

Early harvesting: an efficient technique for speed breeding in soybean

L.F.L. Mescouto¹, M.R. Piza¹, J.C. Costa², L.O. Pessoni¹, A.T. Bruzi², C.E. Pulcinelli¹ and T.T.T. DA Rocha²

¹ Departamento de Biologia, Universidade Federal de Lavras, Lavras, MG, Brasil

² Departamento de Agricultura, Universidade Federal de Lavras, Lavras, MG, Brasil

Corresponding author: A.T. Bruzi
E-mail: adrianobruzi@ufla.br

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ABSTRACT. Autogamous plant breeding programs require the advancement of many inbreeding generations to obtain a line with the most fixed loci. The time requested to obtain a new cultivar can be reduced through speed breeding protocols. This study aimed to evaluate the viability of soybean seeds at different phenological stages of development, at R6 (full developed seed) R7 (beginning of maturity) and R8 (full maturity); estimate genetic and phenotypic parameters associated with the physiological quality of immature soybean seeds; and study the feasibility of early harvesting as an alternative for soybean speed breeding protocol under tropical conditions. Thirty-two commercial and non-commercial soybean lines were utilized, sourced from cultivation and value-in-use trials within the soybean genetic improvement program at the Federal University of Lavras (UFLA). The plants were brought to the field, and the seeds were harvested at various phenological stages. After the plants in each plot reached the desired phenological stage, 10 plants were collected per plot at each evaluated phenological stage. Seed quality was assessed using the standard germination test on germitest paper, and seedling length and emergence tests were conducted in trays maintained in a plant growth chamber at a temperature of 25°C, with subsequent uniform irrigation as needed. The average percentage of cycle reduction gain with early harvest was 18.5% in the experiment aimed at precocity and 17% in the experiment

targeting grain yield. The gain in days was 18 days for the early trials and 20 days for the yield trials. It is inferred that with the adoption of an early harvest, up to four generations of endogamy can be performed per year in soybean in a high-altitude tropical climate compared to one generation in the field or 2-3 generations in winter nurseries.

Key words: Germination; Physiological quality seed; Generations of endogamy

INTRODUCTION

Due to the growing demand for food and the limited availability of land for increasing production, it is necessary to continuously improve crop yield over time. Despite advances in marker technology, statistical predictions, and genetic plant breeding methods that allow the selection of superior cultivars, one of the main bottlenecks preventing breeding programs from being more efficient is the time required from F1 generation to the release of a new cultivar (Lenaerts et al., 2019).

Autogamous species breeding programs, regardless of the method of used to segregate the population, require the advancement of 4-6 inbreeding generations to obtain a line with the most fixed loci of interest, and consequently, the process for release a new cultivar takes approximately 10 to 12 years, when considering the advance of one generation per year.

The time required for the release of a cultivar has been reduced with speed breeding protocols that reduce the recommended time to less than half for some winter crops, such as wheat, barley, chickpea, and canola (Hickey et al., 2019). Speed breeding is a methodology that accelerates inbreeding generations using light quality and intensity adjustments, temperature optimization, early harvests, and the germination of immature seeds, among other approaches (Watson et al., 2018).

For the soybean crop, a protocol using CO₂ supplementation in growth chambers under laboratory conditions increased the success rate of crosses but did not reduce the total crop cycle. CO₂ supplementation increased the growth and yield of soybean plants in growth chambers, producing a greater quantity and quality of flower buds and allowing greater efficiency of crosses when compared to those performed in the field. However, it did not reduce the number of days to flowering, an important factor in reducing generation time (Nagatoshi and Fujita, 2019).

On the other hand, a protocol to accelerate soybean flowering using a 10-hour photoperiod, different light wavelengths, and different light intensities with a light-emitting diode (LED) have been tested. The experiment with the best response used a higher light intensity; however, this approach increased costs due to the use of powerful lighting sources and high energy costs. This protocol for soybean allows up to five generations of inbreeding per year, compared to one generation in the field or 2 to 3 generations in winter nurseries. This protocol cannot be extended to other culture types with short photoperiods, especially because the quality of light needed depends on the culture (Jahne et al., 2020).

Another alternative for accelerated breeding is the use of an early harvest (Obendorf et al., 1980; Adams et al., 1983; Rosenberg and Rinne, 1986; Miles et al., 1988; Roumet and Morin, 1997). In a study with wheat, immature seeds were harvested and dried in greenhouses for three days, and from tests, high viability and vigor were observed. Early

harvesting allows a faster plant cycle when compared to the normal process of seed maturation. In this wheat study, the harvest advancement gain in days (HAGD) was 15 days (Watson et al., 2018).

A similar approach has been reported in the literature for the lentil crop. Immature seeds were removed from the pods, scarified, and placed on plates with 12 cells in a solution of 0.5 ml/cell of gibberellic acid (GA₃) (100 μM) for germination. An average cycle of 56 days was obtained with each generation. Thus, it can be inferred that by adapting this strategy, six inbreeding generations can be conducted per year, greatly reducing the number of years for the launch of a new cultivar (Lulsdorf and Banniza, 2018). For soybean crops, there are no reports in the literature on the application of this strategy in the absence of light or CO₂ supplementation.

