

Selection of recombinant soybean lines with high grain productivity performance for low altitude regions

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Abstract

Superior soybean genotype selection for breeding programs involves several processes, which might be considered complex because important traits are mostly quantitative and highly influenced by the environment. This work was developed in order to evaluate the performance of recombinant soybean lines through genetic parameters and the performance of qualitative and quantitative agronomic traits, with emphasis on grain yield in low altitude regions. A total of 126 recombinant F₁₀ soybean lines were evaluated in an augmented block design with three cultivars as interspersed checks. The traits assessed were: plant height (PH), number of pods per plant (NPP), first pod insertion height (FPIH), grain mass per plant (GMP), and grain yield (GY). Mixed models (REML/BLUP) were used to estimate the genetic parameters, and based on the BLUP predicted values, the multi-trait genotype-ideotype distance index (MGIDI) index was applied to select lines closest to the desired ideotype. High heritability values (>0.90) were observed for all characteristics assessed and experimental accuracy was also high. The MGIDI index selected the lines RIL18_IRC001, RIL103_IRC035, RIL73_IRC038, RIL124_IRC039, RIL71_IRC012, RIL115_IRC013, RIL113_IRC017, and RIL114_IRC038, which reached the greatest proximity to the intended agronomic ideotype. The line RIL13_IRC038 was selected simultaneously for reduction of FPIH and increase in PH, NPP, GMP, and GY, thus investment in this line is recommended. The use of mixed models and multi-trait indices maximizes the potential for selecting superior genotypes for future cultivars adapted to low-altitude environments.

Keywords: *Glycine max*; Heritability; Mixed models; multi-trait indices.

Introduction

Soybean (*Glycine max* L.) is the most widely cultivated oilseed in the world, with great agricultural, economic, and social importance. According to the United States Department of Agriculture (USDA, 2025), referring to the 2024/2025 harvest, approximately 47.4 million hectares are cultivated in Brazil, producing a total of 169 million tons of grains. According to the same survey, Brazil is responsible for 40 % of global production of these grains, followed by the United States of America (28 %), Argentina (12 %), and China (5 %). This relevance is due to the fact that soybean grains contain approximately 35 % protein, 22 % oil (lipids),

28 % carbohydrates, and 4 % ash, totaling close to 100 % of their composition (OLIVEIRA et al., 2023; GUARIENTI et al., 2024). In Brazil, soybean is cultivated across wide range of environments, including low-altitude regions, where specific climatic conditions such as higher temperatures, altered photoperiod responses, and increased biotic pressures can directly affect crop development and grain yield, requiring the development of adapted genotypes (BATTISTI et al., 2017).

Because it is grown in different regions of Brazil, soybean presents great variability in its productive performance, which drives genetic improvement programs to select genotypes that

are productive in different environments with the desired characteristics (MATEI *et al.*, 2018). This variability is even more pronounced in low-altitude environments, where genotype performance may be strongly influenced by temperature regimes and environment stability, intensifying genotype (G) x environment (E) interactions and making selection more complex (SENTELHAS *et al.*, 2015; ZDZIARSKI *et al.*, 2018). However, there are great difficulties in obtaining widely adapted genotypes and consider that to mitigate the effects of the G x E interaction, it is necessary to conduct experiments in a larger number of locations, evaluating the magnitude of the interaction and its impact on genotype selection and recommendation (CRUZ *et al.*, 2026).

Thus, selecting superior progeny for breeding programs involves several processes, which might be considered complex, since most important traits are quantitative in nature and highly influenced by the environment. In addition, these traits are often correlated, which allows the use of multi-trait approaches to improve selection efficiency (VIEIRA *et al.*, 2025). To increase the efficiency of trait selection, indirect selection through correlated traits can be used. Correlation analyses between grain yield and its main components are useful for understanding this complex trait (TISOTT *et al.*, 2023).

Thus, some selection practices are optimized when breeders use consolidated parameters available to guide direct and indirect selection methods (WOYANN *et al.*, 2019). Among the essential parameters, heritability, additive genetic variations, and expected genetic gain in progenies stand out (TORRES *et al.*, 2015; TROYJACK *et al.*, 2017). Many models are used to select superior genotypes, but mixed models (REML/BLUP) are particularly noteworthy. These are effective in recommending genotypes for soybean (PRADEBON *et al.*, 2023), white oat (SAVICKI *et al.*, 2023; LORO *et al.*, 2022), and wheat (SEGATTO *et al.*, 2022). Another widely

used model for selecting superior genotypes is the model based on the genetic distance from the genotype to the intended ideotype (MGIDI). This model allows analyzing the affinity of genotypes with the agronomically important traits sought by genetic improvement programs (PRADEBON *et al.*, 2025).

Given the above, this work was developed in order to evaluate the performance of recombinant soybean lines of the F₁₀ generation through genetic parameters, performance of qualitative and quantitative agronomic traits, with emphasis on grain productivity in low-altitude regions, for the future launch of a cultivar.

Material and methods

The study was carried out in the 2023/2024 harvest, at Granja Uruquá, located in the municipality of Caibaté- RS (28°17'56.18" S and 54°40'51.40" W, 286 m). The soil is classified as Dystrophic Red Latosol (SANTOS *et al.*, 2018). According to the Köppen climate characterization, the climate of the region fits the description of subtropical Cfa, with the occurrence of hot summers, without episodes of prolonged droughts and cold and humid winters, with the occurrence of frost (ALVARES *et al.*, 2014).

The experimental design was an augmented block design with intercropping checkplots. The regular treatments consisted of 126 recombinant inbred soybean lines (RILs) of the F₁₀ generation, obtained through the Genetic Improvement Program of Unijuí. The common treatments (interspersed checks) consisted of three cultivars: TMG 7067 IPRO (T1), BMX Zeus IPRO (T2), and BMX Raio IPRO (T3), arranged in four replicates.

