progenies because the estimates of the genetic variance were different from zero for all the traits in the joint analysis (Table 1). The existence of variability can again be confirmed by estimates of heritability. This parameter ranged from 0.33 (grain productivity) to 0.94 (absolute ripening and days to flowering) (Table 1).

To observe the influence of the environments on the average of the progenies, for the grain yield trait, the prediction of the effect of each environment was obtained, considering the combination of site and agricultural year as the environment (Table 2).

The prediction of the effect of each environment showed how much that environment affected the average of the trait. The values of different magnitude and the effect of each environment showed once again that the progeny behavior was not similar across the evaluated environments.

The frequency distributions, for all the traits, considering all evaluated environments, are presented in Figure 1.

Similar to the estimates of the variance components, the frequency distributions of the BLUP averages highlighted the existence of variability among progenies and denoted the quantitative nature of the traits due to the continuous distribution (Figure 1).

From the graphs of genotypic value and associated errors (Figure 2), it was possible to verify that, considering the 20 best progenies evaluated in the two generations, the selection intensity was 20%, except for the productivity trait, and the others presented values different from zero—that is, there was a possibility of success with selection.

Among the traits evaluated, grain yield was the most important. Taking this as a reference, it was found that progeny 98 was the most prominent (Figure 2). However, it must be emphasized that the genotypic value associated with this treatment could assume a value of zero, that is, it can be null.

One of the major goals of soybean breeding is to increase the yield potential and reduce absolute ripening. It was possible to verify that all the estimates differed from zero. Thus, it is possible to obtain gains from the selection of progenies that show less absolute ripening.

When evaluating progenies/lineages, estimation of the gain from the selection of superior genotypes is beneficial. In this work, we obtained estimates for the joint analysis, considering different selection intensities (Table 3).

Estimates varied according to the selection intensities used. As expected, higher selection intensity, that is, selecting fewer individuals, produced a higher gain but with reduced variability (Table 3). It is also important to emphasize that the expected gain from selection, with the exception of grain yield, is negative because the selection for these traits is performed to reduce them (Table 3).