Therefore, this study aimed to evaluate the viability of soybean seeds at different phenological stages of development, at R6 (full developed seed) R7 (beginning of maturity) and R8 (full maturity); estimate genetic and phenotypic parameters associated with the physiological quality of immature soybean seeds; and study the feasibility of early harvesting as an alternative for soybean speed breeding protocol under tropical conditions.

MATERIAL AND METHODS

Environments

The early harvest of soybean seeds evaluated in this study were from two different crop seasons and at four locations. For the 2018/2019, the seeds were produced in the experimental area of Itutinga (21°17'53" S, 44°39'28" W) and Ijaci (21° 9'51.94" S and 44°55'6.17" W), and in the 2019/2020 in the experimental area of Ijaci, Nazareno (21°12'46" S and 44° 35' 54" W), and Lavras (21°11'54.86" S and 44°58'51.09" W), Minas Gerais state, Brazil.

The climatological data for the environments in the crop seasons 2018/2019 and 2019/2020 seasons (Inmet, 2021) are shown in Figure 1 A and B, respectively.

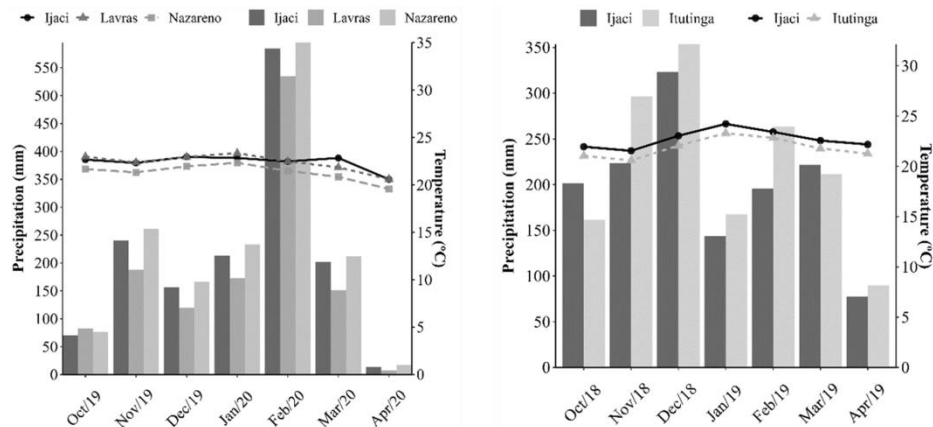


Figure 1. Monthly averages of rainfall (mm) and temperature (°C) occurring in the municipalities of Itutinga and Ijaci during the 2018/2019

Genetic Treatments

Seed of 32 genotypes from the soybean breeding program of the Federal University of Lavras (UFLA) were evaluated for their physiological quality. The lines are described in Table S1 of the [supplementary material](#).

The lines were evaluated in the field in the spring/summer crop season of 2018/2019 and 2019/2020, adopting a plot of four rows of five meters with three replicates. The seeds were harvested at stages R6, R7, and R8 according to the Fehr and Caviness (1977) scale. After the plants in the plots reached the desired phenological stage, ten plants were harvested per plot in each phenological stage. Immediately after harvest, the pods were manually threshed, and next, the laboratory tests were performed. For the cycle indeterminate cultivars, the plants were harvested in the plots, and the pods that best characterized the desired phenological stage for seed quality analysis were selected.

Laboratory analysis

All the following physiological seed quality tests were performed in the Laboratory of Seed Analysis at UFLA (LSA-UFLA) at the Department of Agriculture-DAG/UFLA:

Germination test: It was carried out in a completely randomized design (CRD) with four replications of 50 seeds, on germitest paper, moistened with distilled water, in an amount equivalent to 2.5 times the mass of the dry paper. The rolls were placed in a germinator at 25°C. The evaluations were carried out five days after sowing, and the results expressed in percentage of normal seedlings (GP) according to Brazil (2009).

Seedling length test: Performed in the CRD with four repetitions of 10 seeds on germitest paper, moistened with distilled water, in an amount equivalent to 2.5 times the mass of the dry paper and the soybean seeds were positioned so that the micropyle was facing the bottom of the paper. The rolls were placed in a germinator at 25°C. The evaluations were carried out seven days after sowing, where the radicle (RL) and hypocotyl (HL) lengths were measured using a ruler. The average results per seedling were expressed in centimeters (Nakagawa, 1999 adapted from AOSA, 1983).

Emergence test: Sowing was carried out in soil + sand substrate in a 2:1 ratio, moistened at 60% of the retention capacity. Four replications were performed in CRD with 25 seeds per treatment. After sowing, the trays were kept in a plant growth chamber at a temperature of 25° C, with subsequent uniform irrigations as needed. From the emergence of the first seedling (cotyledon completely out of the substrate) the number of seedlings emerged until stabilization was computed, with a final count 14 days after sowing. The average final percentage of emergence was considered to define the percentage of emergence (EP) value.