The experimental units consisted of three seed rows, spaced 0.45 m apart and ten meters long, totaling a useful area of 4.5 m². For all genotypes, a density of 18 seeds per linear meter was used, with a base fertilization of 220 kg ha⁻¹ of NPK (03-28-00) and 120 kg ha⁻¹ of potassium

chloride with 60 % potassium applied at the V 4 stage. Phytosanitary management was carried out to minimize biotic effects (insect pests and weeds).

Subsequently, when the crop reached the physiological maturity stage, five plants were randomly selected in each experimental unit and the following were measured: plant height (PH, cm), measuring the distance from the plant collar to the last expanded trifoliate; number of pods per plant (NPP, units); first pod insertion height (FPIH, cm), distance from the plant collar to the first legume on the main stem; grain mass per plant (GMP, grams); the legumes were harvested and threshed, with seed moisture adjusted to 13 %; subsequently, the grain yield per hectare (GY, kg ha⁻¹) was estimated.

Data regarding meteorological variables, maximum air temperature (Tmax, °C), mean air temperature (Tmean, °C), minimum air temperature (Tmin, °C), precipitation (Prec, mm) were obtained through the Nasa Power platform (NASA POWER, 2025).

The data obtained were subjected to the diagnosis of normality of residual variances using the Shapiro-Wilk test, homogeneity of residual variances using the Bartlett test, and additivity of the statistical model. Once the assumptions were met, the method based on Restricted Maximum Likelihood (REML) was used to estimate the variance components and genetic parameters, as well as their interactions in the model. Significance was obtained through deviance analysis at 5 % probability using the chi-square (χ^2) test.

The restricted logarithm of the likelihood (LogLik), the Akaike criterion (AIC) and the Maximum Likelihood Ratio (LRT) were computed together. The significant model by the χ^2 probability allowed estimating the parameters: genetic variance (σ^2G); residual variance (σ^2R); phenotypic variance (σ^2P), and the genetic

parameters: broad-sense heritability (H^2); accuracy (Acc); genotypic coefficient of variation (CVg); residual coefficient of variation (CVr); ratio between the genotypic and residual coefficient of variation (CVratio). Subsequently, the Best Linear Unbiased Prediction (BLUP) model was used, based on the mathematical model:

$$y_{ij} = \mu + \alpha_i + \tau_j + \varepsilon_{ij},$$

Where: y_{ij} is the observed value for the i th genotype in the j th repetition; μ is the overall mean; α_i is the effect of the i th genotype; τ_j is the effect of the j th repetition; ε_{ij} is the random error.

Based on the values estimated by BLUP, the multi-trait index based on the distance between the genotype and a desired agronomic ideotype (MGIDI) (OLIVOTO, NARDINO, 2021) was used. In this study, the ideotype was defined a priori by the researcher, specifying the desired direction of selection for each trait. Thus, the objective of multiple selection was to increase (positive direction) NPP, PH, and GY, while reducing FPIH. Although the MGIDI index performs the ranking and selection of genotypes automatically based on the distance to the ideotype, it allows flexibility in defining the desired direction of selection according to breeding objectives. The MGIDI method allowed estimating the following parameters: observed mean (X_o), mean of the selected lines (X_s), selection differential (S_d , %), commonality (Com), and selection direction. This multivariate index is based on the model obtained from the model:

$$MGIDI_i = \left[\sum_{j=1}^f (\gamma_{ij} - \gamma_j)^2 \right]^{0,5}$$

Where: $MGIDI_i$ is the distance index from the genotype to the ideotype sought in the lineage; γ_{ij} represents the score of the i th progeny for the j th factor e ; γ_j consists of the score of the j th ideotype. Thus, the lineage with the lowest $MGIDI$ index is closest to the desired ideotype. The line i of the progeny, explained by the j th factor (ω_{ij}), is used to highlight the potentialities and deficiencies of the progenies (OLIVOTO; NARDINO, 2021). Through the model:

$$w_{ij} = \frac{\sqrt{D^2_{ij}}}{\sum_{j=1}^f \sqrt{D^2_{ij}}}$$

Thus: D^2_{ij} = means the distance between the i-th progeny and the ideotype for the j-th factor. Low contributions from a given factor indicate that the traits are closer to the intended ideotype (OLIVOTO, NARDINO, 2021). The analyses were performed using R software (R CORE TEAM, 2025) using the *metan* (OLIVOTO, LUCIO, 2020), and *ggplot2* (WICKHAM, 2016) packages.

Results and discussion

Variance components were estimated using restricted maximum likelihood (Table 1), and

deviance analysis revealed significant effects ($p > 0.05$) for all traits evaluated. This analysis was effective in identifying genetic variability for soybean grain yield (KNEBEL *et al.*, 2021; PRADEBON *et al.*, 2023; PORT *et al.*, 2024), white oat grain cycle and yield (PRADEBON *et al.*, 2025), and wheat grain quality (SEGATTO *et al.*, 2022). These results demonstrate the presence of genetic variability among the lines and the promising prospects for selecting superior genotypes.

It was observed that for all variables analyzed, the genetic variance (σ^2G) was greater than 91 %, as well as residual variance less than 6.2 %. These findings reveal that most of the variation is attributed to genetic effects and the low contribution of the environment in the expression

Table 1. Estimates of variance components and genetic parameters (RELM) for 126 soybean lines and three controls.