The correlated response estimates, presented in Table 4, evaluate the behavior of the progenies, for the absolute ripening and days to flowering, after selection for grain yield.
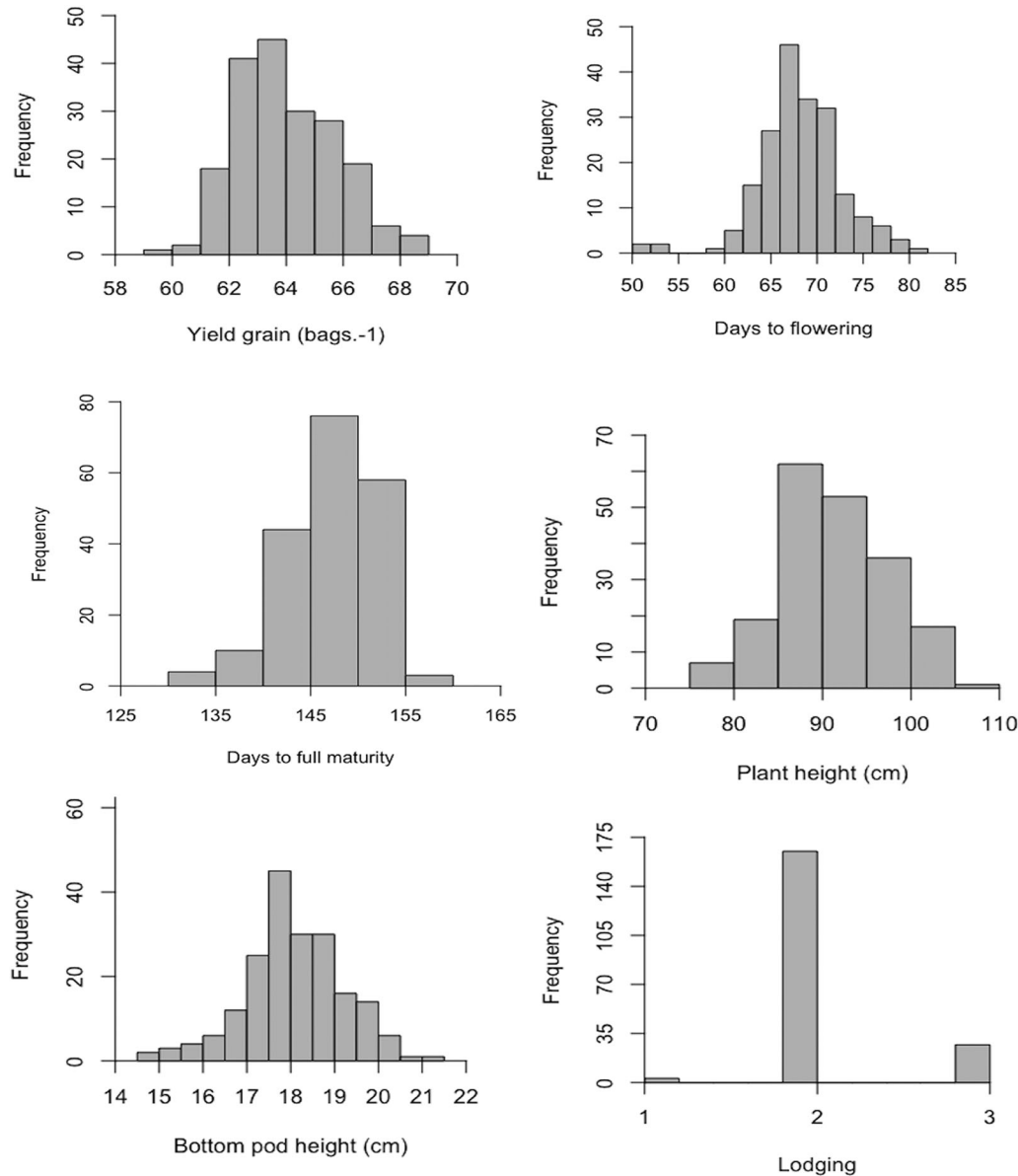
FIGURE 1 Frequency distribution for joint BLUP means of progenies $F_{3:4}$ and $F_{3:5}$ in the agricultural years 2016–2017 and 2017–2018, respectively

From the results, once the most productive progenies were selected, for the selection intensities from 1 to 15%, there was also an increase in the traits in question, with a decrease occurring for the same traits for the other selection intensities.

The estimates of achieved heritability from selection, for different selection intensities, considering progenies $F_{3:4}$ and $F_{3:5}$ in Lavras-MG, and later in Itutinga-MG, are presented in Tables 5 and 6, respectively.

The interaction genotype × years/generations is unpredictable and directly affects the results of achieved heritability. The estimation of achieved heritability considering the same site in different agricultural years allows quantifying the influence of the interaction progenies × agricultural years (unpredictable environmental factors). It is evident that there

was a change in the magnitude compared with the estimates of heritability in the restricted sense (h^2) (Table 1). For some traits, the value was negative, indicating that this component is null. However, it is important to note that, within the interaction genotype × years, the generation effect was also contained.