Statistical analysis of phenotypic data

The statistical analyses were performed using the computational environment R (R Core Team, 2021). First, an individual analysis of variance was performed for each environment, according to model:

$$y_{ij} = \mu + \tau_i + \epsilon_{ij} \quad (\text{Eq. 1})$$

where y_{ij} is the value observed in j -th repetition of the i -th treatment, μ is an overall mean associated with all observations, τ_i is the fixed effect of i -th line, and ϵ_{ij} is the experimental error due to chance.

Subsequently, a joint analysis was carried out involving: (a) the two environments of the 2018/2019 and the three environments of the 2019/2020 for the yield trials; (b) the three environments of the 2019/2020 season for the early trials. The two joint analyzes were carried out according to the model:

$$y_{ijk} = \mu + \tau_i + a_k + (\tau a)_{ik} + \epsilon_{ik} \quad (\text{Eq. 2})$$

where y_{ijk} is the value observed in the j -th repetition of the i -th line of the k -th environment, μ is an overall mean associated with all observations, τ_i is the fixed effect of the i -th line, a_k is the fixed effect of the k th environment, $(\tau a)_{ik}$ is the fixed effect of the interaction of the i -th row in the k -th environment, and ϵ_{ik} is the experimental error due to chance.

The following parameters were estimated: genotypic quadratic component (QC_g), the component variation of the environment (CV_e), the component variation of the genotype-by-environment interaction (CV_{gxe}), the genetic coefficient of determination (GCD), the coefficient of variation (CV%), harvest anticipation gain in days (HAGD) and harvest anticipation gain in percentage (HAG%).

The GCD at the genotype level was obtained according to the estimator proposed by Cruz and Regazzi (1997):

$$GCD = \frac{QC_g}{QC_g + [t/t-1] (1/a) CV_{gxe} + [CV_e/e]} \quad (\text{Eq. 3})$$

where is QC_g estimator of the genotypic quadratic component, CV_{gxe} is the estimator of the variance in the G x E interaction, CV_e is the environmental variance estimator, and t is the number of treatments and e is number of environments.

In this study, the experimental precision was measured using the coefficient of variation (CV%), which was obtained according to the estimator:

$$CV\% = [(CV_e^{1/2})/m] * 100 \quad (\text{Eq. 4})$$

where CV_e is the environmental variance estimator and m is the general phenotypic mean.

The estimated HAGD was obtained according to the estimator:

$$HAGD_{(days)} = HD_{R8} - HD_{R6} \quad (\text{Eq. 5})$$

$$HAGD_{(days)} = HD_{R8} - HD_{R7} \quad (\text{Eq. 6})$$

where HD_{R6} is the harvest date at R6, HD_{R7} is the harvest date at R7, and HD_{R8} is the harvest date at R8.

In turn, the estimated gain with HAG% was obtained according to the estimator:

$$HAG\% = [(\sum ma / t) * (1/ma - HAGD_{(days)}) * 100] - 100 \quad (\text{Eq. 7})$$

where ma is full maturation of the line.

RESULTS AND DISCUSSION

According to the joint analysis of variance, there was a significant difference ($p \leq 0.05$) in the physiological potential of immature (R6 and R7) and mature (R8) soybean seeds between genotypes, except for the variables EP and RL in R8, and between environments, showing that the genotypes differed from each other and that there was an effect of the environment on the phenotypic manifestation of the trait. The GxE interaction was significant for all traits (Table 1), showing a variation in the behavior of genotypes in the different environments.

Table 1. Summary of the joint analysis of variance ($\text{prob} > F_c$) of data of seedlings from seeds harvested at phenological stages R6, R7, and R8 in the state of Minas Gerais, Brazil.

Source of variation	Df	$\text{prob} > F_c$											
		R6				R7				R8			
		EP	GP	RL	HL	EP	GP	RL	HL	EP	GP	RL	HL
Early trials													
Genotype (G)	15	**	**	**	**	**	**	**	**	ns	**	ns	**
Environment (E)	2	**	**	**	**	**	**	**	**	*	**	**	**
GxE	28	**	**	**	**	*	**	**	**	*	**	**	**
General mean		73.9	32.3	4.9	4.8	93.5	68.7	12.0	10.	96.8	95.1	15.4	10.9
CV (%)		17.7	19.2	17.9	11.5	6.7	8.39	36.8	38.5	3.9	3.1	25.5	5.6
Yield trials													
Genotype (G)	15	**	**	**	**	**	**	**	**	**	**	**	**
Environment (E)	4	**	**	**	**	**	**	**	**	**	**	**	**
GxE	58	**	**	**	**	**	**	**	**	**	**	**	**
General mean		74.3	44.1	7.8	7.0	88	60.2	10.8	8.5	88.4	62.4	12.5	7.9
CV%		13.1	14.5	13.5	12.2	6.4	9.6	10.0	9.1	6.3	6.4	8.5	8.7

Emergence percentage (EP), germination percentage (GP), radicle length (RL), and hypocotyl length (HL), degrees of freedom (Df) and coefficient of variation in percentage (CV). *Significant at 5%, ns not significant according to the F test.

In the joint analysis, the CV% observed for most of the traits evaluated in stages R7 and R8 was of excellent quality, below 10%, and of good quality, and that observe for most of the traits evaluated in stage R6 was between 10% and 20%. Malosetti et al. (2016) noted that the GxE interaction can be attributed to predictable and unpredictable environmental factors. In the present study, as genotype evaluations were available not only at different locations but also in different season, both factors influenced the magnitude of the interaction. Considering the climatological data during the seed production period in the field experiments, it was possible to observe that there were differences mainly due to the average rainfall and temperature (Figure 1).