VAR	Model	LogLik	AIC	LR	PR (>Chisq)
PH	Genotype	-239	486	8.07	4.49e-3
FPIH	Genotype	-170	349	6.84	8.94e-3
NPP	Genotype	-317	641	39.2	3.83e-10
GMP	Genotype	-270	548	33.3	7.74e-9
GY	Genotype	-366	741	13.2	2.81e-4
Parameters	PH	FPIH	NPP	GWP	GY
σ^2G	192.33	17.06	2175.41	444.93	2457806.958
σ^2G (%)	94.33	91.19	99.78	99.41	93.80
σ^2R	11.54	1.64	4.61	2.62	162369.76
σ^2R (%)	5.66	8.80	0.21	0.58	6.19
σ^2P	203.88	18.70	2180.02	447.56	2620176.72
H^2	0.94	0.91	0.99	0.99	0.93
H^2 mg	0.98	0.96	0.99	0.99	0.97
Acc	0.99	0.98	1.00	0.99	0.98
CVg	14.19	20.19	39.37	44.29	33.10
CVe	3.47	6.27	1.81	3.40	8.51
CVratio	4.08	3.21	21.70	13.01	3.89

PH: plant height; **FPIH:** first pod insertion height; **NPP:** number of pods per plant; **GMP:** grain mass per plant; **GY:** grain yield; σ^2G : genotypic variance; σ^2G (%): percentage of genotypic variance; σ^2R : residual variance; σ^2R (%) percentage of residual variance; σ^2P : individual phenotypic variance; H^2 : broad-sense heritability; H^2 mg: narrow-sense heritability of genotypes; **Acc:** genotype selection accuracy; **CVg:** genotypic coefficient of variation; **CVr:** residual coefficient of variation **CV ratio:** ratio between CVg and CVe.

Source: authors (2025).

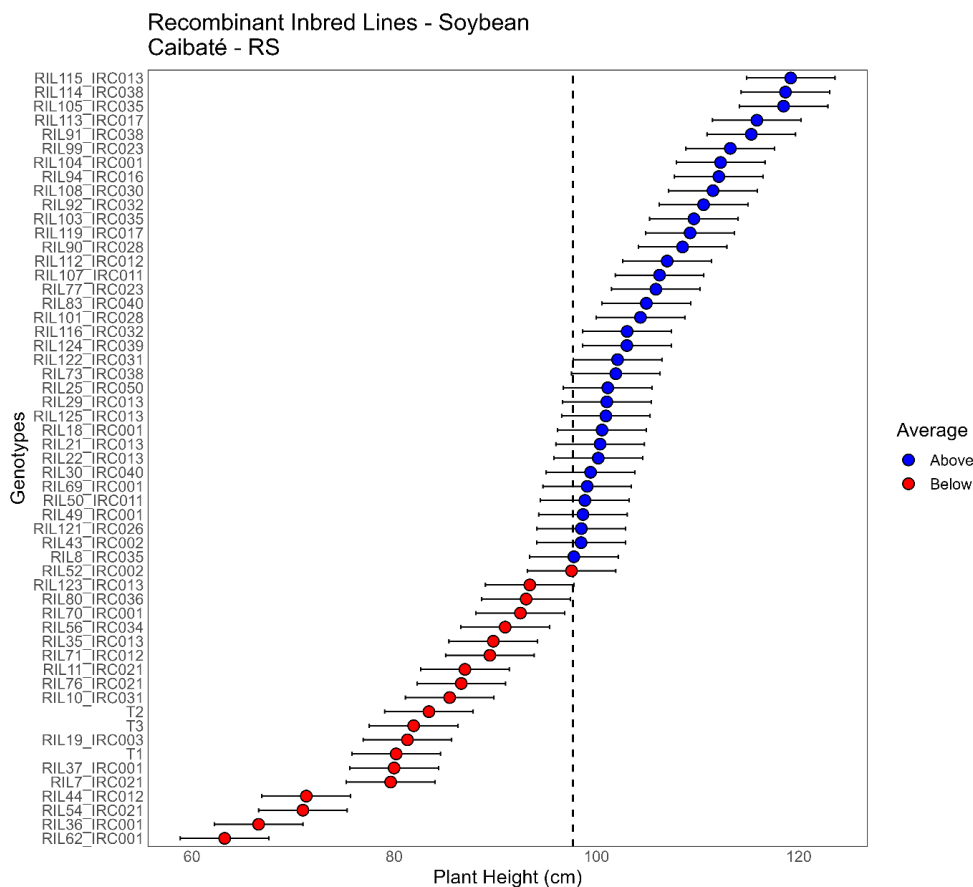
of the character (PORT *et al.*, 2024; PRADEBON *et al.*, 2025). In summary, the results confirm the genetic predominance in the determination of PH, FPIH, NPP, GWP, and GY, with minimal environmental contribution, in addition to revealing the possibility of selection among the lines for all characters under study. Heritability had values of 0.91, 0.93, 0.94, 0.99, and 0.99 for FPIH, GY, PH, NPP, and GWP, respectively. Similar results for PH heritability were found by Silva *et al.* (2021), in 360 soybean lines with a value of 0.86. In another study carried out by Tisott *et al.* (2023), heritability of 0.75 was observed for NPP and NGP and 0.69 for GY, values lower than those of the present study. Under the conditions where this study was carried out, it was found that these traits had high H^2 (>0.90), which was enhanced by the large number of lines with high genetic

variability intrinsic to the basis of the breeding program and control of residual variations during the conduct of the trials.

The accuracy values were high (>0.70), revealing the precision of the study. According to Da Costa *et al.* (2000), high accuracies provide high experimental precision, effectiveness in selection strategies, and genetic gains to the characters under study. The ratio between the coefficient of genotypic and residual variance (CVratio) was 4.08, 3.21, 21.70, 13.01, and 3.89 for PH, FPIH, NPP, GWP, and GY, respectively, which are very high (Table 1). The occurrence of values greater than 1 indicates favorable and promising selection.

