

Genotypic and phenotypic parameters associated with early maturity in soybean





Abstract – The objective of this work was to estimate genotypic and phenotypic parameters associated with early maturity, and to select soybean (*Glycine max*) progenies that are high yielding and early maturing. F_{3:4} and F_{3:5} progenies were evaluated during the 2016/2017 and 2017/2018 crop years in five environments. Data on days to full maturity, days to flowering, and grain yield were collected and analyzed using the mixed model approach. Genotypic and phenotypic parameters, expected and achieved selection gains, and correlated responses were estimated. The components genetic variation and genotype x environment interaction were significant. Heritability fluctuated from 50.14%, for grain yield, to 90.37%, for full maturity. The achieved genetic gain for full maturity ranged from -0.17 to -2.57%. A positive correlation was observed among the three evaluated traits. The selection of 5.0% of the earliest-maturing soybean progenies would reduce mean grain yield by about 5.02%, but also reduce time to reach full maturity from 125 to 119 days, in detriment of 210.5 kg ha⁻¹ potential yield. Five progenies reached full maturity up to 120 days. Progeny 51 overperformed the more productive parent (NK 7074 RR), with a grain yield of 4,975 kg ha⁻¹ and 128 days to full maturity.

Index terms: *Glycine max*, mixed models, soybean breeding, succession cropping.

Parâmetros genéticos e fenotípicos associados à precocidade em soja

Resumo – O objetivo deste trabalho foi estimar parâmetros genéticos e fenotípicos associados à precocidade, e selecionar progênies de soja (*Glycine max*) que associem alta produtividade de grãos e precocidade. Progênies F_{3:4} e F_{3:5} foram avaliadas durante os anos agrícolas de 2016/2017 e 2017/2018, em cinco ambientes. Dados de dias para o florescimento, dias para maturação plena e produtividade de grãos foram coletados e analisados via abordagem de modelos mistos. Foram estimados parâmetros genéticos e fenotípicos, ganhos esperados e realizados com a seleção, e respostas correlacionadas. Os componentes variância genética e interação genótipos por ambientes foram significativos. A herdabilidade oscilou de 50,14%, para produtividade, a 90,37%, para maturação plena. O ganho realizado para maturação plena variou de -0,17 a -2,57%. Observou-se correlação positiva entre os três caracteres avaliados. A seleção de 5,0% das progênies mais precoces reduziria a média produtiva em cerca de 5,02%, mas também reduziria o tempo até maturação plena de 125 para 119 dias, em detrimento de 210,5 kg ha⁻¹ do potencial produtivo. Cinco progênies apresentaram maturação plena até 120 dias. A progênie 51 superou o parental mais produtivo (NK 7074 RR), com rendimento de grãos de 4.975 kg ha⁻¹ e 128 dias até maturação plena.


Termos para indexação: *Glycine max*, modelos mistos, melhoramento de soja, sucessão de culturas.

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Introduction

The Brazilian agricultural system is based on the double-cropping system, in which the soybean [*Glycine max* (L.) Merr.] crop is cultivated during spring and summer, followed by the cultivation of a second crop such as corn (*Zea mays* L.), which is one of the best options for the annual crop production system (Pires et al., 2016).

The state of Minas Gerais is the sixth largest soybean producer in Brazil, and the double-cropping system is widely adopted in different regions of the state (Acompanhamento..., 2021). For the southern region of Minas Gerais, the cultivation of soybean, as a major crop, has increased in importance every year, leading to several studies on: the identification of the best cultivars adapted to the growing conditions of the southern region of the state (Gesteira et al., 2015, 2018; Carvalho et al., 2020), the adaptability and stability of soybean cultivars and progenies (Silva et al., 2017; Soares et al., 2017), and the selection of soybean progenies (Ribeiro et al., 2020).

In order to maintain the double-cropping system, some traits are desirable in the spring-summer crop. Soybean breeding programs focus primarily on the development of early-maturing genotypes, which allows the second crop to be sown during periods with better rainfall (Nóia Júnior & Sentelhas, 2019). In addition, early-maturing soybean genotypes are less affected by end-of-cycle diseases, since the crop remains in the field for a shorter time (Ribeiro et al., 2020). Some early-maturing genotypes have already been selected in a study on the $S_{0.1}$, $S_{0.2}$, and $S_{0.3}$ soybean progenies (Ribeiro et al., 2020). In this scenario, Gesteira et al. (2015) highlighted the importance of adopting early-maturing soybean cultivars in the southern region of the state of Minas Gerais.