The range of water requirements for a soybean crop to complete its physiological cycle ranges from 450 to 800 mm (Embrapa, 2013). In the 2019/2020 season, high rainfall was observed near the end of the crop cycle, reaching 600 mm only in the month of February, in all environments where the experiments were conducted (Figure 1B).

The early genotypes showed a mean emergence of 73.95% in R6. It can be observed that the plants showed a good emergence rate using immature seeds. Regarding germination, a low rate was observed in immature seeds. For the early genotypes, the emergence rate was 32.39% at R6. In turn, the later and more productive genotypes showed a 44.18% emergence rate at R6 (Table 1). The lower germination rates may be related to

fungal proliferation due to the high-water content found in the immature seeds (Table 1). Jahne et al. (2020) also obtained a low germination rate by harvesting immature soybean seeds developed in a controlled environment and in LED chambers.

The average germination at phenological stage R5.3 (56 days after sowing) was 50%. It increased to 90% at the R5.6 stage, 77 days after sowing. Even with lower germination rates in the early harvest, it was possible to obtain seedlings in sufficient quantities to advance the generations, which in practice enables early harvest for early breeding purposes. Evaluating the early harvest of oat panicles, Barrios et al. (2020) concluded that at 21 days after flowering it was possible to obtain acceptable germination levels for all evaluated genotypes.

Regarding RL, there was an increase in the means from R6 to R8, which was observed in the early and late genotypes. The HL of the early genotype seedlings increased from R6 to R8, with a lower mean at R6, 4.83 cm, and a greater mean at R8, 10.91 cm. In turn, the HL of late genotypes showed similar behavior in all stages, at 7.01 cm at R6, 8.52 cm at R7, and 7.9 cm at R8 (Table 1).

This result may have occurred because immature seeds have fewer reserves accumulated in the cotyledons, and therefore, fewer reserves are available to the embryos when they are developing to form the seedlings. For seed weight, Teng et al. (2009) showed a difference depending on their developmental stages, showing that it is a dynamic process and depends on time. According to these same authors, the numbers of QTL (Quantitative Trait Loci) related to the average soybean seed weight and their genetic effects vary at different stages of development, especially in the early stages. In this study, the mean RL and HL at stage R8 were higher than those obtained by Monteiro et al. (2021), who worked with soybean seeds in different environments in Minas Gerais.

Monteiro et al. (2021) observed that a correlated response indicated that more productive genotypes had better physiological soybean seed quality. This assertion is in agreement with the means obtained in this study for the seeds harvested at R6. It was found that the productive genotypes obtained higher rates for all evaluated attributes of physiological seed quality compared to those of the early genotypes. However, the opposite was observed for the seeds at R7 and R8 (Table 2).

A possible explanation for this response at the more advanced stages of maturation can be attributed to the high volume of rainfall in the last stages of soybean in the 2019/2020 crop season. The main environmental factor associated with reduced germination potential is the occurrence of rainfall during harvest. The increase in moisture allowed the seeds to deteriorate more easily and increased the potential for pathogens to occur in the seeds (Zambiazzi et al., 2017).

It was observed that the CV_{gxe} was high, especially for the emergence and germination of the immature seed attributes. On the other hand, the RL and HL were low (Table 2). Monteiro et al. (2018) obtained estimates similar to those found in this study. However, it is important to emphasize that in their study, only soybean seeds harvested at the absolute maturation stage (R8) were used.

The estimates of the QC_g of the experiments were lower than the CV_{gxe} and the CV_e for all evaluated traits (Table 2). This indicates that the variation observed for these parameters, in most cases, was due to environmental effects. The GxE in soybean is frequently reported in the literature, especially for morpho-agronomic characteristics

(Amaral et al., 2019; Carneiro et al., 2019; Gesteira et al., 2018; Monteiro et al., 2018; Zambiazzi et al., 2017; Soares et al., 2015; Silva et al., 2015).

In this study, the GxE was expected because the genotypes were evaluated in different environments. Differences in soil fertility, temperature, rainfall, and other factors are common in high-altitude tropical regions (Malosetti, et al., 2016).

The GCD is a parameter related to heritability, and its greatest importance is linked to its predictive function (Ramalho et al., 2012). The estimates of GCD corroborate the estimates observed for the QC_g s since the estimates obtained were low to average values, ranging from 8.09 to 65.66% (Table 2). All variations in these characteristics, i.e., approximately half of them, were of genetic origin, and the other variation was possibly related to environmental effects or experimental deviations. These results for the GCD allowed us to infer that the characteristics related to seed quality were largely influenced by environmental factors, thus corroborating the results reported by Zambiazzi et al. (2017) in an evaluation of soybean seed quality in different environments of southern Minas Gerais.

Table 2. Estimates of genetic and phenotypic parameters of the soybean genotypes from the early and yield trials of the seedlings from seeds harvested at phenological stages R6, R7, and R8 in the state of Minas Gerais, Brazil.