The use of a mixed model such as REML/BLUP allows exploring the genetic variability

Figure 1. Prediction of the means of the best unbiased linear predictor (BLUP) for the variable plant height (PH), in 129 soybean genotypes, in the municipality of Caibaté - RS.



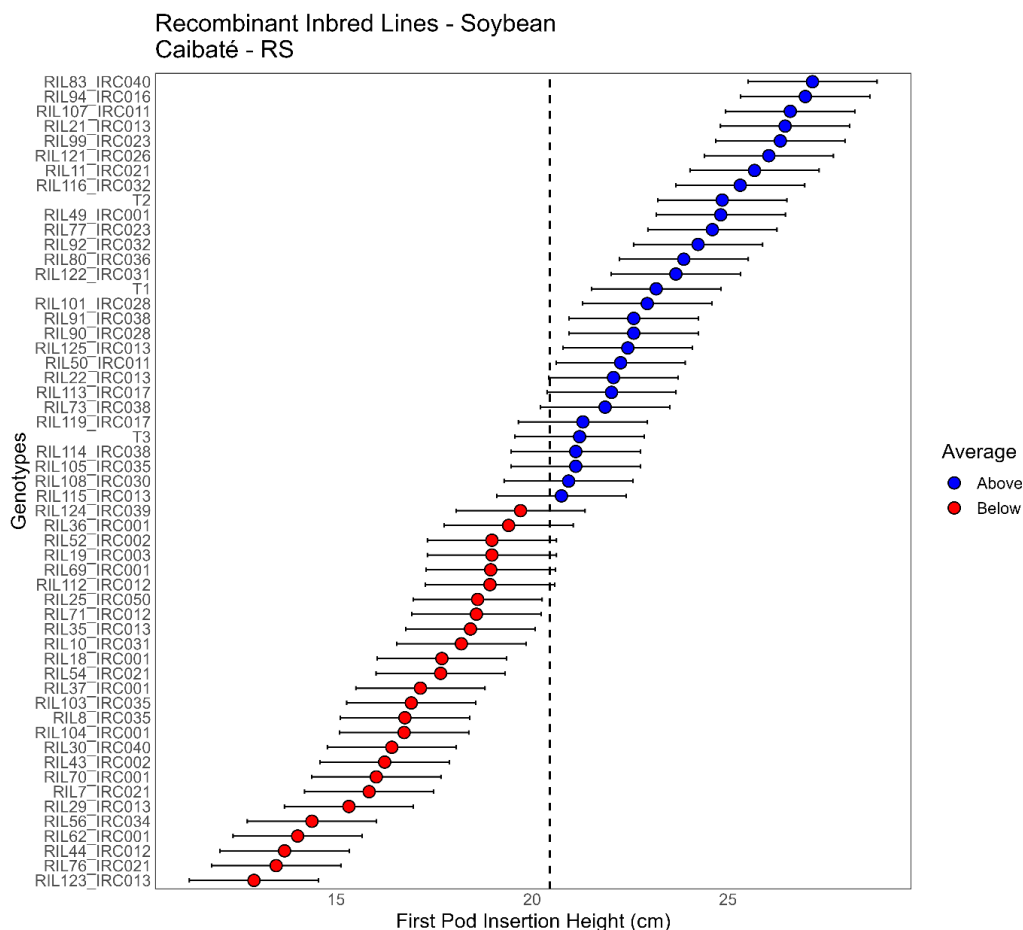
Source: authors (2025).

present in the study population, aiding breeder decision-making and maximizing the efficiency of selecting superior genotypes (SILVEIRA *et al.*, 2022). Plant height (PH) among the lines varied between 63 and 119 cm, with an overall average of 97.68 cm (Figure 1). The highest PH was observed for the line RIL115_IRC013, with 119 cm, while the lowest PH was recorded for the line RIL8_IRC035, with 63 cm. Although there is no defined ideotype for soybean plant height, it is believed that genotypes with height up to 90 cm are ideal (SEDIYAMA *et al.*, 2015). In a study carried out by Yang *et al.* (2021), using 168 F_9 soybean lines, observed that PH varied between 63 and 191 cm. The authors suggest that this trait is additive in origin, with the parents contributing equally to its expression.

Therefore, understanding plant height variability and its additive nature is essential for the careful selection of parents, allowing for more precise and efficient selection strategies to obtain compact genotypes, reducing lodging and maximizing mechanized harvesting.

First pod insertion height (FPIH) is an agronomically relevant trait in soybean crops, as it directly influences the efficiency of mechanized harvesting, as very low insertions can result in harvest losses. The best unbiased linear predictor revealed high genetic variability for this trait, with values ranging from approximately 12.90 cm to 27 cm and an overall average of 20.45 cm (Figure 2). According to Szareski *et al.* (2015), plants with FPIH greater than 10 cm are desired,

Figure 2. Prediction of the means of the best unbiased linear predictor (BLUP) for the variable first pod insertion height (FPIH) in 129 soybean genotypes, in the municipality of Caibaté - RS.