For the selection of agronomically important traits in soybean crops, the estimation of genotypic and phenotypic parameters has been widely used (Leite et al., 2016; Follmann et al., 2019). Silva et al. (2018), for example, estimated and compared genotypic parameters to evaluate different selection methods and strategies when studying 20 soybean populations, while Andrade et al. (2016) assessed the genetic gain due to selection using mixed models and multivariate approaches. Liu et al. (2019) showed how the genotype x environment (GxE) interaction impacts soybean test weight, whereas Soares et al. (2020) concluded that the

estimates of genetic and phenotypic parameters are key in soybean recurrent selection programs.

These studies show that the estimation of genotypic and phenotypic parameters is important for the success of any breeding program because it allows a better genetic understanding of the breeding populations, aiding in the decision-making process and guiding future studies.

The objective of this work was to estimate genotypic and phenotypic parameters associated with early maturity, and to select soybean progenies that are high yielding and early maturing.

Materials and Methods

Eight soybean cultivars were crossed in 2014, originating four different populations: population 1, CD 2630 RR × CD 215 RR; population 2, V-TOP RR × NK 7074 RR; population 3, CD 250 RR × NA 5909 RG; and population 4, BMX Força RR × 5D 690 RR (Table 1). Parents were selected according to the performance of these cultivars in previous experiments, conducted in the southern region of Minas Gerais, such as that of Gesteira et al. (2015), who evaluated 25 soybean cultivars during the 2012/2013 and 2013/2014 crop years. For the present work, 5 of the best-adapted cultivars, considering grain yield and full maturity, as well as 5D 690 RR, V-TOP RR, and NK 7074 RR, were selected as parents (Table 1).

The F_1 generation was cultivated in a greenhouse, and all F_2 seeds of each population were harvested.

Table 1. List of the used soybean (*Glycine max*) cultivars and their respective owner company, maturity group, and growth habit.

Cultivar	Owner company ⁽¹⁾	Maturity group	Growth habit
CD 2630 RR	Coodetec	6.3	Indeterminate
CD 215 RR	Coodetec	5.9	Determinate
CD 250 RR	Coodetec	5.5	Indeterminate
5D 690 RR	Coodetec	6.9	Indeterminate
V-TOP RR	Syngenta Ltda.	5.9	Indeterminate
NK 7074 RR	Syngenta Ltda.	7.4	Determinate
NA 5909 RG	Nidera	6.9	Indeterminate
BMX Força RR	GDM	6.2	Indeterminate

⁽¹⁾Coodetec, Coodetec Desenvolvimento, Produção e Comercialização Agrícola Ltda; Nidera, Nidera Seeds Brasil Ltda; GDM, GDM Genética do Brasil S.A.

In the field, the populations were grown in bulk up to the F₃ generation, from which the 55 most-early maturing plants were visually selected, considering their branching capacity and architecture. Plants were individually harvested, and the 34 highest yielding ones from each population were selected. The F_{3,4} and F_{3,5} progenies from all four populations were evaluated during the summer crop season of 2016/2017 and 2017/2018, respectively.

During the summer crop of 2016/2017, the F_{3,4} progenies were assessed in two municipalities in the state of Minas Gerais: Lavras (21°14'00"S, 45°00'00"W, at 918 m above sea level) and Itutinga (21°17'52"S, 44°39'28"W, at 969 m above sea level). A 12×12 simple lattice design (136 progenies + 8 parents) was used, with 2.0 m wide rows spaced 0.5 m apart.

In the summer crop of 2017/2018, a total of 56 high-yielding and early-maturing F_{3,5} progenies were selected for evaluation in the municipalities of Lavras and Itutinga, as well as in Ijaci (21°09'00"S, 44°54'00"W, at 920 m above sea level). In this case, an 8×8 triple lattice design (56 progenies + 8 parents) was used, with 3.0 m wide rows spaced 0.5 m apart.

The F_{3,4} and F_{3,5} soybean progenies were used to obtain data on grain yield (kg ha⁻¹) after conversion to 13% moisture, days required to full flowering (DTF), and days required to full maturity (DTFM) (Fehr & Caviness, 1977). DTF and DTFM were evaluated when 50% of the plot reached the R2 and R8 stages, respectively, while grain yield was measured based on the total weight of the plot.