Paramet.	R6				R7				R8			
	EP	GP	RL	HL	EP	GP	RL	HL	EP	GP	RL	HL
Early trials												
QC_g	33.7	96.0	0.8	0.4	5.8	100.7	1.3	0.7	0.9	9.0	1.0	0.2
CV _e	56.9	33.1	1.1	0.2	3.4	2.7	0.4	0.2	0.3	5.5	0.0	0.2
CV _{gxe}	204.9	224.2	2.3	1.3	8.6	449.5	5.6	4.5	2.5	8.3	1.5	1.9
CV _r	172.1	38.8	0.7	0.3	40.3	33.3	1.9	1.5	14.3	8.9	1.5	0.3
GCD (%)	26.7	51.1	40.3	44.4	57.8	38.2	37.4	30.0	48.8	65.0	65.5	25.5
Yield trials												
QC_g	88.4	152.0	2.0	0.9	46.8	97.5	3.2	1.0	18.3	14.5	0.9	0.5
CV _e	62.3	146.1	1.6	0.7	24.7	796.2	2.8	7.3	40.7	775.6	9.6	7.6
CV _{gxe}	401.4	283.5	3.7	1.6	113.1	366.9	6.2	3.2	88.4	45.3	1.7	1.1
CV _r	95.8	41.0	1.1	0.7	32.2	34.2	1.1	0.6	31.9	15.5	1.1	0.4
GCD (%)	47.3	62.8	64.6	65.6	61.6	29.1	62.8	32.7	40.3	8.0	29.6	23.5

Paramet: Parameters, Emergence percentage (EP), germination percentage (GP), radicle length (RL), and hypocotyl length (HL), Genotypic quadratic component (QC_g), component of variation of the environment (CV_e), Component of variation of the genotype-by-environment interaction (CV_{gxe}), Residual variation component (CV_r) and genetic coefficient of determination (GCD).

It was observed that the early genotypes that showed the best performance for most of the traits evaluated were 4, 28, 31, 33, and the control M5947. The productive genotypes that showed the best performance for most traits were 2 and the control CZ48B32 IPRO. Analyzing only the immature seeds (R6 and R7), compared to that of plants germinated on the germitest paper, the emergence of plants in the tray performed better (Figure 2). Because these seeds had higher water content, they were possibly more prone to fungal attacks, which decreased the germination potential on the germitest paper. These same outcomes were observed by Zambiazzi et al. (2017) and corroborate the findings of this study.

The genotypes that showed better seed quality attributes did not coincide with the genotypes that obtained greater HAGD. Considering these two factors, the CZ48B32 IPRO genotype is notable as it showed high HAGD and had high EP, GP, and RL values and a lower HL value (Figure 2).

Plants from immature seeds at R6 and R7 showed good development under growth chamber conditions of 25 °C, 12 h of light, and 12 h of dark, in trays with soil and sand substrate at a ratio of 2:1 and moistened to 60% of the retention capacity.

