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Crop Breeding & Genetics

Genetic improvement of soybeans in Brazil: South and Midwest regions

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Abstract

Soybean [*Glycine max* (L.) Merrill] is one of the main crops produced worldwide, and on-farm yields have increased considerably in the last decades in Brazil. We evaluated the genetic gain for agronomic, phenological, and end-use quality traits in 29 cultivars in the South Region, and in 38 cultivars in the Midwest Region in Brazil, released from 1966 to 2011. Field trials were conducted in Macroregions 1, 2, and 4, in 2016–2017, 2017–2018, and 2018–2019 crop seasons. The best linear unbiased predictors (BLUP) of the cultivars were obtained for each trait using a linear model. The BLUPs were regressed with the year of release using linear and quadratic regression models. The rates of genetic gain for seed yield ranged from 11.98 to 15.31 kg ha⁻¹ yr⁻¹

Abbreviations: BLUP, best linear unbiased predictor; BPH, bottom pod height; DF, days to flowering; DM, days to maturity; LS, lodging score; MG, maturity group; MR, Macroregion; OIL, seed oil content; OILY, oil yield; PH, plant height; PROT, seed protein content; PROTY, protein yield; RP, reproductive period; RR, Roundup Ready; SY, seed yield; TSW, thousand-seed weight.

(0.33 to 0.42% yr⁻¹) in the South Region, and from 13.58 to 21.84 kg ha⁻¹ yr⁻¹ (0.47 to 0.77% yr⁻¹) in the Midwest Region. New cultivars presented taller plants and more seed oil content, oil and protein yield, and lower seed weight, days to flowering, days to maturity, and seed protein content than old cultivars in the South Region, although with differences between the Macroregions. In the Midwest Region, new cultivars showed higher seed oil content, oil and protein yield, and lower bottom pod height and seed protein content than old cultivars. Our results showed that breeding programs have been efficient to improve soybean yield and other traits across the years, without yield plateaus in sight.

1 | INTRODUCTION

Soybean [*Glycine max* (L.) Merrill] is one of the most important crops produced on a large scale worldwide and is one of the main commodities currently traded. World soybean production in the 2019–2020 crop season was 339.42 million t (USDA, 2021), and Brazil became the world's largest producer with 124.84 million t (Conab, 2021). The United States and Argentina ranked as the world's next largest producers, with 96.67 and 48.80 million t yr⁻¹, respectively. Collectively, these three countries account for approximately 80% of the total amount of soybean produced worldwide (USDA, 2021).

Although the first reports of soybean cultivation in Brazil date from 1882, only after the 1970s did the crop begin to present significant economic importance in the country (Specht et al., 2014). At that time, the cultivation was concentrated mainly in the South Region (lat. 22 to 30°S), in an area of only 6.95 million ha and production of 12.15 million t, using plant introductions from southern United States (Conab, 2020; Specht et al., 2014). Since then, soybean has grown from a secondary crop to one of the most important crops in Brazilian agribusiness. In the 2019–2020 crop season, the crop area in Brazil was 36.95 million ha (Conab, 2021).

In addition to the expansion of the cultivated area, the soybean on-farm yield in Brazil has also increased considerably in recent decades, from 1,748 kg ha⁻¹ in the mid-1970s to 3,379 kg ha⁻¹ in the 2019–2020 crop season (Conab, 2020). The yield increases are the result of improvements in management practices, as well as the performance of the breeding programs over the years, which were responsible for release increasingly productive cultivars that met the needs of growers.

Several institutions have contributed to the release of soybean cultivars in Brazil. Primarily, the public sector, including state and national research institutions, and universities, was responsible for a great part of breeding efforts. Subsequently, successful public–private associations were developed, and

other institutions, including private foundations and cooperatives, also contributed significantly to cultivar release (Specht et al., 2014). However, the number of cultivar releases in Brazil significantly increased with the approval of the Variety Protection Law on April 25, 1997 (Brasil, 1997; Specht et al., 2014). This law allowed the investments of large national and multinational companies to become viable. Initially, they had not shown interest in the Brazilian cultivar market due to the absence of regulatory legislation. Investments included advances in biotechnology and the establishment of breeding programs, which have contributed significantly to yield increases in recent years (Specht et al., 2014).

Several recent studies conducted in important producing countries, mainly in the United States, China, and Argentina, have reported positive genetic gains for soybean crops, with rates ranging from ~6 to 43 kg ha⁻¹ yr⁻¹ (Boehm Jr. et al., 2019; de Felipe et al., 2016; Rincker et al., 2014; Rogers et al., 2015; Wang et al., 2016; Wu et al., 2015). In Brazil, several authors have also observed significant genetic gains, mainly in the South Region, with rates of genetic gain of up to 84.3 kg ha⁻¹ yr⁻¹, varying with maturity group, period evaluated, and set of genotypes tested (Alliprandini et al., 1993; Lange & Federizzi, 2009; Pagliosa, 2016; Rubin & Santos, 1996; Toledo et al., 1990). However, the rates of genetic gain obtained in Brazil over decades of breeding and involving a wide cultivation area are still unknown.

In addition to yield, studies carried out in several countries have also evaluated other important traits including thousand-seed weight (Morrison et al., 2000; Specht & Williams, 1984), plant height (Keep et al., 2016; Ustun et al., 2001), lodging resistance (Rogers et al., 2015; Voldeng et al., 1997), days to flowering and maturity (Cober & Voldeng, 2012; de Felipe et al., 2016; Rowntree et al., 2014), oil and protein contents (Boehm Jr. et al., 2019; Rincker et al., 2014), and other traits of agronomic importance.

The evaluation of genetic gain in soybean, using sets of cultivars from five decades of breeding and covering a wide cultivation area, is unprecedented in Brazil. This information

is important, as it allows the identification of the main changes that occurred over the years via direct or indirect selection. The objective of this study was to estimate the genetic gain for seed yield, and for agronomic, phenological and end-use quality traits in the South and Midwest Regions of Brazil.

2 | MATERIALS AND METHODS

2.1 | Plant materials and experimental details

Twenty-nine soybean cultivars recommended for the South Region and 38 cultivars recommended for the Midwest Region of Brazil released for cultivation between 1966 and 2011 were evaluated. The cultivars were selected for their importance in each decade, being responsible for a wide cultivation area during the recommendation period and included conventional (nontransgenic) and Roundup Ready 1 (RR1) technologies (Supplemental Tables S1 and S2).

The trials were conducted in locations of Macroregions 1 (MR1) and 2 (MR2) in the South Region, and of Macroregion 4 (MR4) in the Midwest Region of Brazil, in the 2016–2017, 2017–2018, and 2018–2019 crop seasons (Supplemental Figures S1 and S2). The seeds for conducting the trials were obtained from the germplasm bank of Embrapa Soja and from breeding companies. In Pato Branco, PR, the trials were conducted in the experimental area of the Federal University of Technology, Paraná, and in other locations trials were conducted by the project partner companies (Embrapa Soja, Embrapa Trigo, GDM Genética do Brasil, TMG Tropical Melhoramento e Genética, Fundação MT, Nidera, and Syngenta). The experimental design used in all locations was a randomized complete block (RCBD) with three replications. The experimental plots consisted of four 5-m-long rows spaced 0.5 m apart (10 m²), with a population density standardized for 30 seeds m⁻² in the South Region and 40 seeds m⁻² in the Midwest Region. Sowing was carried out within the agroclimatic zoning for each region and was adequate for the breeding programs of the project partner companies. Fertilization and cultivation practices for pest, disease, and weed control were carried out according to the technical recommendations for soybean crops.

During the field trials in both regions, there were locations where the trials were not carried out in the three crop seasons, and locations with more than one trial conducted in the same crop season (Supplemental Tables S3 and S4). For data analysis, each location × year combination was considered as an environment. The total number of environments (location × year) in which each trait was evaluated is shown in Supplemental Tables S5 and S6.

Core Ideas

- We observed positive genetic gain for seed yield in both evaluated regions
- The breeding efforts over the years have changed important soybean traits
- The seed yield has not reached its plateau in the South and Midwest Regions of Brazil

2.2 | Evaluated traits

In the full maturity stage (R8; Fehr & Caviness, 1977), the lodging score (LS) was evaluated by attributing visual scores on a scale from 1 (fully erect) to 9 (fully prostrate). Plant height (PH) and bottom pod height (BPH) were measured from the soil surface to the apex of the stem and the first bottom pod of the plant, respectively. Seed yield (SY) was obtained from the harvest of the two central rows of each plot (5 m²), corrected to 13% moisture, and estimated for kg ha⁻¹. Thousand-seed weight (TSW) was obtained by weighing three samples of 100 seeds and estimating for 1,000 seeds.

Phenological stages were evaluated according to the growth scale proposed by Fehr and Caviness (1977). Days to flowering (DF) were determined by the period in days between emergence (VE) and the beginning of flowering (R1); days to maturity (DM) was determined by the period between VE and full maturity (R8), and the reproductive period (RP) was determined by the period between stages R1 and R8.

After harvesting the trials, 50 g of clean and undamaged seeds from each replication were separated for determination of seed oil (OIL) and protein (PROT) contents, which were expressed at 13% moisture. The most representative locations in each region were selected for analysis. The OIL and PROT were determined by Near Infrared Reflectance (NIR) in the Embrapa Soja laboratory (Heil, 2010). Readings were performed in quadruplicate, with equipment Thermo, model Antaris II, equipped with an integration sphere with a resolution of 4 cm⁻¹, an average of 32 scans, and background at each reading (Quirino et al., 2014). The methodology described by Quirino et al. (2014) was used for the prediction of values. The average values of each quadruplicate for each repetition of the field trials were used for statistical analysis. The oil (OILY) and protein (PROTY) yields were obtained as the product of their percentage levels and SY and presented in kg ha⁻¹.