For the 2016/2017 and 2017/2018 crop years, seed were sown in the first half of November. In-furrow fertilization was performed using 7.0, 105.0, and 70.0 kg ha⁻¹ N, P₂O₅, and K₂O, respectively. At the time of planting, *Bradyrhizobium japonicum* (Kirchner 1896) Jordan 1982 bacteria were inoculated, in the furrows, using 10.8×10⁶ colony-forming units (CFU) per seed of the Nitragin Cell Tech HC liquid inoculant (3×10⁹ CFU mL⁻¹) (Cooperoste, Pará de Minas, MG, Brazil), containing the 5079 and 5080 SEMIA strains (Universidade Federal de Lavras, Lavras, MG, Brazil). The application rate and the volume of the broth were 18 mL kg⁻¹ and 150 L ha⁻¹, respectively.

For pest control, insecticides with the following active ingredients were applied as necessary: neonicotinoid (Engeo Pleno, Syngenta Brasil, São Paulo, SP, Brazil), at a rate of 0.25 L ha⁻¹; pyrethroid

(Fastac, BASF S.A., São Paulo, SP, Brazil), at 0.2 L ha⁻¹; and chlorpyrifos (Lorsban, Dow AgroSciences Industrial Ltda., São Paulo, SP, Brazil), at 0.5 L ha⁻¹. Postemergence weed control was performed using 2.0 L ha⁻¹ glyphosate.

The data were analyzed through the R software (R Core Team, 2019), using the mixed model approach. The joint analysis of all five studied environments – combination of sites and crop seasons, i.e., Lavras 2016/2017, Itutinga 2016/2017, Lavras 2017/2018, Itutinga 2017/2018, and Ijaci 2017/2018) – was performed with the following model:

$$Y = X\beta + Zu + Wr + Tp + Qpa + \varepsilon$$

where Y is the vector of phenotypic data; X is the incidence matrix for the fixed effect of the environments; β is the vector of the fixed effect of the environments; u, r, p, and pa are the vectors of the random effects of the blocks within the replicate in the environments, the replicate within the environments, the progenies, and the progenies × environments interaction, respectively; Z, W, T, and Q are the incidence matrix for the random effects of the blocks within the replicate in the environments, the replicate within the environments, the progenies, and the progenies × environments interaction, respectively; and ε is the vector of residuals.

According to individual analyses of the joint analysis assumptions, the ratio of the higher and lower residual variance was smaller than 7 for all evaluated traits, showing that the joint analysis can be performed (Pimentel-Gomes, 2009). Moreover, based on the residual variances across the five studied environments, a homogeneous residual variance structure was chosen.

The random effects were assumed to follow a normal distribution with means and variances defined as:

$$\begin{bmatrix} u \\ r \\ p \\ pa \\ \varepsilon \end{bmatrix} : N \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} I\sigma_u^2 & 0 & 0 & 0 & 0 \\ 0 & I\sigma_r^2 & 0 & 0 & 0 \\ 0 & 0 & I\sigma_p^2 & 0 & 0 \\ 0 & 0 & 0 & I\sigma_{pa}^2 & 0 \\ 0 & 0 & 0 & 0 & I\sigma_\varepsilon^2 \end{bmatrix} \right)$$

where σ_u^2 , σ_r^2 , σ_p^2 , σ_{pa}^2 , and σ_ε^2 are the components of variance of blocks, replicate, progenies, progenies x environments interaction, and residuals, respectively.

The components of variance were estimated using the restricted maximum likelihood method, through

the R-package lme4 (Bates et al., 2015), and tested by the likelihood-ratio test, using the lmerTest R-package (Kuznetsova et al., 2017). Graphs were plotted with the aid of the GGplot2 R-package (Wickham, 2016).

Experimental quality was measured by the coefficient of variation (CV, %) and selective accuracy (\widehat{r}_{gg}) (Gezan et al., 2014), using the following equations:

$$CV(\%) = \frac{\sqrt{\sigma_E^2}}{\bar{Y}} * 100$$

where σ_E^2 is the component of variance of residuals, and \bar{Y} is the phenotypic mean of the trait.

$$\widehat{r}_{gg} = \sqrt{1 - \left(\frac{PEV}{\sigma_G^2} \right)}$$

where PEV is the variance of prediction errors, and σ_G^2 is the component of the genetic variance of the progenies.