To better understand the behavior of the genotypes under different environmental effects, achieved heritability estimates were also obtained for the progenies $F_{3:4}$ in the Lavras-MG and Itutinga-MG sites in the agricultural year 2016–2017, progenies $F_{3:5}$ in the Lavras-MG and Itutinga-MG sites in the agricultural year 2017–2018, and the joint analysis considering all the environments of the present study (Tables 7, 8, and 9).
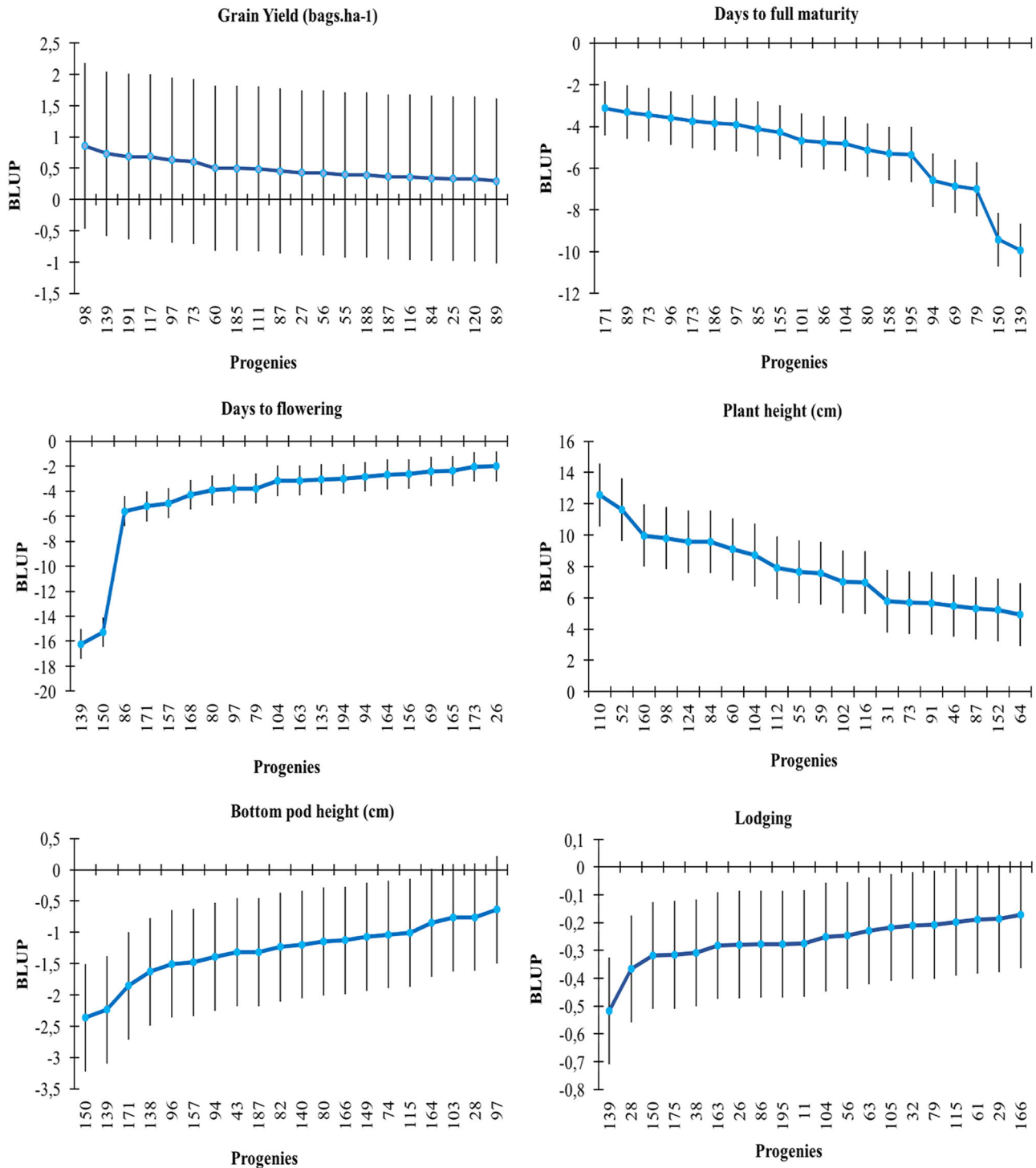
FIGURE 2 Genotypic values (BLUP) and associated errors of the 20 best progenies evaluated in the five environments for the traits grain yield, days to full maturity, days to flowering, plant height, bottom pod height, and lodging

When considering the behavior of the same genotype, in the same agricultural year, altering only the site, the effect of the interaction genotype × site is evident. Considering the observed results, it is evident that the sites have significantly altered the progeny behavior, as well as the magnitude of the estimates (Tables 7 and 8).