2.3 | Statistical analysis

The statistical analyses were performed using a linear model, considering cultivar, environment, repetitions within each

environment, and genotype \times environment interaction as random effects, whereas the mean effect was considered fixed in the model (Alvarado et al., 2015, 2020). In this case, all random effects were assumed to be normally distributed. The best linear unbiased predictors (BLUPs) and variance components were obtained according to Alvarado et al. (2015). For the analysis combining data across environments and considering the RCBD, the model was:

$$Y_{ijk} = \mu + \text{Env}_i + \text{Rep}_j(\text{Env}_i) + \text{Gen}_k + \text{Env}_i \times \text{Gen}_k + \varepsilon_{ijk}$$

where Y_{ijk} is the evaluated trait; μ is the mean effect; Env_i is the effect of the i th environment; $\text{Rep}_j(\text{Env}_i)$ is the effect of the j th replicate within the i th environment; Gen_k is the effect of the k th genotype; $\text{Env}_i \times \text{Gen}_k$ is the effect of the environment \times genotype interaction; and ε_{ijk} is the error associated with the i th environment, j th replication, and k th genotype, which is assumed to be normally and independently distributed, with mean zero and homoscedastic variance σ^2 (Alvarado et al., 2015, 2020).

The annual estimates of genetic gain were obtained as the slope of the regression analysis performed with the BLUPs of each evaluated trait (ordinate) against the year of development and/or release of the cultivars (abscissa). For each trait, the absolute and relative rates of genetic gain were presented. The relative rates were calculated by dividing the absolute gain rates by the values for each trait predicted for the beginning of the historical series (Boerma, 1979; de Felipe et al., 2016). The genetic gain estimates for the SY were obtained considering the full set of 29 cultivars in the South Region, as well as separating the set of cultivars into two groups according to their maturity groups (MG): 13 early cultivars in Group I (MG ≤ 6.3) and 16 medium cultivars in Group II (MG 6.4–7.4). In the same way, for the Midwest Region, the gain estimates for the SY were obtained for the full set of 38 cultivars, as well as separating the set of cultivars into three groups: 13 early cultivars in Group I (MG ≤ 7.8), 14 medium cultivars in Group II (MG 7.9–8.5) and 11 late cultivars in Group III (MG ≥ 8.6), according to the classification proposed by Kaster and Farias (2012).

The BLUPs of the joint analysis considering all environments (location \times year) where each trait was evaluated were used for the presentation of the results. Simple linear and quadratic regression models were tested to identify whether the rates of genetic gain were constant or discontinuous across the years. The parameters in the linear and quadratic regression models were as follows:

$$\text{LinearModel} : y = a + bx$$

$$\text{QuadraticModel} : y = a + bx + cx^2$$

where y is the dependent variable (agronomic, phenological, and end-use quality traits), x is the independent variable (year of cultivar release), a is the intercept, and b and c are the regression coefficients in different phases of the independent variable (Wang et al., 2016).

The analyses were carried out using Meta-R software (Multi Environment Trial Analysis with R for Windows), version 6.0 (Alvarado et al., 2015). Regression analyses to obtain estimates of genetic gain, and construction of graphs were performed using SigmaPlot software, version 11.0. Pearson's correlation analysis between the BLUPs of the traits was performed using the Genes software (Cruz, 2016). The significance of the regression and correlation coefficients was verified by the t test, considering the levels of 5% ($p < .05$), 1% ($p < .01$) and 0.1% ($p < .001$) of error probability.

3 | RESULTS AND DISCUSSION

3.1 | South region

There were significant differences ($p < .01$) for genotype, environment, and genotype \times environment interactions for all evaluated traits in both regions, except for the genotype and environment effects for BPH in MR1. The SY across the evaluated environments ranged from 3,238 to 5,540 kg ha⁻¹ in MR1, 2,154 to 4,931 kg ha⁻¹ in MR2, and 2,154 to 5,540 kg ha⁻¹ over the South Region as a whole. The respective average yields in these regions were 4,308, 3,876, and 4,118 kg ha⁻¹ (data not shown).

3.1.1 | Yield improvement

The results showed significant and positive genetic gains for SY in the South Region (Figure 1). The absolute rates of genetic gain were 15.31, 13.83, and 14.13 kg ha⁻¹ yr⁻¹ for the full set of cultivars, and for the early and medium sets (Figures 1a, 1b and 1c). These gains correspond to relative rates of 0.42, 0.36, and 0.39% yr⁻¹, respectively. In MR1 the rates of genetic gain were 14.89, 14.17 and 13.75 kg ha⁻¹ yr⁻¹, which is equivalent to 0.39, 0.35, and 0.36% yr⁻¹ for the full, early and medium sets, respectively (Figures 1d, 1e, and 1f). In MR2, the estimated rates of genetic gain were 14.47, 11.98 and 13.48 kg ha⁻¹ yr⁻¹ for the full, early and medium sets, which represents 0.42, 0.33, and 0.39% yr⁻¹, respectively (Figures 1g, 1h, and 1i). For the full set of cultivars in both the South Region overall, and MR1 (Figures 1a and 1d), there were trends towards an increase in the rates of genetic gain from the 1990s to 2000s onwards, although the quadratic model did not reach significance in either region ($p = .060$ and $.059$, respectively).

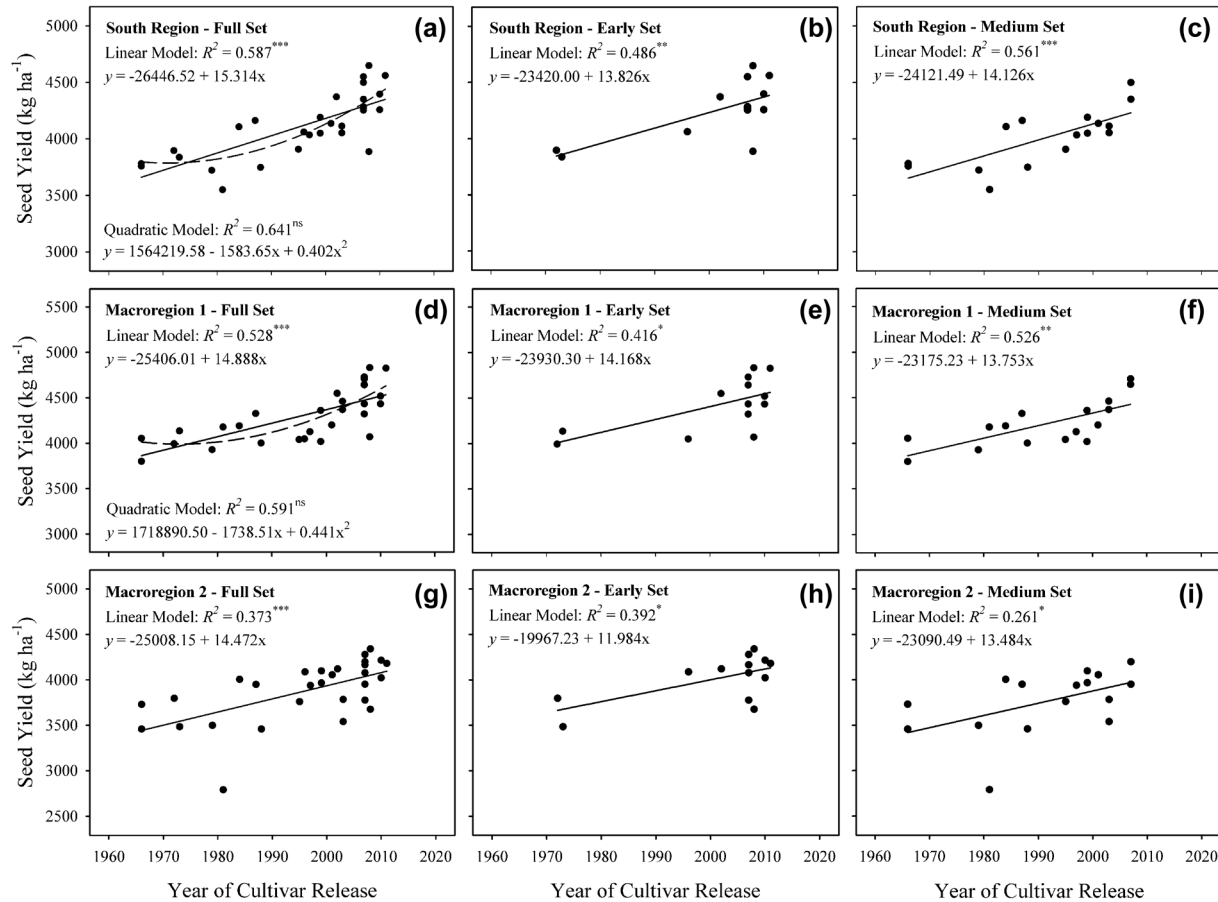


FIGURE 1 Regressions between the year of release and seed yield for the full set of soybean cultivars, and for the early and medium sets, in the South Region of Brazil (a, b, and c); Macroregion 1 (d, e, and f); and Macroregion 2 (g, h, and i). Each data point is the best linear unbiased predictor (BLUP) of seed yield for a cultivar, generated for sets of 25, 14, and 11 environments (location \times year) in the South Region, Macroregion 1, and 2, respectively. *Significant at the .05 probability level. **Significant at the .01 probability level. ***Significant at the .001 probability level. ^{ns}Not significant