Broad-sense heritability (h^2) at the progeny level was estimated using the equation proposed by Piepho & Möhring (2007):

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

where σ_G^2 , σ_{GxE}^2 , and σ_E^2 are the components of variance of progenies, progenies x environment interaction, and residuals, respectively; n is the number of sites; and r is the harmonic mean of the number of replicates.

The expected selection gain (SG) and the achieved gain (AG) for selection intensities of 5.0 to 40% were calculated as:

$$SG(\%) = \frac{\overline{BLUP's}}{\bar{Y}} * 100$$

where $\overline{BLUP's}$ is the best linear unbiased prediction (BLUP) mean of the selected progenies, and \bar{Y} is the phenotypic mean of the trait.

$$AG(\%) = \frac{\overline{BLUP's_{j/i}}}{\bar{Y}_j} * 100$$

where $\overline{BLUP's_{j/i}}$ is the BLUP mean of generation j progenies selected on generation i, being $j = i + 1$; and \bar{Y}_j is the phenotypic mean of the trait on generation j.

The correlated response (CR), using the full maturity trait as a reference, was obtained through the equation:

$$CR_{y/y'}(\%) = \frac{\overline{BLUP's_{y/y'}}}{\bar{Y}} * 100$$

where $\overline{BLUP's_{y/y'}}$ is the BLUP mean of trait y of the progenies selected for trait y', and \bar{Y} is the phenotypic mean of trait y.

The means of the progenies by environments were plotted in an interaction plot. Spearman's rank correlations of progenies across the environments were also estimated.

Results and Discussion

For all evaluated traits, the components of genetic variance were significant, indicating the existence of genetic variability among the progenies (Table 2). These results were expected due to the different backgrounds and characteristics – growth habits and maturity groups – of the used parents (Table 1).

The quality of the experiments ranged from good to optimal (Resende & Duarte, 2007). The CV for grain

Table 2. Joint estimation of genotypic and phenotypic parameters associated with the agronomic traits of F_{3:4} and F_{3:5} progenies of soybean (*Glycine max*) grown in the municipalities of Lavras, Itutinga, and Ijaci, in the state of Minas Gerais, Brazil, during the 2016/2017 and 2017/2018 crop years.

Parameter ⁽¹⁾	Agronomic trait		
	Grain yield (kg ha ⁻¹)	Days to full maturity	Days to flowering
σ_{GxE}^2	218,613.10**	1.99**	0.49**
σ_G^2	102,667.00**	11.98**	1.58**
σ_E^2	729,892.30	10.99	2.29
\widehat{h}^2 (%)	50.14	90.37	84.88
\widehat{r}_{gg} (%)	59.20	90.31	85.76
CV (%)	19.06	2.65	2.94
Maximum ⁽²⁾	4975.54	132.14	55.32
Minimum ⁽²⁾	3909.19	115.22	48.13
Mean ⁽²⁾	4481.54	125.30	51.53
Range ⁽²⁾	1066.35	16.92	7.19

⁽¹⁾ σ_{GxE}^2 , genotype x environment interaction; σ_G^2 , genetic variance; σ_E^2 , residual variance; \widehat{h}^2 (%), broad-sense heritability; \widehat{r}_{gg} (%), selective accuracy; and CV, coefficient of variation. ⁽²⁾ Magnitudes of the means of the best linear unbiased prediction. **Significant by the likelihood-ratio test, at $p < 0.01$.

yield was 19.06%, higher than that of 2.65% estimated for DTFM and of 2.94% for DTF. Furthermore, selective accuracy was the lowest for grain yield, which indicates that the variance of prediction errors associated with this trait was higher than that of DTFM and DTF (Table 2).

Heritability ranged from 50.14%, for grain yield, to 90.37%, for DTFM; the lowest value for grain yield can be attributed to the complexities involved in determining this trait, which is greatly affected by external factors. Andrade et al. (2016), Leite et al. (2016), and Pereira et al. (2017) reported similar

results when evaluating grain yield in soybean. This is indicative that lower genetic gains are expected for selection based on grain yield due to the trait's lower genetic nature in total phenotypic variation.