Considering the joint analysis, with all the environments of the present study (Table 9), we observed that, for the characteristics grain yield, plant height, and lodging, the estimates were negative, assuming zero heritability (Table 9). For the traits absolute ripening and days to flowering, the values ranged from 0.10 to 0.25 and 0.09 to 0.29, respectively,

TABLE 3 Estimates of the expected gain from the selection (EG) of the traits grain yield (Yield), days to full maturity (DFM), days to flowering (DTF), plant height (PH), bottom pod height (BPH), and lodging (Lodg.) at different selection intensities. The data refer to progenies $F_{3:4}$ and $F_{3:5}$ in the agricultural years 2016–2017 and 2017–2018, respectively

Selection intensity	EG%					
	Yield bags ha^{-1}	DFM	DTF	PH	BPH	Lodg.
		———————days———————		———————cm———————		
1%	4.61	−28.30	−23.90	−13.46	−3.31	−0.70
5%	3.75	−8.41	−14.83	−11.37	−2.65	−0.55
10%	3.17	−6.53	−10.96	−10.30	−2.14	−0.50
15%	2.87	−5.63	−9.34	−9.30	−1.84	−0.47
20%	2.60	−4.95	−8.09	−8.40	−1.59	−0.44
25%	2.36	−4.43	−7.23	−7.66	−1.41	−0.41
30%	2.15	−3.95	−6.51	−7.01	−1.26	−0.39

TABLE 4 Estimates of the correlated response after selection for grain yield, days to full maturity (DFM), and days to flowering (DTF) at different selection intensities. The data refer to progenies $F_{3:4}$ and $F_{3:5}$ in the agricultural years 2016–2017 and 2017–2018, respectively

Selection intensity	DFM	DTF
	——————days——————	
1%	1.12	1.51
5%	0.68	0.46
10%	0.49	0.15
15%	0.01	0.02
20%	−0.19	−0.11
25%	−0.49	−0.21
30%	−0.61	−0.86

being much lower than those obtained for the heritability in the restricted sense (Table 1). The results show the effect of the interaction on all evaluated traits.

4 | DISCUSSION

To be successful in plant breeding programs, the existence of genetic variability is critical (Bernardo, 2010; Ramalho et al., 2012). This study demonstrated that the components of genetic variance were significant for all evaluated traits. Thus, it is possible to infer the existence of genetic variability. The amplitude of variation observed between the BLUP averages, for the evaluated traits, also denotes the existence of variability. The significance of the genetic variance component and observed variability are due to the choice of progenitors.

In the present work, the biparental cross between elite genotypes (BRS Favorita RR × P 98Y11 RR) with excellent agronomic performance in the region and a different genetic background was used to obtain the base population. The cultivar BRS Favorita RR is a strong growth cultivar in ripening group

7.9 and is resistant to the root knot nematode. The cultivar P 98Y11 RR shows strong growth, ripening group 8.1, and resistance to the cyst nematode races 1 and 3. The use of elite and contrasting genotypes as progenitors provided the variability and good agronomic performance among the progenies, thus allowing success in the selection of superior individuals (Bernardo, 2010; Ramalho et al., 2012).

There was also the effect of the environment on the expression of the traits. In the present study, progenies were evaluated at different sites and agricultural years. Under the current condition, predictable environmental factors as well as unforeseeable ones were expected to have an effect (Allard & Bradshaw, 1964). The variation in the different environments is evident when the contribution of each environment to the averages of the progenies is observed (Table 2). Notably, the environmental variation observed in the present study was not only due to the agricultural/site year effect but also to the generation effect.

The combination of the environmental factors associated with the progenies was critical for the existence of the interaction G × Y. Thus, the progenies did not exhibit similar behavior in the different environments. Much of the interaction found was due to the complex interaction, indicating the existence of conspicuous progeny in specific environments and making selection difficult (Gesteira et al., 2018; Ramalho et al., 2012).