In studies performed in South Brazil, several authors have also reported significant genetic gains in soybean. Toledo et al. (1990) evaluated trials of lines developed between 1981 and 1986 in Paraná state and reported rates of genetic gain of 45.1 and 36.8 kg ha⁻¹ yr⁻¹ (1.80 and 1.32% yr⁻¹) for the early and semi-early MGs, respectively. In a similar study, Alliprandini et al. (1993) evaluated trials of genetic lines from 1986 to 1990, also in Paraná state, and reported rates of genetic gain of 24.16, 10.83, and -8.17 kg ha⁻¹ yr⁻¹ (0.89, 0.38, and -0.28% yr⁻¹) for the early, semi-early and medium MGs, respectively. In addition, Rubin and Santos (1996), evaluated a period of 40 yr of improvement in Rio Grande do Sul state and observed rates of genetic gain of 17.7, 5.1, and 22.7 kg ha⁻¹ yr⁻¹ for early, medium and semi-late to late MGs, respectively, which corresponded to an average gain rate of 19.0 kg ha⁻¹ yr⁻¹ (1.1% yr⁻¹). Similarly, Lange and Federizzi (2009) reported rates of genetic gain from 0.0 to 71.5 kg ha⁻¹ yr⁻¹ (0.0 to 3.49% yr⁻¹) in Rio Grande do Sul state, over the period from 1979 to 1999. In a more recent study Pagliosa (2016) evaluated the value of cultiva-

tion and use (VCU) trials conducted in the crop seasons from 2001–2002 to 2013–2014 and reported rates of genetic gain of up to 84.32 kg ha⁻¹ yr⁻¹ (3.25% yr⁻¹). Although previous studies have reported higher rates of genetic gain than those obtained in the present study, the rates varied considerably between the MGs, regions, and periods evaluated. In addition, the results obtained are highly dependent on the number of environments and the set of genotypes evaluated, especially when evaluating lines from specific breeding programs. In most of the previously cited studies in South Brazil, the rates of genetic gain were obtained from phenotypic averages, in contrast to the present study where BLUPs were used, representing the true genotypic effect of the cultivars regardless of environmental effects (de Felipe et al., 2016).

The absolute rates of genetic gain obtained in the present study were similar to those reported in several studies conducted in the United States, which ranged from 10.3 to 23.1 kg ha⁻¹ yr⁻¹ (Boehm Jr. et al., 2019; Boerma, 1979; Rincker et al., 2014; Rogers et al., 2015; Salado-Navarro et al., 1993;

Ustun et al., 2001). Similar results have been reported from other countries. Rates of genetic gain ranging from 5.8 to 16.2 kg ha⁻¹ yr⁻¹ were reported from China (Jin et al., 2010; Wang et al., 2016; Wu et al., 2015). Similarly, rates of genetic gain similar to those found in the present study and within the intervals of studies already mentioned were reported by studies conducted in Canada (10.2 kg ha⁻¹ yr⁻¹) and India (23.1 kg ha⁻¹ yr⁻¹) (Morrison et al., 2000; Ramteke et al., 2011). However, in a study conducted in Argentina, de Felipe et al. (2016) reported a genetic gain of 43 kg ha⁻¹ yr⁻¹. In a more recent study, the same authors reported similar results, with a genetic gain of 42 kg ha⁻¹ yr⁻¹ or approximately 1% yr⁻¹ (de Felipe et al., 2020); estimated rates of genetic gain higher than those obtained in our study and those reported in the previously mentioned studies performed in other countries. The studies by de Felipe et al. (2016, 2020) evaluated crops in only three and two environments (location × year), respectively. In contrast, the present study and most of the previously mentioned studies involved several environments and a wide cultivation area, where the average yield of the cultivars tended to be lower.

Soybean breeding in Brazil began with plant introductions from the southern United States in the 1960s and 1970s (Specht et al., 2014). Therefore, we expected to observe similar or lower rates of genetic gain than those reported from the United States. Hiromoto and Vello (1986) evaluated 69 of 74 cultivars used in the 1983–1984 crop season in Brazil and reported that 11 ancestors were responsible for approximately 89% of their pedigrees. In a more recent study, Wysmierski and Vello (2013) evaluated 444 soybean cultivars available for cultivation in Brazil between 1943 and 2009 and reported that the number of ancestors has increased over time, but that the genetic base is still narrow. According to the authors, 14 ancestors represented 92.4% of the genetic base, and the four top ancestors alone contributed more than 55%. However, although these studies have shown that the genetic base of the crop in Brazil is still narrow, yield plateaus were not observed in the main studies carried out in Brazil, nor in the present study.

In the recent studies, de Felipe et al. (2016, 2020) evaluated soybean genetic gain arising from conventional (nontransgenic), RR1, and RR2 IPRO technologies from 1980 to 2015 in Argentina. These authors did not observe discontinuities in rates of genetic gain across the years, suggesting that there were no qualitative yield advantages associated with the biotechnological events, although the importance of these technologies for the management of the crop is incontestable. Similarly, Cober and Voldeng (2012) reported that after its introduction into Canada, the RR1 technology did not seem to have changed the soybean genetic gain rates. In the present study, the available dataset does not allow us to conclude whether the RR1 technology conferred any yield advantage over conventional genotypes. It is more likely that

the upward trend in rates of genetic gain from the 1990s–2000s (Figures 1a and 1d) was the result of the approval of the Variety Protection Law of April 25, 1997 (Brasil, 1997). This law allowed investments of national and multinational private companies in Brazil, resulting in the establishment of new breeding programs and biotechnology advances that increased the yield potential of new cultivars (Specht et al., 2014). This behavior was also observed in the US following the Plant Variety Protection (PVP) Act of 1970 which promoted significant investments in breeding programs and gave breeders exclusive control over new cultivars, and likely positively affected the genetic gain of the soybeans in United States (Rincker et al., 2014; Specht et al., 2014).

Although several studies performed in Brazil and worldwide have demonstrated significant yield increases, these cannot be attributed solely to genetic improvement, because the cultivation environment has also been continuously improved (Boehm Jr. et al., 2019; Rogers et al., 2015; Ustun et al., 2001). In addition, genetic and agronomic advances have occurred simultaneously over the years, making it difficult to measure the exact contribution of each of them to on-farm yield increases (Messina et al., 2009; Specht et al., 2014). However, some authors have reported that between half and two-thirds of yield gains are due to breeding efforts, whereas the other part is attributed to agronomic and environmental improvements (de Felipe et al., 2016; Rincker et al., 2014; Rowntree et al., 2013; Specht et al., 2014). Among the environmental improvements that have been associated with yield gains are improvements in management practices, adoption of agronomic technologies, and synergistic interaction between agronomic practices and new cultivars (Boehm Jr. et al., 2019; Rowntree et al., 2013; Specht et al., 2014).

3.1.2 | Agronomic traits

The SY has been the target trait of soybean improvement in Brazil and worldwide. However, positive rates of genetic gain in SY were followed by changes in several other important traits via direct or indirect selection. Despite the positive genetic gains for SY observed in the present study, the TSW showed a reduction across the years, with annual rates of -0.33 , -0.38 , and -0.26 g yr⁻¹ in the South Region, MR1, and MR2, respectively (Figures 2a, 2b, and 2c). These reductions are equivalent to -0.18 , -0.21 , and -0.15% yr⁻¹, although without reaching statistical significance in the South Region nor in MR2 ($p = .072$ and $.158$, respectively). The quadratic model showed that the reduction occurred until the end of the 1990s, followed by stabilization and increase in the last years of the historical series for both regions, but also without reaching statistical significance in MR2 ($p = .056$).

The negative rates of genetic gain for the TSW suggest that the yield increases across the years were caused by an increase