The GxE interaction component was significant for all assessed traits, which means that genotype ranking varies across the environments, affecting the selection process. Interaction plots between the mean grain yield and DTFM of the progenies across the environments are presented in Figure 1.

The GxE interaction had greater effects on grain yield than on DTFM. This result is expected for

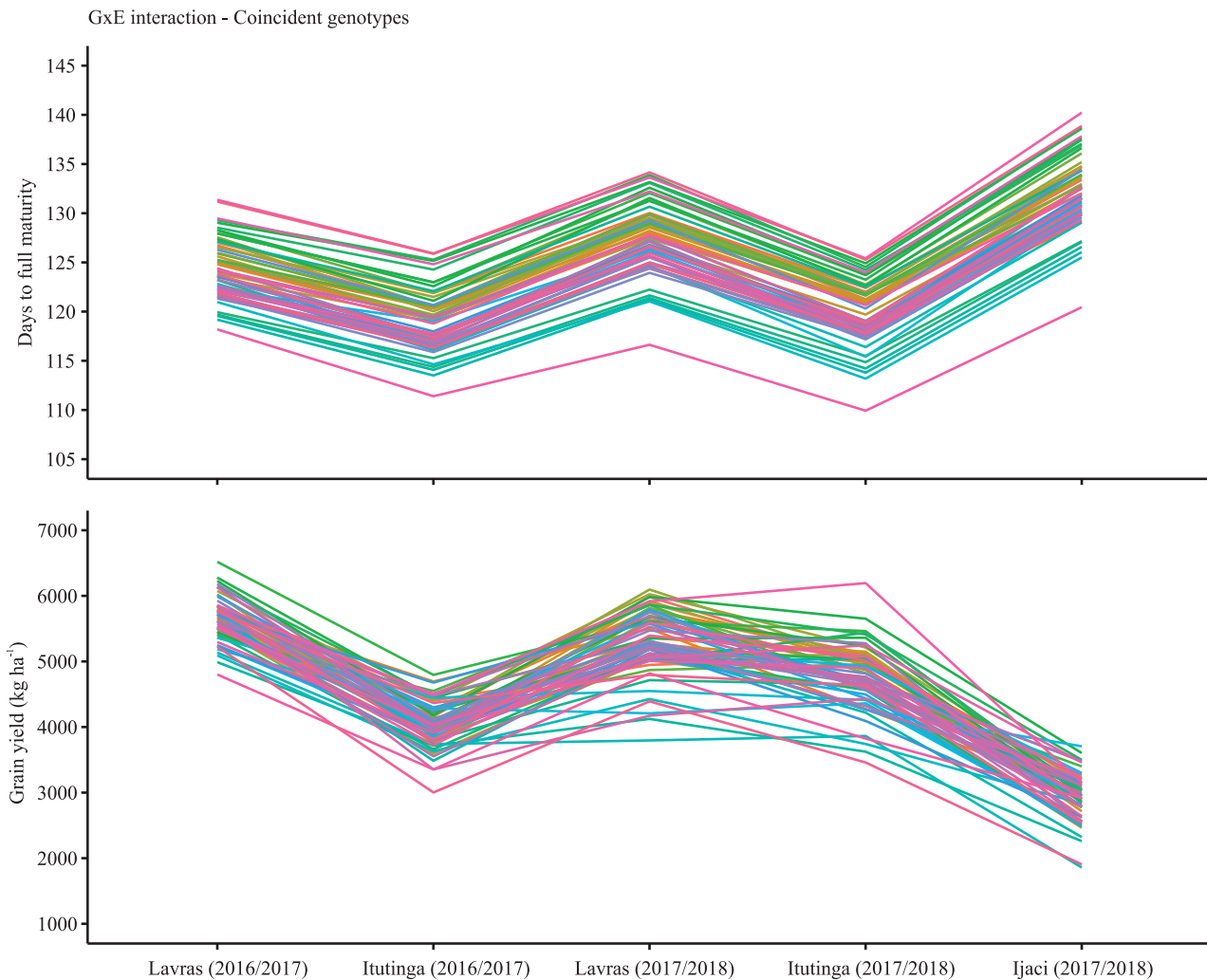


Figure 1. Interaction plot of genotype means for days to full maturity and grain yield across the five evaluated environments, i.e., municipalities in the state of Minas Gerais, Brazil, combined with crop years. Only coincident genotypes across all environments were considered.

quantitative traits, such as grain yield, as reported by Soares et al. (2020) and Ribeiro et al. (2020). Although there was a significant GxE interaction for DTF and DTFM, weaker effects are expected on the selection of early-flowering and early-maturing genotypes. Spearman's rank correlations of the genotypes in each environment emphasize these results (Figure 2).