In any selection strategy, success is measured by quantifying the expected gain from the selection (Table 3). Higher selection intensities—that is, when fewer individuals are selected—result in higher than expected gains because individuals with a higher frequency of favorable alleles are selected. However, when using a higher selection intensity, reduced variability occurs.

The correlated response was performed by selecting the progenies with the highest grain yield and response to the absolute ripening and flowering days. A small variation was observed in the estimates for the traits in question, and, by

TABLE 5 Achieved heritability estimates for the traits grain yield (Yield), days to full maturity (DFM), days to flowering (DTF), plant height (PH), bottom pod height (BPH), and lodging (Lodg.) at different selection intensities. The data refer to progenies $F_{3:4}$ and $F_{3:5}$ in Lavras-MG in the agricultural years 2016–2017 and 2017–2018, respectively

Selection intensity	Yield bags ha^{-1}	DFM days	DTF	PH cm	BPH	Lodg.
1%	−1.77	−0.04	0.05	−0.84	1.91	−0.30
5%	−2.11	−0.05	0.07	−1.07	2.26	−0.38
10%	−2.40	−0.07	0.09	−1.21	2.56	−0.43
15%	−2.67	−0.08	0.10	−1.35	2.82	−0.50
20%	−2.97	−0.09	0.12	−1.52	3.07	−0.58
25%	−3.26	−0.10	0.13	−1.67	3.32	−0.69
30%	−3.59	−0.11	0.14	−1.87	3.64	−0.77

TABLE 6 Achieved heritability estimates for the traits grain yield (Yield), days to full maturity (DFM), days to flowering (DTF), plant height (PH), bottom pod height (BPH), and lodging (Lodg.) at different selection intensities. The data refer to progenies $F_{3:4}$ and $F_{3:5}$ in Itutinga-MG in the agricultural years 2016–2017 and 2017–2018, respectively

Selection intensity	Yield bags ha^{-1}	DFM days	DTF	PH cm	BPH	Lodg.
1%	0.06	0.35	−0.01	0.29	0.47	0.56
5%	0.07	0.40	−0.01	0.37	0.54	0.61
10%	0.08	0.50	−0.02	0.44	0.68	0.70
15%	0.09	0.59	−0.02	0.51	0.81	0.79
20%	0.11	0.68	−0.02	0.55	0.90	0.89
25%	0.12	0.78	−0.02	0.60	1.01	1.00
30%	0.13	0.89	−0.03	0.65	1.11	1.10

TABLE 7 Achieved heritability estimates for grain yield (Yield), days to full maturity (DFM), days to flowering (DTF), plant height (PH), bottom pod height (BPH), and lodging (Lodg.) at different selection intensities. The data refer to the progenies $F_{3:4}$ in the Lavras-MG and Itutinga-MG sites in the agricultural year 2016–2017

Selection intensity	Yield bags ha^{-1}	DFM days	DTF	PH cm	BPH	Lodg.
1%	−0.67	0.24	−0.13	0.96	−0.76	0.35
5%	−0.79	0.30	−0.20	1.22	−0.90	0.44
10%	−0.90	0.37	−0.26	1.38	−1.02	0.51
15%	−1.01	0.44	−0.30	1.55	−1.13	0.59
20%	−1.12	0.50	−0.35	1.74	−1.23	0.68
25%	−1.23	0.56	−0.39	1.91	−1.32	0.78
30%	−1.35	0.64	−0.42	2.14	−1.45	0.90

TABLE 8 Achieved heritability estimates for the traits grain yield (Yield), days to full maturity (DFM), days to flowering (DTF), plant height (PH), bottom pod height (BPH) and lodging (Lodg.), at different selection intensities. The data refer to the progenies $F_{3:5}$ in the Lavras-MG and Itutinga-MG sites in the agricultural year 2017–2018