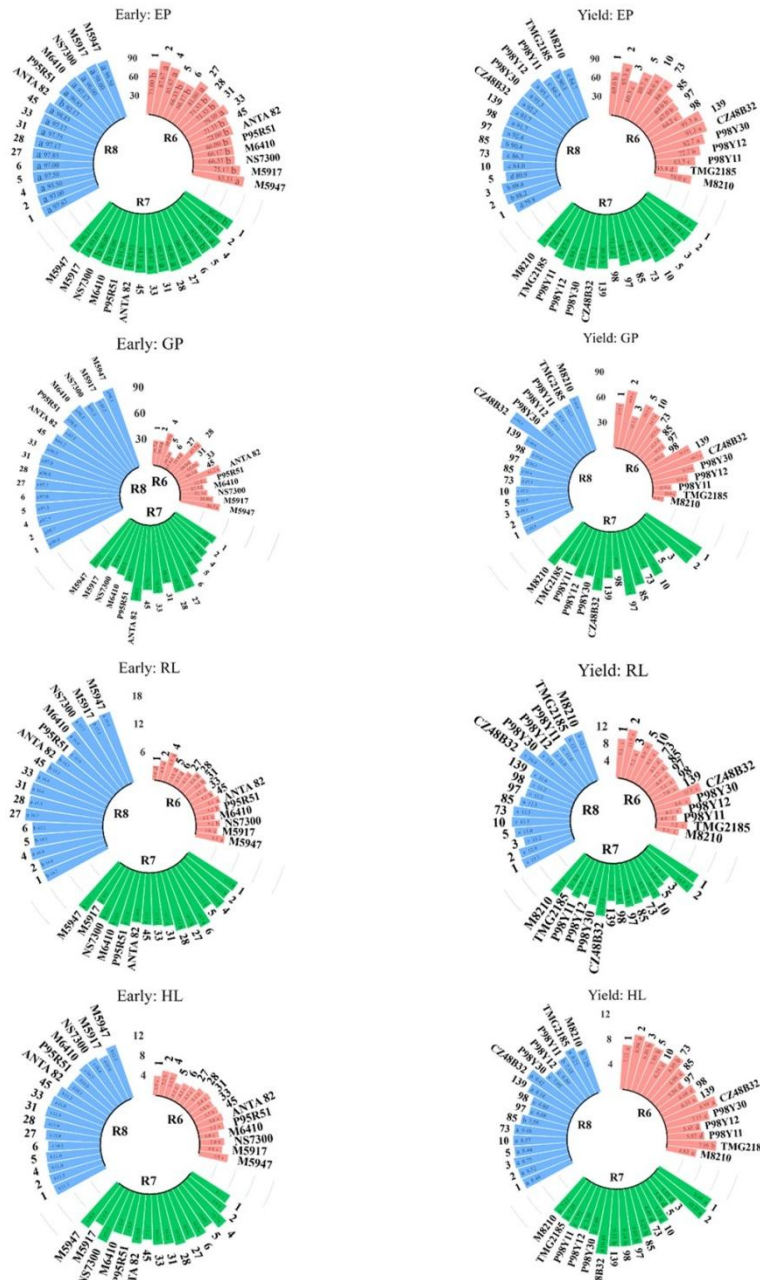


Figure 2. Mean values of emergence percentage (EP), germination percentage (GP), radicle length (RL), and hypocotyl length (HL) of the seedlings from seeds harvested at phenological stages R6, R7, and R8 of the early and the yield trials in the state of Minas Gerais, Brazil.

Regarding RL and HL, the productive genotypes showed greater variation and greater length than the early genotypes (Figure 2). Considering that speed breeding protocols usually use growth chambers with a controlled environment, in which space is a limiting factor, the objective is to obtain plants with shorter HLs that are more uniform.

The early genotypes had the most desirable traits (Figure 3A). These results corroborate the behavior of these genotypes in the field. In comparison to productive genotypes, early genotypes are shorter, more compact, and generally less productive (Sediyama et al., 2015).

Fungi are the main pathogens associated with soybean seeds (Santos et al., 2016). They can reduce germination and vigor and serve as the primary foci of diseases (Danielli et al., 2011). In soybean seeds recently harvested in the southern region of Minas Gerais, the main types of fungi found in the evaluation were *Cercospora kikuchii*, *Fusarium*, and *Alternaria* (Zambiazzi et al., 2017). These pathogens in the soybean seeds are the most frequently found in Brazil and are of great importance, as they can cause significant losses in production and reduction in seed quality (Goulart, 2018).

The estimated HAGD was determined for each genotype (early or yield) in each environment per harvest, as shown in Figures 3 and 4. The HAGD indicates the advancement in harvest gain for each genotype in relation to absolute maturation. The early genotype of the 2019/2020 harvest that obtained the highest average HAGD in the three environments was the ANTA 82 RR cultivar at 25 days. The environment that provided the greatest HAGD for the genotypes was Nazareno, with a mean of 18 days (Figure 3A).

In comparison to the other environments, this environment is higher in altitude with milder temperatures. In general, milder temperatures occur at high altitudes. Thus, the cultivars showed lengthened vegetative cycles, excessive plant growth, lengthened nodes, flower and pod death, and greater plant lodging.

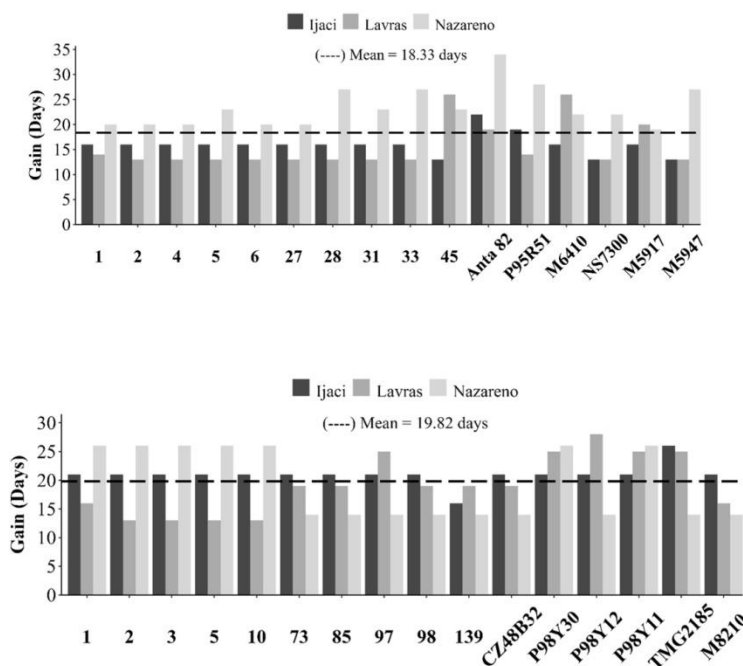


Figure 3. Harvest advancement gain in days for immature seeds (stage R6) of the soybean genotypes early trials(A) and yield trials (B) in the state of Minas Gerais, Brazil.

The yield genotypes of the 2019/2020 harvest that obtained the highest HAGD in the three environments were P98Y30 and P98Y11 at 24 days. The environment that provided the greatest gain for the late genotypes was also Nazarene, with a mean of 20 days (Figure 3B). The productive genotypes of the 2018/2019 harvest had the same average HAGD considering the two environments. The environment that provided the greatest HAGD in the stage R7 for the genotypes was Ijaci, with a mean of 17 days (Figure 4).