Spearman's rank correlations indicate highly positive correlations among the environments for DTF and DTFM (Figure 2). The studied genotypes tend to perform constantly for these two traits across all environments, making genotype selection easier. However, no strong correlations (>0.6) were found for grain yield, since genotype rankings, based on this trait, tend to fluctuate in the different environments despite the positive correlations observed across them.

Soares et al. (2015), Silva et al. (2017), Zambiazzi et al. (2017), and Gesteira et al. (2018) reported a significant GxE interaction when evaluating soybean progenies in the southern region of the state of Minas Gerais. To overcome GxE interaction challenges, several strategies might be applied. In the present study, selection was performed based on the BLUPs of the main effect of the genotypes obtained in the joint analysis of variance.

Estimates of the expected genetic gain and of the achieved genetic gain for the $F_{3;4}$ and $F_{3;5}$

generations were determined at different selection intensities (Table 3). A high variation was observed in the expected genetic gains, as a function of the intensity of selection. When a few individuals are selected for a determined trait, higher selection gains are expected; however, Ramalho et al. (2012) and Cobb et al. (2019) concluded that a rigorous selection would strongly reduce genetic variability among progenies, which means that misselection in early stages would greatly impact the efficiency of the breeding pipeline.

In general, the expected genetic gain fluctuated from 3.59 to 7.42% for grain yield, and the expected reduction in time ranged from -2.06 to -3.02% and -0.91 to -2.40% for DTFM and DTF, respectively (Table 3). Ribeiro et al. (2020) reported higher expected gains when assessing the $S_{0.1}$, $S_{0.2}$, and $S_{0.3}$ soybean progenies in the southern region of Minas Gerais. Although many factors affect genetic gain, in the present work, for grain yield, the GxE interaction component was two times greater than the genetic component (Table 2), directly affecting the genetic gain (Bianchi et al., 2020).

The achieved genetic gain ranged from 0.02 to 0.23, -0.17 to -2.57, and -0.17 to -2.55% for grain yield, DTFM, and DTF, respectively (Table 3). The lower estimates for grain yield can be explained by the complexity of the trait, which is harshly affected

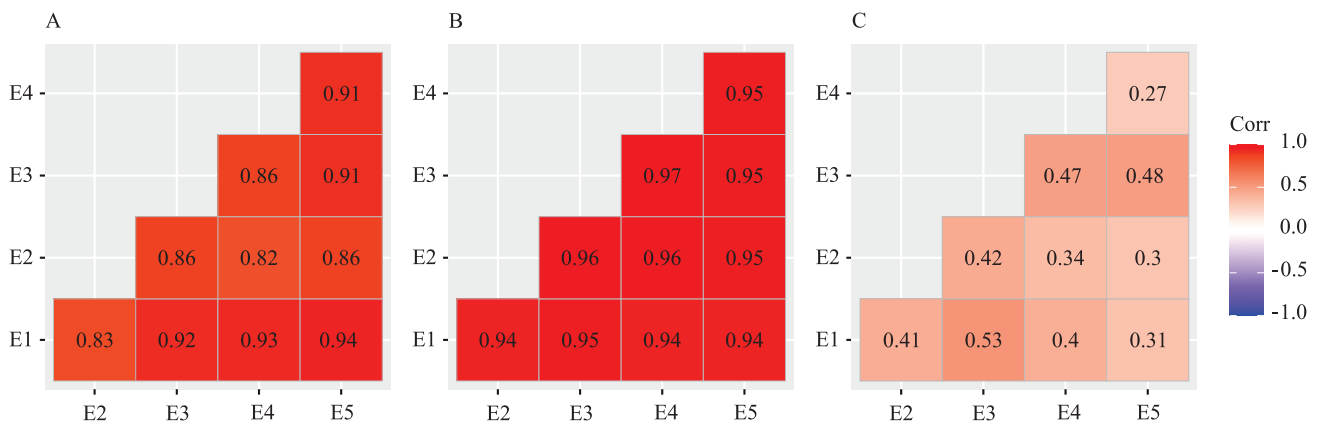


Figure 2. Spearman's rank correlation of genotypes for: A, days to flowering; B, days to full maturity; and C, grain yield across five environments (E1 to E5), i.e., municipalities in the state of Minas Gerais, Brazil, combined with crop years. E1, Lavras 2016/2017; E2, Itutinga 2016/2017; E3, Lavras 2017/2018; E4, Itutinga 2017/2018; and E5, Ijaci 2017/2018.