Selection intensity	Yield bags ha^{-1}	DFM days	DTF	PH cm	BPH	Lodg.
1%	0.48	0.99	0.24	2.12	−1.96	0.34
5%	0.56	1.35	0.30	2.35	−2.56	0.60
10%	0.64	1.73	0.37	2.69	−2.92	0.90
15%	0.70	1.98	0.41	3.01	−3.30	1.12
20%	0.75	2.18	0.46	3.28	−3.71	1.37
25%	0.82	2.41	0.51	3.52	−4.15	1.67
30%	0.88	2.71	0.56	3.79	−4.56	1.99

TABLE 9 Achieved heritability estimates for the traits grain yield (Yield), days to full maturity (DFM), days to flowering (DTF), plant height (PH), bottom pod height (BPH), and lodging (Lodg.) at different selection intensities. The data refer to progenies $F_{3:4}$ and $F_{3:5}$ in the agricultural years 2016–2017 and 2017–2018, respectively

Selection intensity	Yield bags ha^{-1}	DFM days	DTF	PH cm	BPH	Lodg.
1%	−3.16	0.10	0.09	−1.03	2.00	−0.04
5%	−3.85	0.12	0.13	−1.23	2.34	−0.04
10%	−4.53	0.15	0.17	−1.36	3.01	−0.04
15%	−5.13	0.17	0.20	−1.50	3.58	−0.05
20%	−5.71	0.20	0.23	−1.66	4.14	−0.07
25%	−6.21	0.22	0.26	−1.83	4.66	−0.09
30%	−6.74	0.25	0.29	−2.00	5.17	−0.11

selecting the most productive progenies at selection intensities from 1 to 15%, an increase in the expression of the traits was noted and a small decrease for the other intensities (Table 4). The parents used to obtain the population were highly productive and late for the region, explaining the low variations of the correlated response.

To study the implications of the G × E interaction, the methods to assess adaptability and phenotypic stability are most commonly discussed in the literature. However, these statistical tools are recommended to study the interaction in the final stages of breeding programs, i.e., few genotypes evaluated in different environments. A question that arises for soybean breeders is the influence of the interaction in the estimation of genetic and phenotypic parameters in the early stages, when progenies are normally evaluated at different sites and agricultural years.

In this context, a little explored option by researchers is obtaining achieved heritability (h_R^2). In the present work, we obtained estimates of this genetic parameter considering the combinations genotype × years/generations (G × Y), genotype × site (G × S), and genotype × site × years (G × S × Y). Note that the estimates of h_R^2, considering the different combinations (Tables 5–9), have assumed values from negative to greater than 1.00. Estimates of h_R^2 greater or lower than the heritability in the restricted sense in the reference generation (Table 1) demonstrate the interaction effect (Lima, Ramalho, & Abreu, 2010).

The interaction influenced the performance of the evaluated progenies, especially for the effect of the G × Y interaction. Borém and Miranda (2013) commented that this phenomenon occurs frequently, especially when the sites are restricted to a smaller region, as in the present study.

The results suggest that, to minimize the effects of the G × E interaction, progeny evaluation should be performed in the greatest number of possible sites per agricultural year and that the selection of the best genotypes should also be considered in previous generations to minimize the implications of the interaction in the classification of the superior progenies.

5 | CONCLUSION

The estimates of the components of variance show the existence of variability among the progenies, allowing the selection of superior genotypes. The G × E interaction influences the estimates of genetic and phenotypic parameters in soybean. Achieved heritability is a tool to study the G × E interaction.

ORCID
Mariane Cristina Bianchi iD
https://orcid.org/0000-0001-9630-4284
Adriano Teodoro Bruzi iD
https://orcid.org/0000-0001-6909-5157
Igor Oliveri Soares iD
https://orcid.org/0000-0001-8372-2145
Flaviane De Oliveira Ribeiro iD
https://orcid.org/0000-0001-8430-9715
Gabriel De Siqueira Gesteira iD
https://orcid.org/0000-0002-4106-7346

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