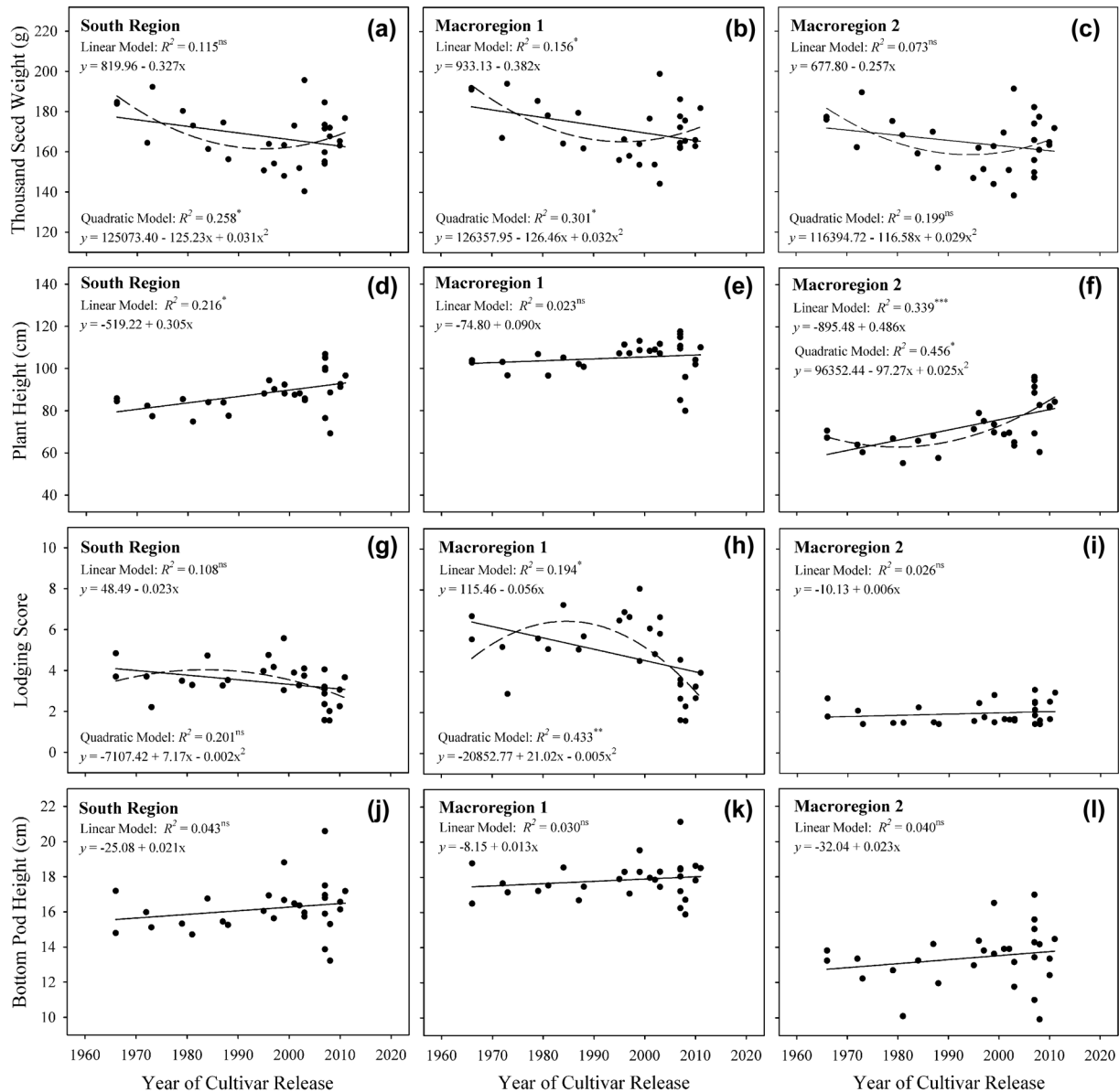


FIGURE 2 Regressions between the year of soybean cultivar release and thousand-seed weight (a, b, and c), plant height (d, e, and f), lodging score (g, h, and i), and bottom pod height (j, k, and l) in the South Region of Brazil, and Macroregions 1, and 2, respectively. Each data point is the best linear unbiased predictor (BLUP) of the agronomic trait for a cultivar, generated for the set of environments (location \times year) of the evaluated region. *Significant at the .05 probability level. **Significant at the .01 probability level. ***Significant at the .001 probability level. ^{ns}Not significant

in the number of seeds per unit area, either by the greater number of seeds per pod, pods per plant, and/or seeds per plant, as reported in other studies (Cui & Yu, 2005; Jin et al., 2010; Todeschini et al., 2019; Wu et al., 2015). Although some studies conducted in the United States (Specht & Williams, 1984) and China (Qin et al., 2017; Wang et al., 2016) have reported an increase in the TSW over the years, other studies conducted in Canada (Morrison et al., 2000), Argentina (de Felipe et al., 2016), China (Jin et al., 2010), and the United States (Boehm Jr. et al., 2019; Rincker et al., 2014) did not identify genetic gains for this trait. These results can

be explained by the lack of positive correlations between TSW and SY and other components, as reported in several studies (Boehm Jr. et al., 2019; de Felipe et al., 2016; Egli et al., 1978; Jin et al., 2010; Morrison et al., 2000).

The results for the PH and LS traits varied significantly among the different regions. A significant increase in PH was identified in both the South Region and MR2, with rates of genetic gain of 0.31 and 0.49 cm yr⁻¹ (0.38 and 0.82% yr⁻¹), respectively (Figures 2d and 2f). However, there was no difference between the old and new cultivars in MR1 (Figure 2e). There was no difference in LS over the years

in MR2 (Figure 2i), but a downward trend was observed in the South Region (-0.023 yr^{-1} , $p = .082$) and a significant reduction of -0.056 yr^{-1} (equivalent to $-0.86\% \text{ yr}^{-1}$ on the score scale) was observed in MR1 (Figures 2g and 2h, respectively). The quadratic model was significant for PH in MR2, showing that the increase in this trait only occurred in the 2000s (Figure 2f). Likewise, the quadratic model was significant for LS in MR1, showing that this trait started to reduce only from the 2000s onwards (Figure 2h). In the South Region LS showed a similar trend, but the quadratic model did not reach statistical significance ($p = .095$, Figure 2g). These results indicate that new cultivars were more resistant to lodging in MR1, even though there were no differences in PH. In contrast, in MR2 there was an increase in PH over the years, but without difference in LS. These results suggest that because lodging resistance was maintained over the years the higher PH of new cultivars in this region is not a negative point.

Several studies performed in China (Jin et al., 2010; Wang et al., 2016) and the United States (Keep et al., 2016; Rincker et al., 2014; Rogers et al., 2015) have shown a simultaneous reduction in PH and LS in new cultivars. Although the results obtained in the present study are in contrast with most of the studies carried out in other countries, Rincker et al. (2014) reported that although PH is an important trait, it does not have the great importance of LS, for which selection is prioritized due to the losses it causes in the field. The authors further state that taller and shorter cultivars have often been released in the United States, providing they present satisfactory SY and LS resistance, as observed in MR2 in the present study. However, because shorter cultivars tend to have lower LS, the trend of reduction of PH that was observed in several studies has been favored by selection for LS resistance (Boehm Jr. et al., 2019; Rincker et al., 2014; Rogers et al., 2015; Ustun et al., 2001). Even so, in some cases increases in PH have been reported for specific MGs and/or evaluated periods (Specht & Williams, 1984; Wilcox, 2001; Wu et al., 2015). The higher PH of the new cultivars observed in the present study, especially after the 2000s, may be the result of the release of indeterminate cultivars, which maintain their vegetative growth after the beginning of flowering, a condition also observed by Pagliosa (2016) in southern Brazil.

The increase in PH did not influence BPH in any of the regions, and there were no significant differences in BPH between old and new cultivars over the years. The lowest values observed for BPH were approximately 13, 16, and 10 cm in the South Region, MR1, and MR2, respectively (Figures 2j, 2k, and 2l). The improvement of BPH is important to avoid losses during mechanized harvesting, and the minimum values observed are acceptable. The absence of genetic gain for this trait has also been reported by Wu et al. (2015) and Wang et al. (2016) in China.

3.1.3 | Phenological traits

A reduction in DM over the years was observed in both evaluated regions. The decrease was -0.15 , -0.18 , and -0.11 d yr^{-1} , which represent -0.11 , -0.13 , and $-0.10\% \text{ yr}^{-1}$ for the South Region, and MR1 and MR2, respectively (Figures 3a, 3b, and 3c). However, the reduction did not reach statistical significance in MR2 ($p = .073$). A similar result was observed for DF, with decreases of -0.13 , -0.16 , and -0.10 d yr^{-1} (equivalent to the relative rates of -0.254 , -0.250 , and $-0.247\% \text{ yr}^{-1}$) observed in the South Region, and MR1 and MR2, respectively (Figures 3d, 3e, and 3f).

Several studies conducted in other countries have also reported that new cultivars presented reductions in DM (Cober & Voldeng, 2012; Ustun et al., 2001) and DF (de Felipe et al., 2016; Rowntree et al., 2014; Wu et al., 2015) compared with old ones. However, no significant differences in RP were observed in any of the regions that were evaluated in the current study (Figures 3g, 3h, and 3i). These results indicate that the reduction in DM of the new cultivars occurred mainly due to the reduction in the DF. Furthermore, the quadratic model was significant for DM and DF in both regions, showing that the reduction was not linear over the years. For both traits, the reduction occurred only from the 2000s onwards, in both regions. Indeterminate germplasm was introduced in Brazil in the 2000s and is characterized by early flowering and this could explain the observations of the present study.

The cultivars with determinate growth habit that were better adapted for the South Region of Brazil until 2000 had a maturity ranging between 120 and 125 d (Specht et al., 2014; Toledo et al., 2006). After 2000 there was a need to obtain earlier cultivars, which allowed double cropping of soybean with corn (*Zea mays*) or cotton (*Gossypium hirsutum* L.) in a single season, and which favored the control of Asian soybean rust (*Phakopsora pachyrhizi*) that was emerging in Brazil (Specht et al., 2014; Toledo et al., 2006). However, determinate-type cultivars that matured in less than 115 to 120 d presented low yield potential, as they needed a minimum period of time before flowering to reach an adequate development (Specht et al., 2014). Therefore, early cultivars could only be obtained by reducing the RP, which would also affect the seed yield (Specht et al., 2014). The solution was found in the introduction of indeterminate germplasm from Argentina and North America. Indeterminate plants characteristically continue their development after the beginning of flowering and thus offer early, productive, and adequate-sized cultivars (Specht et al., 2014). This germplasm introduced a new set of genes not yet explored in Brazil, which contributed even more to yield increases (Godoi et al., 2013; Specht et al., 2014) and could explain the higher rates of genetic gain obtained from the 2000s in the South Region of Brazil (Figure 1).