by location, crop year, planting date, rainfall, and other environmental factors (Gesteira et al., 2018; Ribeiro et al., 2020; Soares et al., 2020). It is important to highlight that the soybean progenies faced drought conditions at the initial stages of development in Ijaci 2017/2018, which affected progeny yield (Figure 1).

The lower estimates of the achieved gains, compared with those of the expected gains, can be primarily attributed to the genotypes x crop year interaction (Table 3). The $F_{3;4}$ progenies were evaluated at two distinct sites during the 2016/2017 crop year; therefore, for the selection of superior genotypes, it was possible to isolate the genotype x site interaction component. In the case of the $F_{3;4}$ progenies, the genotypes x crop years interaction was not considered in the estimate of the expected genetic gain due to selection. However, reports in the literature have shown that fluctuations in different crop years have a greater influence on the estimation of components of variance than site variations (Rocha et al., 2002; Zhe et al., 2010).

Table 3. Estimates of expected and achieved genetic selection gain under different selection intensities of traits of soybean (*Glycine max*) cultivated in the municipalities of Lavras, Itutinga, and Ijaci, in the state of Minas Gerais, Brazil, during the 2016/2017 and 2017/2018 crop years.

IS ⁽¹⁾ (%)	Expected genetic gain ⁽²⁾ (%)			Achieved genetic gain ⁽³⁾ (%)		
	Grain yield	DTFM	DTF	Grain yield	DTFM	DTF
5	7.42	-3.02	-2.40	0.23	-2.57	-2.55
10	6.43	-2.91	-1.99	0.15	-1.98	-1.73
15	5.89	-2.83	-1.81	0.36	-1.68	-1.25
20	5.28	-2.70	-1.59	0.99	-1.34	-0.87
25	4.75	-2.54	-1.27	0.87	-1.38	-0.76
30	4.31	-2.36	-1.14	0.63	-0.92	-0.61
35	3.91	-2.19	-1.02	0.48	-0.50	-0.48
40	3.59	-2.06	-0.91	0.02	-0.17	-0.17

⁽¹⁾Intensity of selection. ⁽²⁾Estimated expected gains for the 2016/2017 crop year. ⁽³⁾Estimated achieved gains for the 2017/2018 crop year. DTFM, days to full maturity; and DTF, days to flowering.

The full maturity trait has direct relationships with flowering and grain yield; the earlier full maturity occurs, the earlier the flowering and the lower the grain yield (Table 4). Likewise, Enideg et al. (2016), Gesteira et al. (2018), and Pereira et al. (2019) found a positive correlation between these traits.

The BLUP means of the grain yield of the 136 soybean progenies are plotted in Figure 3. Progeny 51 overperformed NK 7074 RR, the more productive parent, considering both yield (4,975 vs 4,967 kg ha⁻¹) and DTFM (128 vs 131 days).

According to Gesteira et al. (2015), for the southern region of the state of Minas Gerais, soybean cultivars with full maturity up to 125 days could be considered as early-maturing genotypes. In the present study, 59 of the 136 progenies reached full maturity in less than 125 days (Figure 3), with an overall BLUP mean of 4,432 kg ha⁻¹. Moreover, 5 progenies reached full maturity up to 120 days (Figure 3): progeny 77, with 4,431 kg ha⁻¹; progeny 75, with 4,368 kg ha⁻¹; progeny 89, with 4,319 kg ha⁻¹; progeny 93, with 4,152 kg ha⁻¹; and progeny 82, with 4,011 kg ha⁻¹. Considering these results, it is evident that it is possible to select early-maturing progenies, with grain yield performances superior to the average soybean grain yield in Brazil, which was 3,529 kg ha⁻¹ in 2020/2021 (Acompanhamento..., 2021).