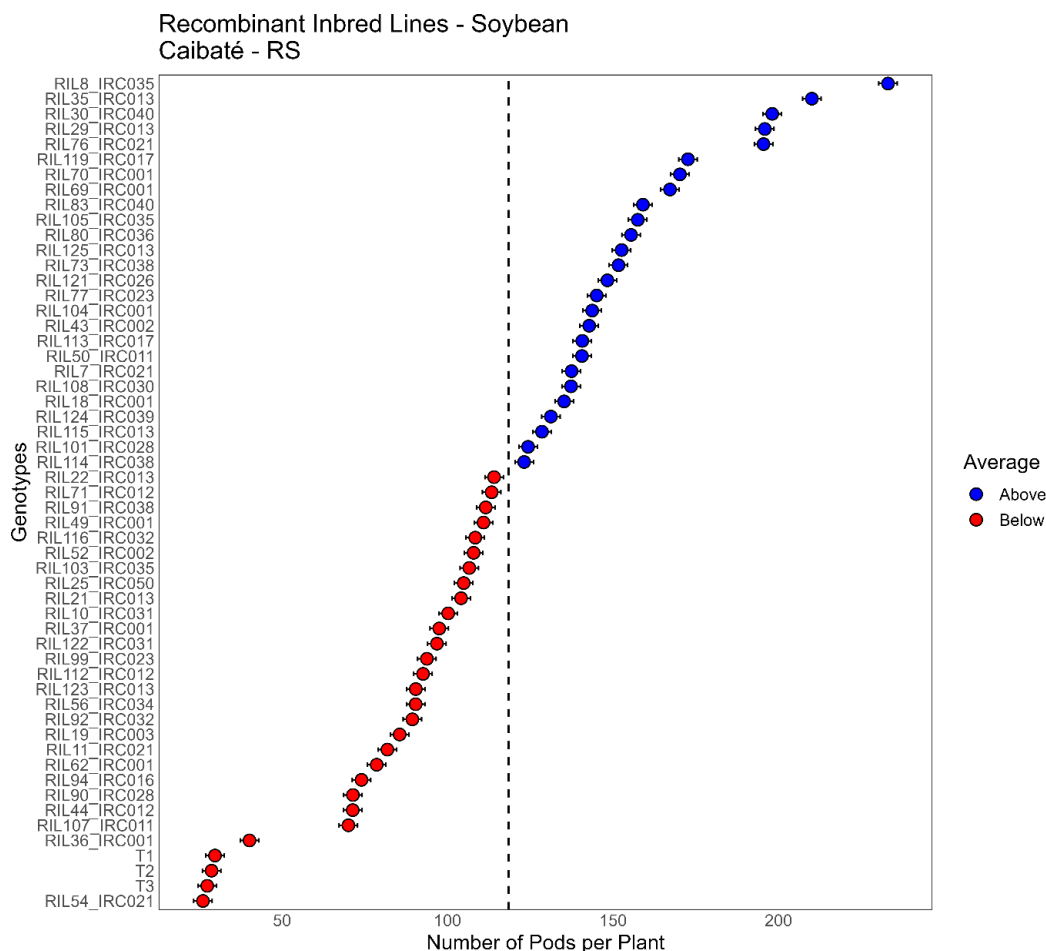
Source: authors (2025).

as they maximize harvest. However, Ribeiro *et al.* (2017) describe that high FPIH can be disadvantageous, as it leads to the formation of plants with a smaller production zone, reducing the crop's production potential. Thus, Rocha *et al.* (2012) report that, for most soybean crop conditions, the ideal height of insertion of the first legume is around 15 cm. Thus, the lines that come closest to this measurement are RL29_IRC013, RL7_IRC021, RL70_IRC001, RL43_IRC002, RL30_IRC040.

According to the BLUP analysis for the number of pods per plant (NPP), it was observed that there is great variability between the lines with values between 26 and 233 legumes per plant, with an overall average of

118 units (Figure 3). It was observed that the lines RIL76_IRC021, RIL29_IRC013, RIL30_IRC040, RIL35_IRC013 and RIL8_IRC035, accumulated 195, 196, 198, 210 and 233 pods respectively. In contrast, the line RIL54_IRC021 and the controls T1 (TMG 7067 IPRO), T2 (BMX Zeus IPRO) and T3 (BMX Raio IPRO) accumulated the lowest NPP values. According to Paraginski *et al.* (2024), the number of pods per plant is related to the number of grains per plant and, consequently, to grain yield. Selection for this variable occurs intensively in breeding programs. In the same study, the authors observed a high positive correlation between the number of pods and the number of grains per plant ($r=0.97$). These results corroborate

Figure 3. Prediction of the means of the best unbiased linear predictor (BLUP) for the variable number of pods per plant (NPP), in 129 soybean genotypes, in the municipality of Caibaté - RS.



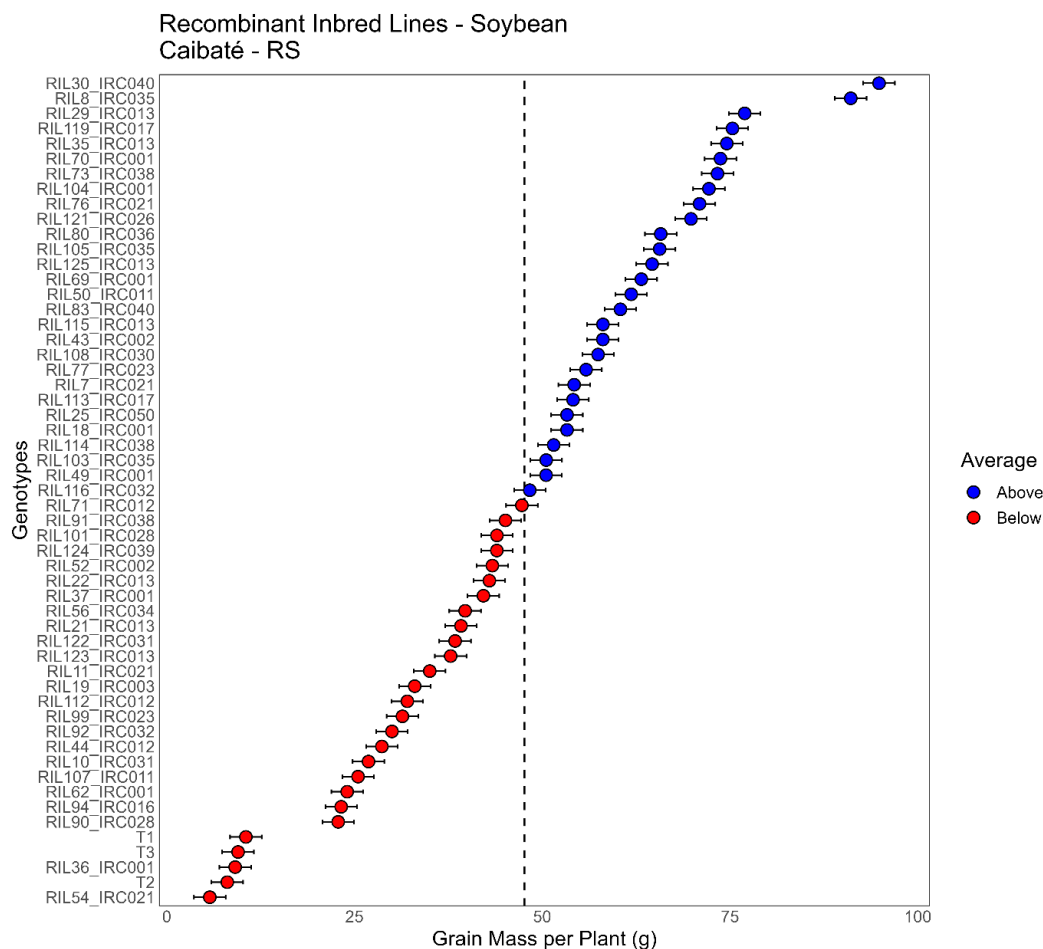
Source: authors (2025).