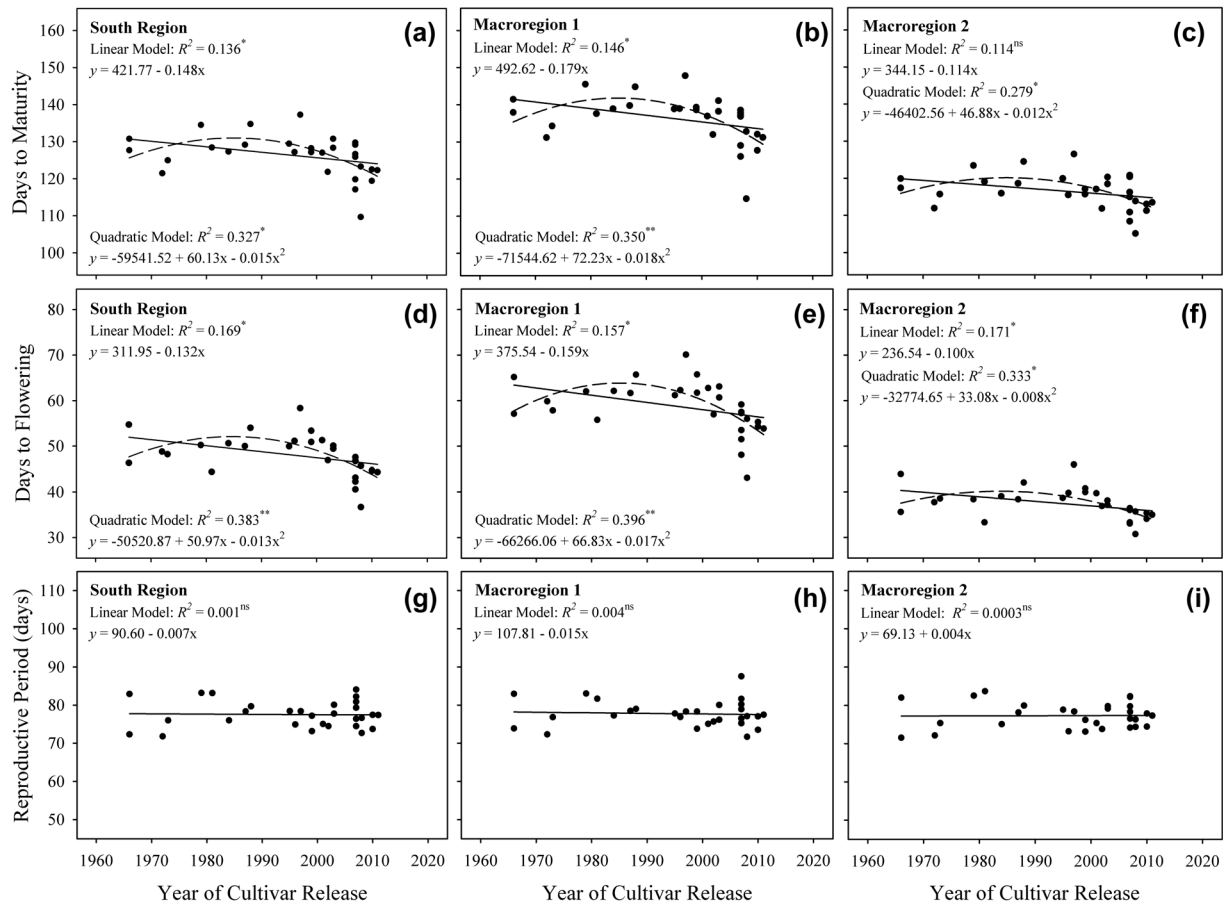


FIGURE 3 Regressions between the year of soybean cultivar release and days to maturity (a, b, and c), days to flowering (d, e, and f) and reproductive period (g, h, and i) in the South Region of Brazil, and Macroregions 1, and 2, respectively. Each data point is the best linear unbiased predictor (BLUP) of the phenological trait for a cultivar, generated for the set of environments (location \times year) of the evaluated region. *Significant at the .05 probability level. **Significant at the .01 probability level. ^{ns}Not significant

Rincker et al. (2014) evaluated soybean cultivars released from 1923 to 2008 in the United States and reported positive genetic gain for SY and an average increase of 8 d within each evaluated MG in the total cycle of the new cultivars. According to the authors, late cultivars tend to increase yield because they extend the photosynthesis period and, consequently, assimilate more carbon. However, the present study showed that the new cultivars yielded more even with earlier maturity, as also observed in other studies (Cober & Voldeng, 2012; Ustun et al., 2001). In addition, several authors have associated the yield increases of the new cultivars with their higher photosynthetic rates (Jin et al., 2010; Liu et al., 2012; Morrison et al., 1999; Todeschini et al., 2019), as well as their greater efficiency in converting biomass into seeds (Koester et al., 2014).

The BLUPs of SY were divided by the total cycle of the cultivars to obtain the daily rates of genetic gain. Rates of genetic gain of 0.160, 0.153, and 0.157 kg ha⁻¹ d⁻¹ yr⁻¹ were observed in the South Region, MR1, and MR2, which represent gains of 0.574, 0.561, and 0.545% yr⁻¹, respectively (Supplemental Figure S3). In summary, the reduction in the

total cycle of the new cultivars was associated with higher daily rates of genetic gain. In addition, the quadratic model showed that daily genetic gains remained constant in the first decades of the evaluated historical series, showing an increase only from the beginning of the 2000s in both regions, although without statistical significance in MR2 ($p = .064$).

3.1.4 | End-use quality traits

There were trends towards an increase in OIL and a decrease in PROT over the years in both regions. In the South Region overall a rate of genetic gain of 0.015% yr⁻¹ for OIL and a reduction of -0.024% yr⁻¹ for PROT were observed, although without significant statistical difference for OIL ($p = .082$). These values are equivalent to relative gains of 0.079 and -0.071% yr⁻¹, respectively (Figures 4a and 4d). Similar performances were observed in MR1 and MR2, with increases of 0.011 and 0.019% yr⁻¹ (0.059 and 0.105% yr⁻¹) for OIL (Figures 4b and 4c) and reductions of -0.024 and -0.021% yr⁻¹ (-0.072 and -0.064% yr⁻¹) for PROT (Figures 4e

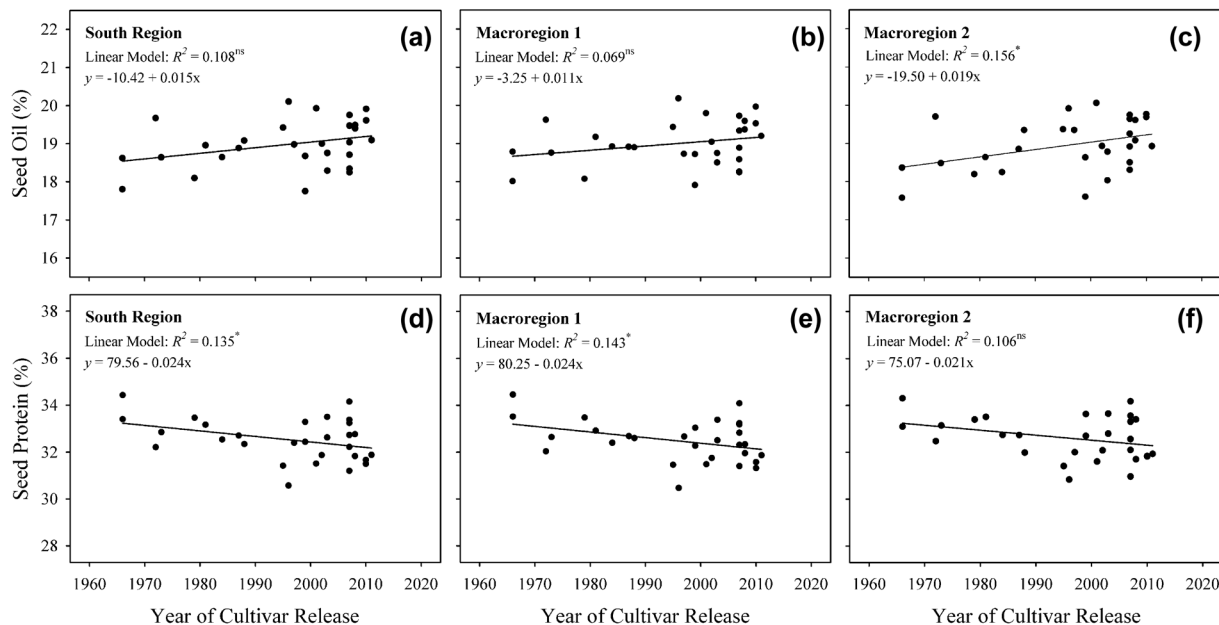


FIGURE 4 Regressions between the year of soybean cultivar release and seed oil (a, b, and c) and seed protein contents (d, e, and f) in the South Region of Brazil, Macroregions 1, and 2, respectively. Each data point is the best linear unbiased predictor (BLUP) of the end-use quality trait for a cultivar, generated for the set of environments (location \times year) of the evaluated region. *Significant at the .05 probability level. ^{ns}Not significant

and 4f), respectively. However, the OIL rates in MR1 and PROT rates in MR2 were not statistically significant ($p = .168$ and $.085$, respectively).

The increase in OIL and decrease in PROT across the years found in the present study corroborate previous studies carried out in Brazil and other countries (Bonato et al., 2000; Morrison et al., 2000, 2008; Rogers et al., 2015; Rowntree et al., 2013; Ustun et al., 2001). However, in a more recent study Boehm Jr. et al. (2019), evaluated MGs V, VI, and VII in the United States and observed a significant reduction in PROT only in MG VI, but with no significant difference in OIL for all MGs studied, in contrast to the previously cited studies. Similarly, de Felipe et al. (2016) observed a significant reduction in PROT in Argentina from 1980 to 2015, but no change was observed for OIL over the years.