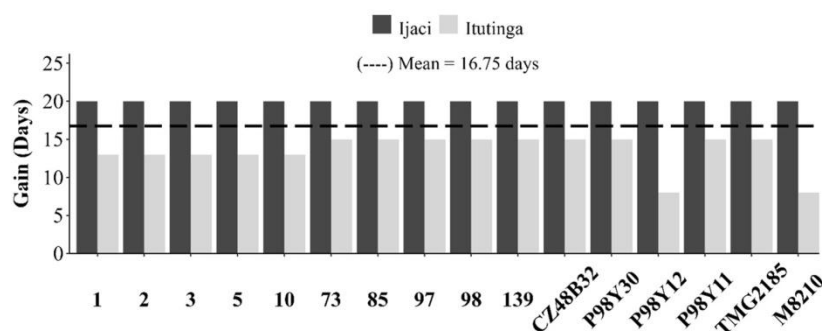


Figure 4. Harvest advancement gain in days for immature seeds (stage R7) of the soybean yield trials in the state of Minas Gerais, Brazil.

The HAGD varied according to the maturity of group. The early genotypes had an average HAGD of 18 days, while the yield genotypes had a higher average HAGD of 20 days. The gain obtained in this study was higher than that obtained by Watson et al. (2018) with wheat seeds harvested while still immature and dried in greenhouses for three days. When compared to the normal process of seed maturation, there was a HAGD of 15 days for this harvest.

Therefore, it can be inferred that the HAGD was more significant in the genotypes of the yield experiment than in those of the early experiment. A possible explanation for this difference is that the former genotypes have greater absolute maturation, they spend more time in the field and take longer to reach absolute maturation, providing greater time between the maturation stages of the plant and, consequently, a greater HAGD when the harvest is advanced to previous stages (Sediyama et al., 2015). This makes this alternative more advantageous for genotypes that have a greater number of days for absolute maturation.

The early genotypes that obtained higher gains and were more stable in all environments were Lines 1, 2, 4, 5, and 6, with a gain of 17 to 30%. The P95R51 cultivar had a gain of 23 to 44%. The gain in percentage of each genotype varied according to the environment. In Nazareno, the HAG% was higher than those in the other environments. The early genotypes that obtained the lowest gains were the NS7300, M5917, and M5947 cultivars, with a HAG% below 15%.

On the other hand, the yield genotypes of the 2019/2020 harvest that obtained the highest HAG% and were most stable in all environments were Lines 1, 2, 3, 5, and 10, with a HAG% of 17 to 33%. The P98Y11 cultivar had a HAG% of 20 to 26%. The Nazarene environment provided greater gains for the genotypes with shorter cycles compared to the environments of Ijaci and Lavras. The production genotypes that obtained the lowest

HAG% were Lines 73, 85, 97, 98, 139 and the control CZ 48B32 IPRO, with HAG% below 15% (Figure 5).

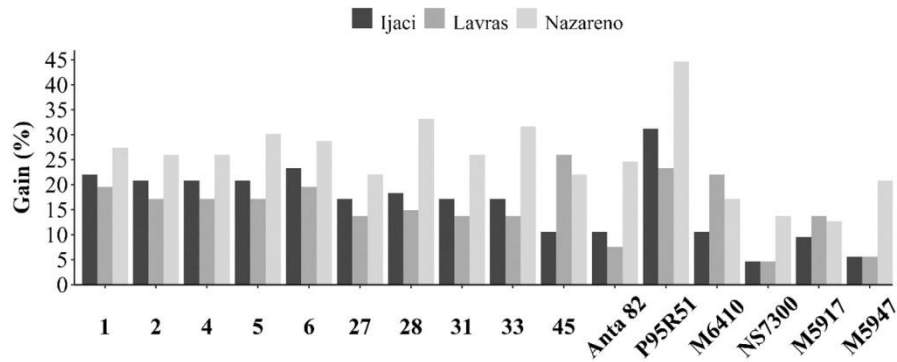


Figure 5. Gain, in percentage, of anticipation of the harvest of immature seeds (stage R6) of soybean genotypes from the early trials in the state of Minas Gerais, Brazil.

The yield genotypes of the 2018/2019 harvest that obtained the highest HAG% were the same as those of the 2019/2020 harvest. It should be emphasized that in this harvest, the HAG% was in relation to the R7 stage, so the HAG% was of lesser magnitude than that of the yield genotypes of the 2019/2020 harvest, which was in relation to the R6 stage. The yield genotypes of the 2019/2020 harvest that had lower HAG% values were the same genotypes as those of the 2018/2019 harvest (Figure 6 A and B).