those found by Smiderle *et al.* (2019). These results confirm the success of the program in obtaining lines with superior performance, with the potential to form groups of elite lines and a germplasm bank for the development of soybean cultivars with high production potential.

It was observed that the grain mass per plant (GMP) ranged from 5.73 to 94.85 grams, with an overall average of 47.62 grams (Figure 4). The low-performance genotypes were RIL36_IRC001 and RIL54_IRC021, as well as T1, T2, and T3, with grain weight below 10.5 grams. However, the genotypes RIL30_IRC040, RIL8_IRC035, RIL29_IRC013, RIL119_IRC017, RIL35_IRC013, RIL70_IRC001, RIL73_IRC038, RIL104_IRC001, RIL76_IRC021, RIL121_IRC026, RIL80_IRC036, RIL105_IRC035, RIL125_IRC013, RIL69_IRC001, RIL50_IRC011, RIL83_IRC040, RIL115_IRC013, RIL43_IRC002, RIL108_IRC030, RIL77_IRC023, RIL7_IRC021, RIL113_IRC017, RIL25_IRC050, RIL18_IRC001, RIL114_IRC038, RIL103_IRC035, RIL49_IRC001, RIL116_IRC032, RIL71_IRC012, RIL91_IRC038, RIL101_IRC028, RIL124_IRC039, RIL52_IRC002, RIL22_IRC013, RIL37_IRC001, RIL56_IRC034, RIL21_IRC013, RIL122_IRC031, RIL123_IRC013, RIL11_IRC021, RIL19_IRC003, RIL112_IRC012, RIL99_IRC023, RIL92_IRC032, RIL44_IRC012, RIL10_IRC031, RIL107_IRC011, RIL62_IRC001, RIL94_IRC016, RIL90_IRC028, T1, T3, RIL36_IRC001, T2, and RIL54_IRC021 presented grain weight per plant greater than 75 grams. A promising performance of the lines

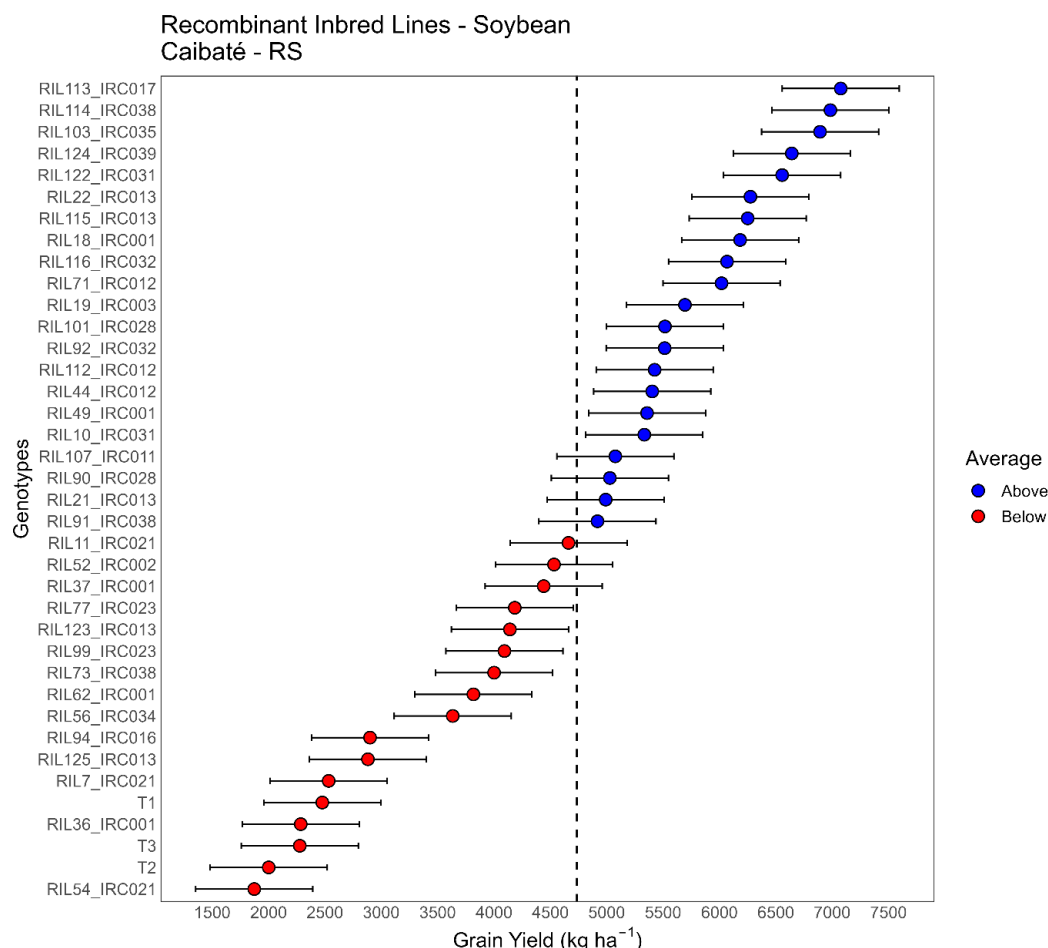
evaluated in the present study was observed, as they were superior to the commercial check plots, with the exception of RIL36_IRC001 and RIL54_IRC021. Recent studies have revealed lower values for grain weight per soybean plant between 3 and 25 grams (LENHARDT *et al.*, 2023). Paraginski *et al.* (2024) state that soybean grain yield is proportional to the thousand grain weight, having presented a positive correlation coefficient ($r=0.56$). Thus, the selection of high-performance soybean genotypes can be carried out indirectly, through characteristics such as thousand grain weight, number of legumes, grains, and nodes per plant (SOUZA *et al.*, 2015; UMBURANAS *et al.*, 2022; PARAGINSKI *et al.*, 2024).