Even though some previously mentioned studies have not identified significant differences for OIL and PROT in soybean, the overall trend of increasing OIL and decreasing PROT over the years is clear. These results suggest that a constant search for yield increases over time has indirectly changed these traits (Rincker et al., 2014; Rogers et al., 2015; Rowntree et al., 2013). A negative correlation between OIL and PROT has been widely reported (Boehm Jr. et al., 2019; de Felipe et al., 2016; Rogers et al., 2015; Ustun et al., 2001), and was also found in the present study in the South Region of Brazil ($r = -.83$, $p < .001$; data not shown), which could explain the results obtained.

Although the PROT has decreased over the years, the PROTY per unit area increased, as did the OILY (Figure 5). Rates of genetic gain of 3.36, 2.98, and 3.44 kg ha⁻¹ yr⁻¹ for

OILY (Figures 5a, 5b, and 5c) and 3.75, 3.35, and 3.73 kg ha⁻¹ yr⁻¹ for PROTY (Figures 5d, 5e, and 5f) were identified in the South Region, MR1, and MR2. These gains correspond to the respective relative rates of 0.49, 0.40, and 0.55% yr⁻¹ for OILY and 0.30, 0.25, and 0.33% yr⁻¹ for PROTY. An increasing trend in the rate of genetic gain for PROTY was observed in the South Region in the last years of the historical series (Figure 5d), although the quadratic model did not reach statistical significance ($p = .078$). This trend may be associated with the higher yield gain rates in the region from the 1990s–2000s onwards (Figure 1a), which also resulted in higher PROTY per unit area. A similar pattern was reported by Rincker et al. (2014), who evaluated soybean cultivars of MG II, III, and IV in the United States. These authors also identified an increase in OIL and a decrease in PROT over the years, but the OILY and PROTY were positive and significant for all MGs studied, except for OIL in MG IV.

Currently, soybean is a major source of oil and protein, and changes in the concentration of these traits are of great importance in the processing industry (Rincker et al., 2014). According to Pípolo et al. (2015), a minimum of 46% of protein in meals is required by legislation (MAPA, 1993), and the industrial sector has shown concern about the difficulty of obtaining this value. Increases in PROTY are not sufficient, as the industry demand is for protein concentration in seeds. However, growers have been paid in the past for the volume produced, and unless an additional value is paid for higher PROT, it is likely that the downward trend in PROT will continue in the coming years. A similar situation has been observed in the United States (Rincker et al., 2014),

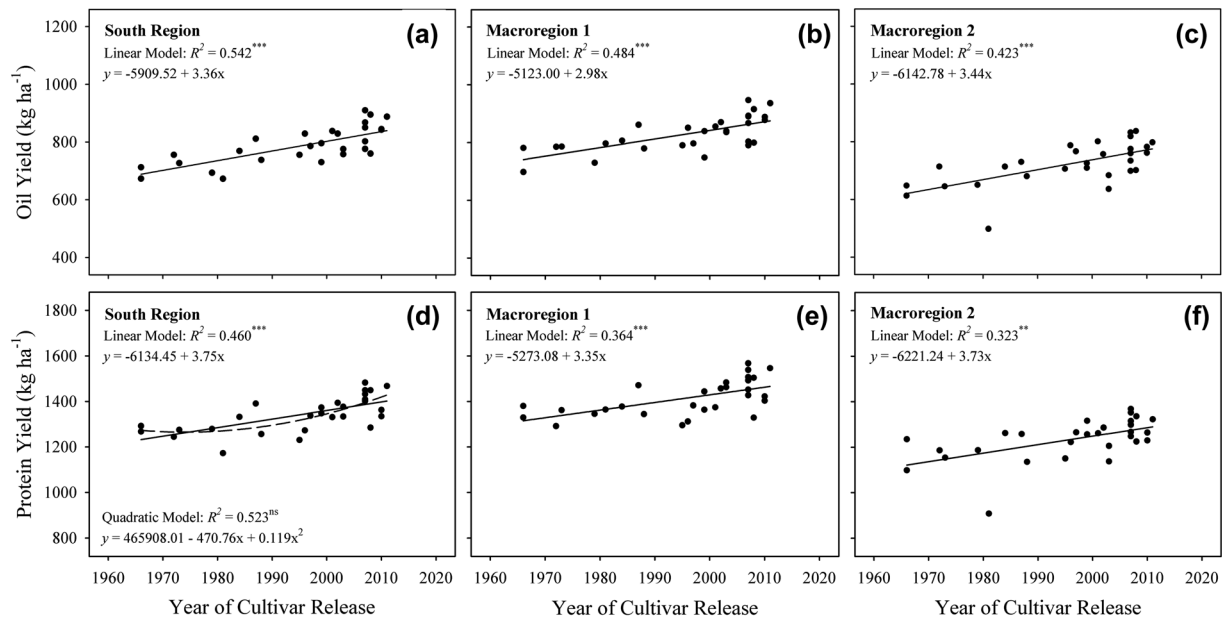


FIGURE 5 Regressions between the year of soybean cultivar release and oil (a, b, and c) and protein yield (d, e, and f) in the South Region of Brazil, and Macroregions 1, and 2, respectively. Each data point is the best linear unbiased predictor (BLUP) of the end-use quality trait for a cultivar, generated for the set of environments (location \times year) of the evaluated region. **Significant at the .01 probability level. ***Significant at the .001 probability level. ^{ns}Not significant

and some authors have highlighted the need for simultaneous selection for SY and PROT to alleviate this problem in the future (Boehm Jr. et al., 2019).

Pearson's correlation analysis showed positive and significant associations between SY and the traits OILY ($r = .92$, $p < .001$) and PROTY ($r = .91$, $p < .001$), as expected, because these traits are the result of multiplication of the oil and protein percentages by yield (Supplemental Figure S4). Similarly, the correlation between SY and PH ($r = .63$, $p < .001$) was also positive and significant, indicating that the most productive cultivars exhibited more height in the South Region of Brazil. This result can be attributed, in part, to the indeterminate cultivars evaluated in the present study, which were released for cultivation after the 2000s.

The SY was negatively and significantly correlated with PROT ($r = -.39$, $p < .05$), but the correlation with OIL was not significant ($r = .31$, $p \geq .05$; Supplemental Figure S4). Despite the lack of significance for this trait in the present study, several studies have shown that increases in yield over time tend to indirectly increase OIL and reduce PROT (Boehm Jr. et al., 2019; Morrison et al., 2000, 2008; Qin et al., 2017; Voldeng et al., 1997). The correlations of the other evaluated traits with SY were not statistically significant. The absence of a significant correlation between SY and TSW ($r = -.22$, $p \geq .05$) was also expected and corroborates several studies performed in other countries (Boehm Jr. et al., 2019; de Felipe et al., 2016; Egli et al., 1978; Jin et al., 2010; Morrison et al., 2000), demonstrating that the productivity increases in soybean over time have been more

associated with other yield components than with TSW, as previously discussed.

3.2 | Midwest region

There were significant differences ($p < .01$) for genotype, environment, and genotype \times environment interaction for all evaluated traits in the Midwest Region. The SY across environments ranged from 2,792 to 4,432 kg ha⁻¹, with an average yield of 3,402 kg ha⁻¹ (data not shown).

3.2.1 | Yield improvement

The results showed significant genetic gain for SY in the Midwest Region (Figure 6). The absolute rates of genetic gain were 17.55, 13.58, 21.84, and 20.83 kg ha⁻¹ yr⁻¹ for the full, early, medium, and late sets of cultivars. These gains correspond to relative rates of 0.62, 0.47, 0.77, and 0.69% yr⁻¹, respectively (Figures 6a, 6b, 6c, and 6d). It is noteworthy that, although the gain observed for the early MG was lower than those obtained for the medium and the late MGs, there was a clear trend towards an increase in the rate of genetic gain in the last years of the evaluated historical series, although the quadratic model did not reach statistical significance ($p = .056$; Figure 6b).

As previously shown, the main studies of soybean genetic gain in Brazil have been conducted in the South Region of the

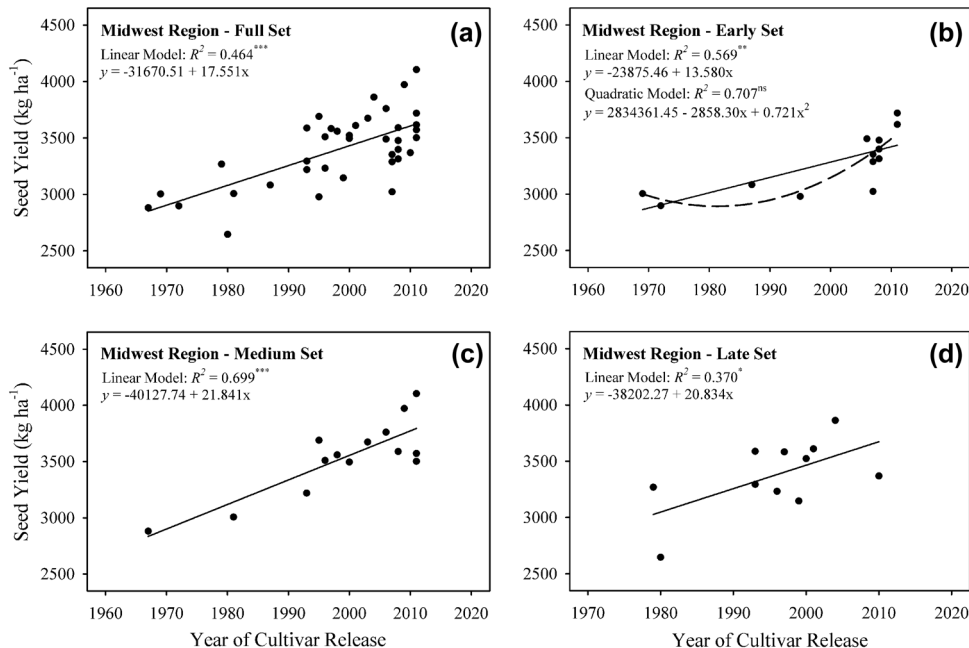


FIGURE 6 Regressions between year of release and seed yield for the full set of soybean cultivars (a), and for the early (b), medium (c), and late (d) sets, in the Midwest Region of Brazil. Each data point is the best linear unbiased predictor (BLUP) of seed yield for a cultivar, generated for the set of 12 environments (location \times year) of the evaluated region. *Significant at the .05 probability level. **Significant at the .01 probability level. ***Significant at the .001 probability level. ^{ns}Not significant

country, and positive rates of genetic gain have been reported, which varied with the set of genotypes, the region, and the periods of evaluation. In the Midwest Region, few studies have been performed, and there is little information about the progress of the crop in the region. However, Mezzalira (2017) evaluated soybean genotypes from value of cultivation and use (VCU) trials in MR3 and MR4 and reported an absolute rate of genetic gain of $18.3 \text{ kg ha}^{-1} \text{ yr}^{-1}$ for MG 8, over the crop seasons from 2006–2007 to 2015–2016. This gain corresponds to a relative rate of $0.59\% \text{ yr}^{-1}$, which is within the range of rates obtained in this study in MR4.