Table 4. Correlated response estimate for selection, aiming to reduce time to full maturity of soybean (*Glycine max*), under different selection intensities, during the 2016/2017 and 2017/2018 crop years.

Intensity of selection (%)	Correlated response (%)	
	Grain yield	Days to flowering
5	-5.02	-1.57
10	-2.97	-1.24
15	-2.32	-0.99
20	-2.26	-0.85
25	-2.52	-0.89
30	-1.41	-0.55
35	-0.49	-0.31
40	-0.12	-0.13

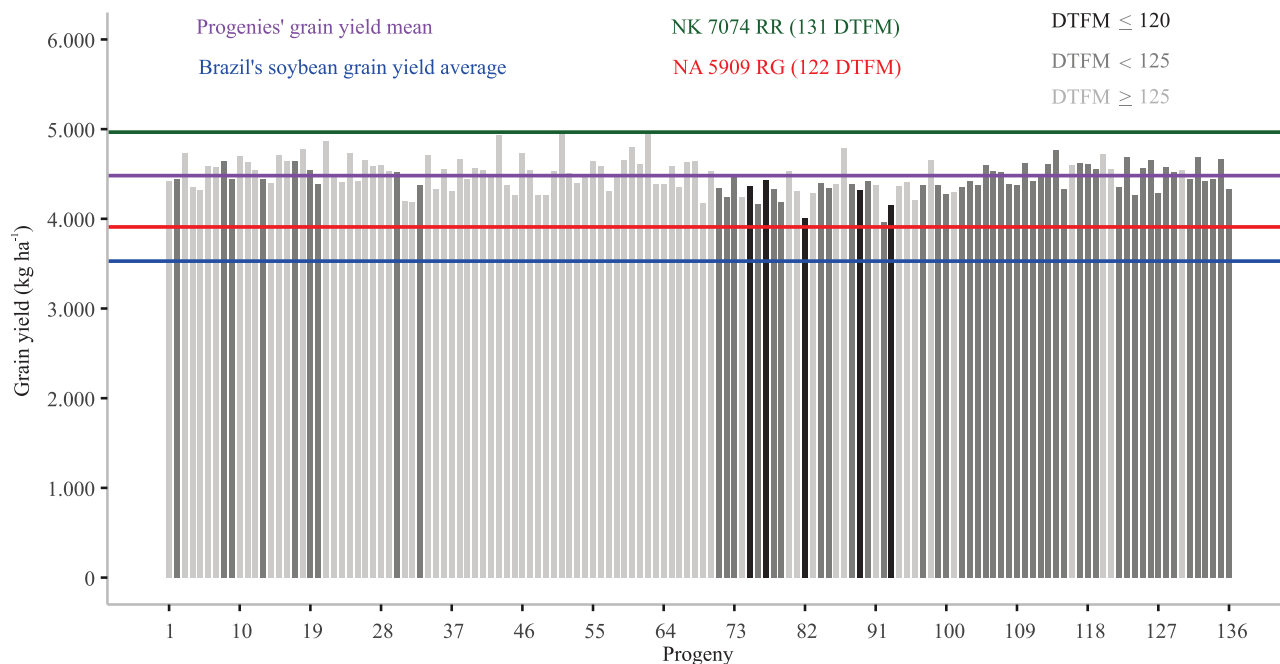


Figure 3. Means of the best linear unbiased prediction for soybean (*Glycine max*) grain yield. The grayscale indicates days to full maturity of the progenies: ≤ 120 , < 125 , and ≥ 125 . The green and red lines indicate the parents with the best (NK7074 RR) and the worst (NA 5909 RG) grain yield performance, respectively. The purple line represents the mean grain yield of the progenies, while the blue line represents the average soybean grain yield in Brazil. DTFM, days to full maturity.

Conclusions

1. It is possible to select high-yielding ($> 3,529 \text{ kg ha}^{-1}$) and early-maturing (up to 125 days to full maturity) soybean (*Glycine max*) genotypes adapted to the southern region of the state of Minas Gerais, Brazil.

2. Among the 136 soybean progenies evaluated, progenies 77, 75, 89, 93, and 82 reached full maturity up to 120 days, and progeny 51 overperformed NK 7074 RR, the more productive parent, with a grain yield of $4,975 \text{ kg ha}^{-1}$ and 128 days to full maturity.

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