Figure 4. Prediction of the means of the best unbiased linear predictor (BLUP) for the variable grain mass per plant (GMP), in 129 soybean genotypes, in the municipality of Caibaté - RS.



Source: authors (2025).

Figure 5. Prediction of the means of the best unbiased linear predictor (BLUP) for the grain yield (GY) variable, in 129 soybean genotypes, in the municipality of Caibaté - RS.



Source: authors (2025).

The predictions for soybean grain yield revealed wide variability among the lines in grain yield (Figure 5), with values ranging from approximately 1872.94 to over 7076 kg ha^{-1} , demonstrating the high genetic potential available for selection. A significant number of RILs were superior to the commercial checkplots, with inferiority only for RIL36_IRC001 and RIL54_IRC021. It is noteworthy that the RILs, RIL114_IRC038, RIL103_IRC035, RIL124_IRC039, RIL122_IRC031, RIL22_IRC013, RIL115_IRC013, RIL18_IRC001, RIL116_IRC032, RIL71_IRC012, reached performance superior to 6 t ha^{-1} of grains, demonstrating high potential. Umburanas *et al.* (2022), when studying the

grain productivity gains of 26 soybean cultivars registered in the last five decades in southern Brazil, observed grain productivity between 700 and 5700 kg ha^{-1} , in the 2017 and 2018 harvests. The authors also reveal productivity increases of 2.1 % per year (45.9 kg ha^{-1}), that is, an increase of 2.3 times between 1965 and 2015.

The potential of these genetic backgrounds, either for the release of new cultivars or as a source of variability in breeding programs, is indicated by the observed data. In addition, the significant genetic gains can be attributed to the recombination performed during the development of these lines.

Table 2. Genotype-ideotype multi-trait distance analysis, multi-trait selection of soybean lines (MGIDI).

VAR ¹	FACTOR	FAI1 ²	FAI2 ³	Xo ⁴	Xs ⁵	Sd(%) ⁶	Com ⁷	Sense
NPP ⁸	FA1	0.95	0.02	118.00	129.00	8.74	0.85	Increase
GMP ⁹	FA1	0.94	-0.01	47.60	54.00	13.40	0.91	Increase
GY ¹⁰	FA1	0.74	0.16	4735.00	6256.00	32.10	0.90	Increase
PH ¹¹	FA2	0.08	0.69	97.70	107.00	9.84	0.88	Increase
FPIH ¹²	FA2	0.62	-0.95	20.50	19.80	-3.04	0.57	Decrease

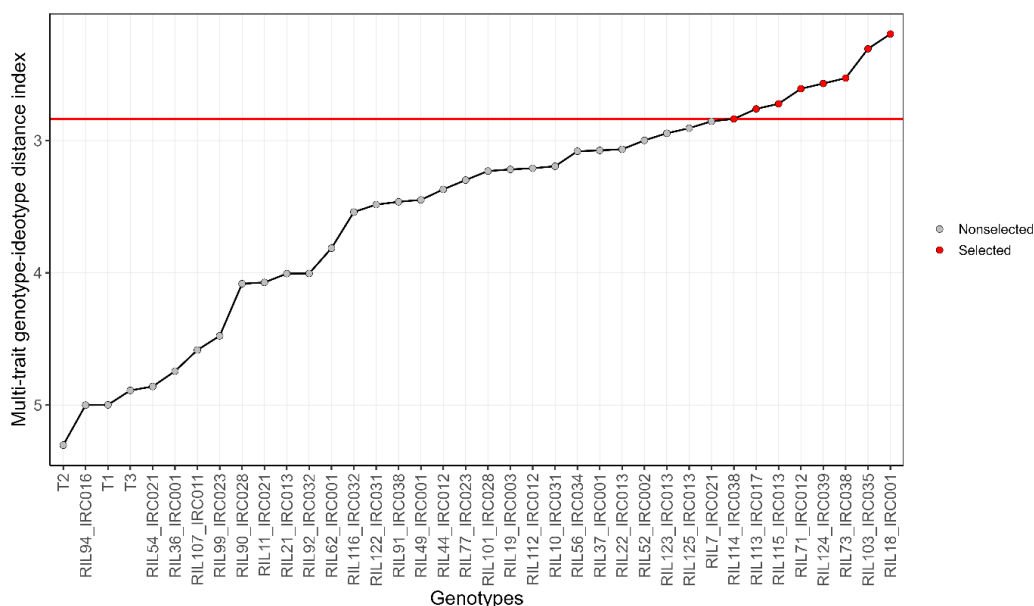
¹Variables: VAR; ²FA1: Factor 1; ³FA2: Factor 2; ⁴Xo: observed mean; ⁵Xs: mean of cultivars (Xs); ⁶Sd, %: percentage difference; ⁷Com: Commonality; ⁸NPP: Number of pods per plant; ⁹GMP: Grain mass per plant; ¹⁰GY: Grain yield; ¹¹PH: Plant height; ¹²FPIH: First pod insertion height.