Studies performed in other important countries, have reported rates of genetic gain similar to those obtained in this study for the Midwest Region, such as in the United States (approximately 10 to $23 \text{ kg ha}^{-1} \text{ yr}^{-1}$), China (approximately 6 to $16 \text{ kg ha}^{-1} \text{ yr}^{-1}$), India (approximately $23 \text{ kg ha}^{-1} \text{ yr}^{-1}$), and Canada (approximately $10 \text{ kg ha}^{-1} \text{ yr}^{-1}$), but lower than those obtained in recent studies (approximately $43 \text{ kg ha}^{-1} \text{ yr}^{-1}$) conducted in Argentina (Boehm Jr. et al., 2019; de Felipe et al., 2016, 2020; Jin et al., 2010; Morrison et al., 2000; Ramteke et al., 2011; Rincker et al., 2014; Rogers et al., 2015; Wang et al., 2016; Wu et al., 2015). However, as previously discussed, the rates of genetic gain are highly dependent on the set of genotypes tested and the number of environments evaluated, which may explain the differences observed in the cited studies.

As previously mentioned, the first plant introductions from southern United States were adapted to latitudes from 22 to

30°S , such as those found in the South Region of Brazil (Specht et al., 2014). Thus, the first genotypes cultivated were not adapted to regions of low latitude because the short photoperiod caused early flowering, thus reducing vegetative development, and, consequently, yield (Almeida et al., 1999). Therefore, given the limitations of soybean cultivation under short day conditions, such as in the Midwest Region of Brazil, breeding efforts were decisive for the adaptation of the crop. Such was the main challenge of the 1970s and 1980s (Specht et al., 2014). The solution found by breeders to cropping soybeans in low latitude regions was to identify and understand the long juvenile period (Almeida et al., 1999; Hartwig & Kiihl, 1979). This finding allowed the cultivation of soybean genotypes with adequate size and yield in regions previously unexplored in Brazil, thereby, moving Brazilian crop production into the tropics and introducing modern agriculture into the extensive flatland areas of Cerrado, the Brazilian savannas (Specht et al., 2014). Currently, the Midwest Region accounts for almost half the soybean production and the cultivated area in the country (Conab, 2020).

3.2.2 | Agronomic, phenological, and end-use quality traits

Despite of the significant yield improvement observed in the Midwest Region, no gain in TSW over the years was

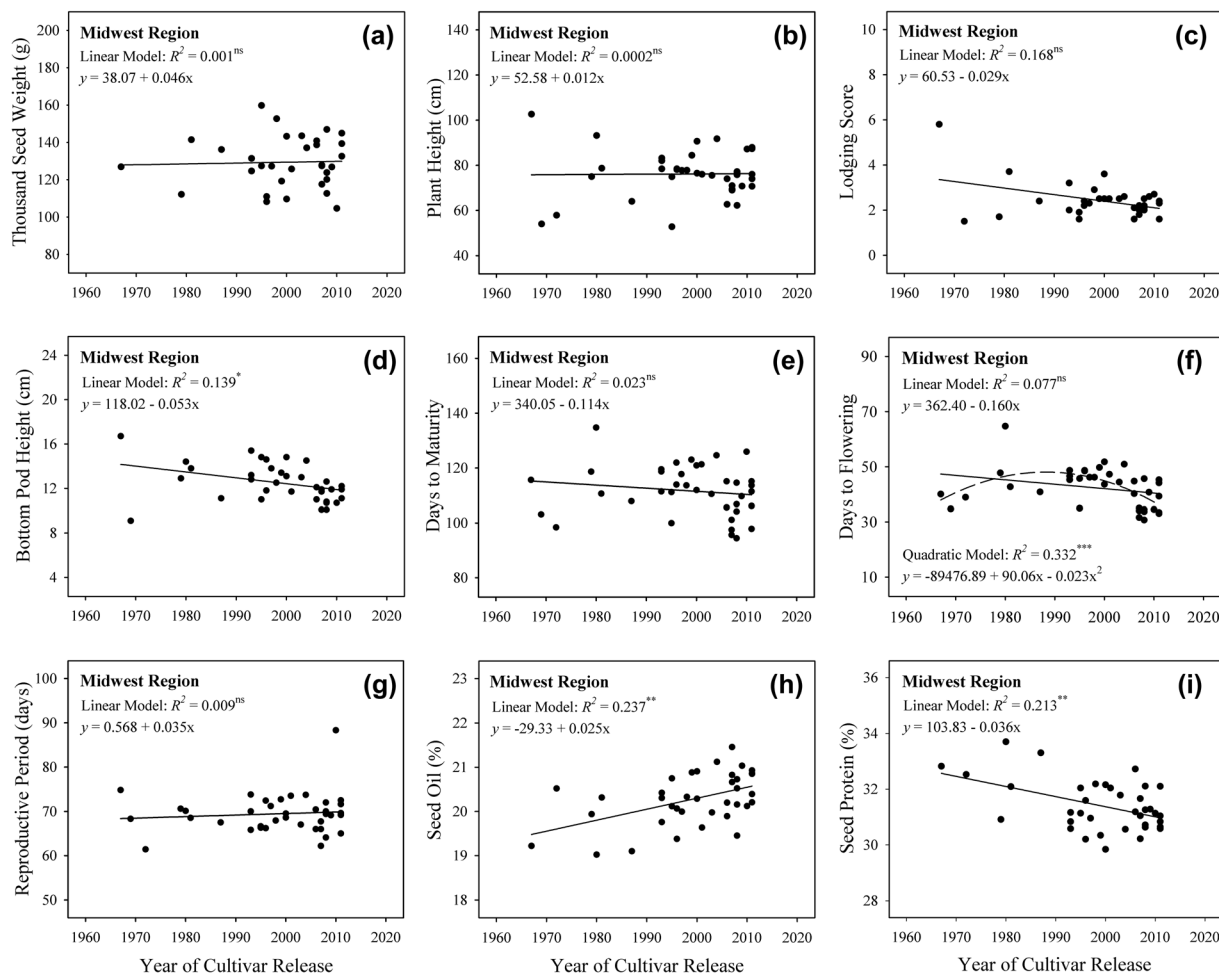


FIGURE 7 Regressions between the year of soybean cultivar release and thousand seed weight (a), plant height (b), lodging score (c), bottom pod height (d), days to maturity (e), days to flowering (f), reproductive period (g), seed oil (h), and seed protein content (i) in the Midwest Region of Brazil. Each data point is the best linear unbiased predictor (BLUP) of the agronomic, phenological, and end-use quality traits for a cultivar, generated for the set of environments (location \times year) of the evaluated region. *Significant at the .05 probability level. **Significant at the .01 probability level. ***Significant at the .001 probability level. ^{ns}Not significant

detected in this study (Figure 7a), corroborating recent studies conducted in the United States (Boehm Jr. et al., 2019; Rincker et al., 2014) and Argentina (de Felipe et al., 2016). This can be explained by the absence of correlation between TSW and SY and other components, as previously reported (Boehm Jr. et al., 2019; Jin et al., 2010; Morrison et al., 2000). Therefore, the higher yields of the new cultivars can be attributed to the greater number of seeds per unit area (seeds per pod, pods per plant, and/or seeds per plant), as observed by other researchers and previously discussed (Cui & Yu, 2005; Kahlon & Board, 2012; Morrison et al., 2000; Rincker et al., 2014).

Plant height and LS did not show significant changes over the years, although there appeared to be a trend towards reduced LS in the new cultivars (Figures 7b and 7c). Despite the limited significance for these traits, average PH of the new cultivars ranged between approximately 70 and 90 cm, maintaining an LS of approximately 2 to 3 units and avoid-

ing significant losses in the field. Several studies performed in other countries, including the United States and China, have shown simultaneous reductions in these traits over the years (Keep et al., 2016; Wang et al., 2016). Further, the trend of decreasing PH has been favored by selection for greater resistance to lodging (Rogers et al., 2015; Ustun et al., 2001), but this was not observed in the study reported herein. Although there were no changes in PH over the years, there was a significant reduction in BPH. However, despite the reduction in BPH in new cultivars, the minimum values remained above 10 cm, thus not compromising mechanized harvesting, and avoiding field losses (Figure 7d).