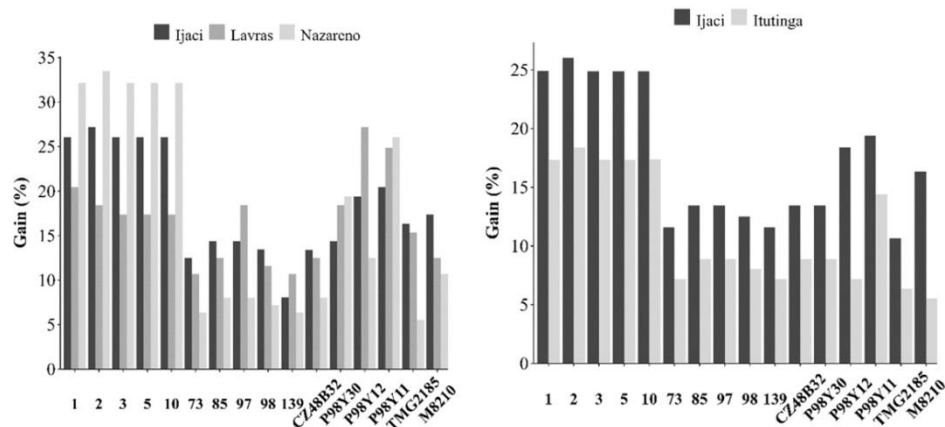


Figure 6. Gain, in percentage, of anticipation of the harvest of immature seeds of soybean genotypes of the yield trials at the R6 stage (A), and at the R7 stage (B) in the state of Minas Gerais, Brazil.

The general mean cycle of the early experiment and the yield experiment are shown in Figure 7. The early experiment had an average cycle of 117 days, and the yield experiment had an average cycle of 136 days in the field, from sowing to harvest after the plant reached absolute maturity (R8), in a normal cycle. In the accelerated cycle, the early experiment had an average cycle of 98 days, and the yield experiment had an average cycle of 116 days, from sowing to harvest of immature seeds in R6.

The reduction gain of the cycle for the early experiment and for the yield experiment is shown in Figure 7. The average HAG% was 18.5% for the early experiment and 17% for the yield experiment. Considering that the HAG% values were different for the early and yield experiments, as well as for the accelerated cycle of each generation and one average cycle of 110 days of soybean cultivars under the high-altitude tropical climate conditions of this study, it is inferred that up to four generations of soybean per year can be obtained using early genotypes and up to three generations per year can be obtained with productive genotypes.

These results were obtained under field conditions in the Campos das Vertentes region of Minas Gerais, which has a high-altitude tropical climate, and these results may vary considering different climatic conditions. In the study by Jahne et al. (2020), performing up to five soybean generations per year in a growth chamber with different lengths of LED lights and high light intensity is recommended to increase speed breeding under different cultivation conditions.

The use of supplemental lighting in a glasshouse environment allows rapid generation cycling through single seed descent (SSD) and potential for adaptation to larger-scale crop improvement programs (Watson et al. 2018). Similar results were obtained by Gallino et al. (2022). These authors used a modified cold room equipped with fluorescent lamps, which allows the development of up to 5 generations per year, instead of the 1-2 generations currently possible under field or greenhouse conditions.

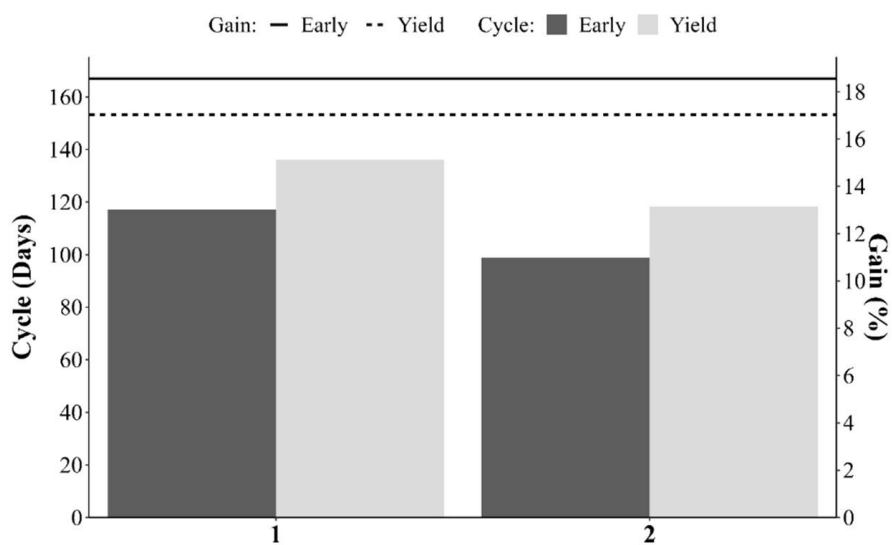


Figure 7. Overall mean cycle of the early experiment and the yield experiment in the field without an early harvest (1) and with an early harvest (2) and their respective cycle reduction gains.

CONCLUSIONS

Immature seeds at stages R6 and R7 showed good growth development under chamber conditions at 25 °C, with 12 h of light and 12 h of dark, in trays with soil and sand substrate at a 2:1 ratio, moistened at 60% of the retention capacity. The estimates of the QC_g

and the GCD were low to medium values, indicating that the characteristics related to seed quality are largely influenced by environmental factors.

The early genotypes obtained an HAGD of 18 days and a reduction of 18.5% in the cycle, and the productive genotypes had an HAGD of 20 days and a reduction of 17% in the average cycle. Early harvesting at R6 can be used in soybean breeding programs, thus enabling up to four inbreeding generations per year for the early genotypes and three generations per year for the late genotypes.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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