Source: authors (2025).

Factor analysis revealed the formation of two important factors, with an average commonality of 0.824 (Table 2). According to Cruz *et al.* (2014), the minimum acceptability for this parameter is 0.64. Among the groups, Factor I was identified, which brought together NPP, GWP, and GY, with a positive direction. Factor II brought together PH and FPIH, with the objective of increasing and reducing, respectively. In this scenario, eight RILs were selected: RIL18_IRC001, RIL103_IRC035, RIL73_IRC038,

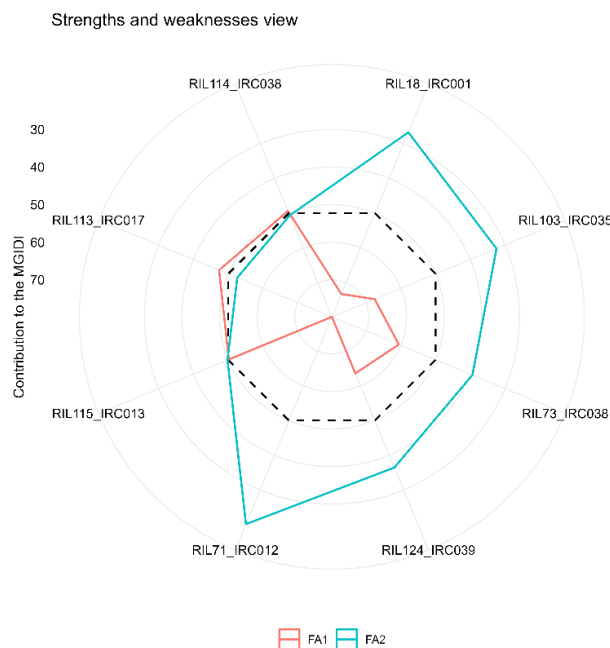
RIL124_IRC039, RIL71_IRC012, RIL115_IRC013, RIL113_IRC017 e RIL114_IRC038. In other words, they met the selection premises imposed by the breeder.

The multi-trait analysis for the soybean lines in relation to the distance of the genotype to the agronomic ideotype of soybean (Figure 6) revealed that the selected RILs were RIL18_IRC001, RIL103_IRC035, RIL73_IRC038, RIL124_IRC039, RIL71_IRC012, RIL115_IRC013, RIL113_IRC017 and

Figure 6. Classification of genotypes in ascending order for the *MGIDI* index, based on the quantitative characteristics of soybeans.

Source: authors (2025).

Figure 7. Proportion of each factor in the calculated genotype-ideotype distance index (*MGIDI*). The smaller the proportion explained by a factor (closer to the outer edge), the closer the characteristics of that factor are to the ideotype. The dashed line indicates the theoretical value if all factors contribute equally.



Source: authors (2025).

RIL114_IRC038, where there was greater proximity to the intended agronomic ideotype, evidencing the potential for using these genotypes in soybean breeding programs.

The proportion of responsiveness of the RILs selected under each selection factor is presented in Figure 7. For Factor 1, which targets increases in NLP, GWP, and GP, the selected lines were RIL71_IRC012, RIL126_IRC039, RIL073_IRC038, RIL103_IRC035, RIL18_IRC001 and RIL15_IRC013. For Factor 2, aimed at increasing PH and reducing IFL, the genotypes with the greatest contribution were RIL13_IRC15, RIL113_IRC017 and RIL114_IRC038.

Considering the focus, in terms of concentration of efforts of the breeding program, for the agronomic ideotype index and the ideotype index for reducing FPIH and increasing PH, NPP, GWP and GP, it is recommended to invest in the potential of the RIL13_IRC15 line, where it was simultaneously selected for these characteristics through the multi-trait index.

Thus, this study gathered valuable information on the characterization of the soybean agronomic ideotype for the selection of genotypes with high number of legumes per plant, grain weight, and grain yield. This ideotype can be used as a reference standard to aid in the selection of superior soybean genotypes through multi-trait selection indices. This allows for targeted genotype selection, thus maximizing the efficiency of the selection process for high-yield plants.

Conclusions

The use of mixed models and multi-trait indices maximizes the potential for selecting superior genotypes for future cultivars adapted to low-altitude environments.

Plant height, insertion of the first legume, number of legumes per plant, grain weight per plant and grain productivity have a high genetic contribution.

The elite lines of the F₁₀ generation RIL36_IRC001 and RIL54_IRC021 were superior to the commercial controls for grain yield. The lines RIL18_IRC001, RIL103_IRC035, RIL73_IRC038, RIL124_IRC039, RIL71_IRC012, RIL115_IRC013, RIL113_IRC017 and RIL114_IRC038 met the intended ideotype for the crop.

Only the RIL13_IRC15 line was selected concomitantly with the multivariate indices, with genes that combine greater plant height, number of legumes per plant, grain weight per plant and grain yield, as well as lower height of the insertion of the first legume.

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