There were no significant changes in phenological traits between the old and the new cultivars over the years (Figures 7e, 7f, and 7g). However, although the linear model was not significant for any of the phenological traits, the quadratic model for DF was significant, showing an initial increase between the 1960s and the 1990s, followed by a

reduction at the end of the evaluated historical series, especially after the 2000s (Figure 7f). It is worth mentioning that, although the set of cultivars evaluated in this study did not show significant changes in DM over the years, the number of early cultivars released in the Midwest Region has increased over the last few years, as observed for the South Region in the present study. In the Midwest Region, there was also a need to use early cultivars that allowed double cropping with corn or cotton in the same season, in addition to favoring the control of Asian soybean rust (Specht et al., 2014; Toledo et al., 2006). The introduction of indeterminate growth-habit germplasm in Midwest Region also showed yield potential combined with earliness, which until then were difficult to obtain with determinate growth-habit cultivars (Specht et al., 2014).

Regarding the traits associated with end-use quality, there was a significant gain of $0.025\% \text{ yr}^{-1}$ ($0.127\% \text{ yr}^{-1}$) for OIL, and a reduction of $-0.036\% \text{ yr}^{-1}$ ($-0.111\% \text{ yr}^{-1}$) for PROT over the years (Figures 7h and 7i). These results corroborate the findings of several studies conducted in Brazil (Bonato et al., 2000), Canada (Morrison et al., 2000, 2008), and the United States (Rincker et al., 2014; Rowntree et al., 2013; Ustun et al., 2001), indicating that these traits were indirectly altered with yield improvement (Rincker et al., 2014; Rogers et al., 2015). As previously discussed, these observations can be explained by the negative correlation between OIL and PROT, which has been widely reported (Boehm Jr. et al., 2019; Cober & Voldeng, 2000; de Felipe et al., 2016; Ustun et al., 2001) and also identified in this study in the Midwest Region of Brazil ($r = -0.67$, $p < .001$; data not shown).

The OILY and PROTY traits also increased over the years, with absolute rates of genetic gain of $3.83 \text{ kg ha}^{-1} \text{ yr}^{-1}$ and $3.67 \text{ kg ha}^{-1} \text{ yr}^{-1}$, respectively. These gains correspond to relative rates of 0.64 and $0.37\% \text{ yr}^{-1}$, respectively (Figures 8a and 8b). Although the yield per unit area of these components is important, the processing industries have great interest in the concentrations of oil and protein in the seeds. As previously mentioned, the reduction in protein levels has caused concern for the crushing industries, because the composition of the seeds has a direct effect on the quality of the final products (de Felipe et al., 2016; Pípolo et al., 2015; Rincker et al., 2014), which highlights the need for simultaneous selection of end-use quality traits and SY in the coming years (Boehm Jr. et al., 2019).

Positive and significant correlations between SY and OILY ($r = .83$, $p < .001$) and PROTY ($r = .84$, $p < .001$) were observed in the Midwest Region, as these traits were obtained as the product of OIL and PROT with the yield (Supplemental Figure S5), similar result to that observed in the South Region. On the other hand, SY was negatively correlated with PROT ($r = -0.35$, $p < .05$), and the correlation with OIL was not significant ($r = .30$, $p \geq .05$), as also observed in the South Region in the present study. Despite the lack of sig-

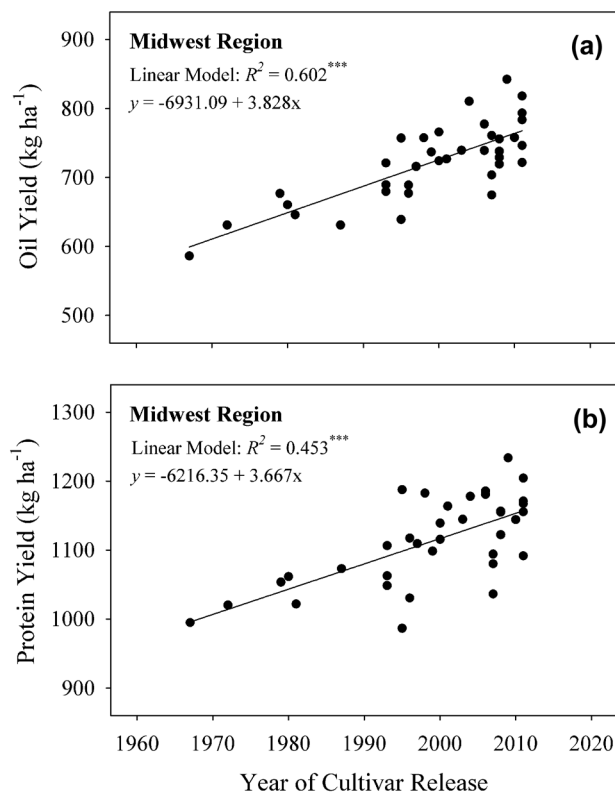


FIGURE 8 Regressions between the year of soybean cultivar release and oil (a) and protein yield (b) in the Midwest Region of Brazil. Each data point is the best linear unbiased predictor (BLUP) of the end-use quality trait for a cultivar, generated for the set of environments (location \times year) of the evaluated region. ***Significant at the .001 probability level

nificance for OIL, several studies have shown that this trait has increased indirectly with yield improvement, followed by reductions in PROT as previously discussed (Boehm Jr. et al., 2019; Morrison et al., 2008; Voldeng et al., 1997). The correlations between SY and the other evaluated traits in the Midwest Region were not significant (Supplemental Figure S5).

Our results showed that the efforts of breeding programs have changed important traits in Brazilian soybean cultivars, and significant genetic gains for SY have been attained. The linear increases over time indicate that the yield has not reached a plateau, showing that there is potential for soybean improvement in the coming years. However, the rates of genetic gain obtained in both evaluated regions during the last five decades are still below those estimated as necessary to feed the projected global population of more than 9 billion people by 2050 (FAO, 2009; Ray et al., 2013), a conclusion also highlighted by Boehm Jr. et al. (2019) for the U.S. conditions. The combined use of the currently available tools of genomics and phenomics will play a key role in increasing future rates of genetic gain for important crop species such as soybean (Crossa et al., 2021).

4 | CONCLUSIONS

There was a significant genetic gain in SY in the South Region of Brazil from 1966 to 2011. The estimated rates of genetic gain ranged from 11.98 to 15.31 kg ha⁻¹ yr⁻¹ for the evaluated maturity groups and Macroregions. These gains are equivalent to relative gains ranging from 0.33 to 0.42% yr⁻¹. In the Midwest Region, the rates of genetic gain obtained from 1967 to 2011 ranged between 13.58 and 21.84 kg ha⁻¹ yr⁻¹, which correspond to relative gains from 0.47 to 0.77% yr⁻¹ for the evaluated maturity groups.

New cultivars presented more PH, OIL, OILY, and PROTY, and less TSW, DF, DM, and PROT than old cultivars in the South Region, although there were differences between the Macroregions. In the Midwest Region, the new cultivars also showed higher OIL, OILY, and PROTY, whereas concomitantly, they showed lower BPH and PROT than the old cultivars.

The results showed that breeding programs have been efficiently improved soybean yield in the South and Midwest Regions of Brazil, with positive rates of genetic gain for all evaluated MGs. The breeding efforts added to the introduction of germplasm were decisive for obtaining the crescent gains over the years. The absence of a yield plateau is another positive result, highlighting that the rates of genetic gain have been maintained over the years and that further gain can be achieved in the future.

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AUTHOR CONTRIBUTIONS

Anderson Simionato Milioli: Conceptualization; Data curation; Formal analysis; Investigation; Methodology; Writing-original draft; Writing-review & editing. Daniela Meira: Data curation; Formal analysis; Investigation; Methodology; Writing-original draft. Maiara Cecília Panho: Data curation; Investigation; Methodology; Writing-original draft. Laura Alexandra Madella: Data curation; Investigation; Methodology; Writing-original draft. Leomar Guilherme Woyann: Formal analysis; Investigation; Methodology; Writing-original draft. Matheus Henrique Todeschini: Investigation; Methodology; Writing-original draft. Andrei Daniel Zdziarski: Investigation; Methodology; Writing-original draft. Otávio Ramos Campagnoli: Investigation; Methodology; Writing-original draft. Caroline Patrícia Menegazzi: Investigation; Methodology; Writing-original draft. Lucas Leite Colonelli: Invest-

igation; Methodology; Writing-original draft. Rogê Afonso Tolentino Fernandes: Investigation; Methodology; Writing-original draft. Carlos Lásaro Pereira de Melo: Conceptualization; Investigation; Resources; Supervision; Writing-review & editing. Marcelo Fernandes de Oliveira: Conceptualization; Resources; Supervision; Writing-review & editing. Paulo Fernando Bertagnolli: Conceptualization; Investigation; Resources; Supervision; Writing-review & editing. Carlos Alberto Arrabal Arias: Conceptualization; Resources; Supervision; Writing-review & editing. Nizio Fernando Giasson: Conceptualization; Investigation; Resources; Supervision; Writing-review & editing. Marcos Norio Matsumoto: Conceptualization; Resources; Supervision; Writing-review & editing. Marcos Quiroga: Conceptualization; Resources; Supervision; Writing-review & editing. Raphael Rossi Silva: Conceptualization; Investigation; Resources; Supervision; Writing-review & editing. Ivandro Bertan: Conceptualization; Investigation; Resources; Supervision; Writing-review & editing. Marcio Andrei Capelin: Investigation; Resources; Supervision; Writing-review & editing. Gilvani Matei: Investigation; Resources; Supervision; Writing-review & editing. Giovanni Benin: Conceptualization; Project administration; Resources; Supervision; Writing-review & editing.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

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