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AGRONOMIC PERFORMANCE AND SELECTION OF IDEAL SOYBEAN GENOTYPES

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RESUMO:

The study aimed to evaluate agronomic performance and select ideal soybean genotypes. The experiment happened at the Missions Agronomic Research and Results Center (CPRAM), located in Entre-Ijuís - Rio Grande do Sul, South Region of Brazil. The experiment used random blocks with 36 different types of soybeans in four different tests. The units of the experiment were 40 square meters. The research evaluated morphological and productive characters and meteorological data from the experiment's environment. The MGIDI index selected the genotypes DM 5958, BMX ZEUS, NS 6601, BMX FIBRA, and P 95R51 by potentiating the variables number of legumes per plant, the number of grains per plant, the thousand-grain weight, and the grain yield. The genotype selection with higher grain yield can be performed indirectly through the number of legumes per plant and legumes on the main stem.

Keywords: Linear correlation, *Glycine max*, Selection index.

DESEMPENHO AGRONÔMICO E SELEÇÃO DO GENÓTIPOS IDEAIS DA SOJA

RESUMO:

O objetivo do estudo foi avaliar o desempenho agronômico e selecionar genótipos ideais da soja. O experimento foi realizado no Centro de Pesquisa e Resultados Agronômicos de Missões (CPRAM), localizado em Entre-Ijuís - Rio Grande do Sul, Sul, Brasil. O experimento utilizou o delineamento de blocos casualizados, sendo avaliados 36 genótipos da soja dispostos em quatro repetições. As unidades experimentais foram formadas por 40 metros quadrados. Foram avaliados caracteres morfológicos e produtivos, bem como dados meteorológicos do ambiente do experimento. Os genótipos DM 5958, BMX ZEUS, NS 6601, BMX FIBRA e P 95R51 foram selecionados pelo índice MGIDI potencializando as variáveis número de legumes por planta, número de grãos por planta, peso de mil grãos e produtividade de grãos. A seleção de genótipos com maior produtividade de grãos pode ser realizada indiretamente através do número de legumes por planta e legumes na haste principal.

Palavras-chave: Correlação linear, *Glycine max*, Índice de seleção.

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INTRODUCTION

Soybean (*Glycine max* L.) is one of the most versatile crops in the world, as it has great agricultural, social, economic, and nutritional relevance (Gazzoni, 2018). In the 2020/21 crop, world soybean production was 362.947 million tons in a cultivated area of 127.842 million hectares. Brazil, as the largest producer of this oilseed, produced 135.409 million tons in an area of 38.502 million hectares of cultivation (Usda, 2021).

Because of the soybean importance, new investments are fundamental for the development of new technologies, cultivars, and management that allow greater sustainability for the soybean production chain (Pradebon et al., 2023). The manifestation of the genetic potential of soybean depends on several environmental elements, such as photoperiod, maximum, average, and minimum temperature, and solar radiation, as well as the specific characteristics of the variety, such as stability and tolerance to insect pests and diseases, which can influence this process (Pradebon et al., 2023).

The choice of cultivars is a major factor that influences both soybean yield and soybean components. To increase the efficiency of the character selection, correlated characters can use indirect selection. Correlation analyses between grain yield and its main components are useful to understand this complex character (Alcantara Neto et al., 2011).

The genotype-environment interaction generates implications for the evaluation of genotypes, which can influence phenotypic value estimates and thus result in limitations in selection gains and make it difficult to recommend cultivars. Predicting the behavior of soybean genotypes in different locations is complex since there is great heterogeneity in climatic conditions within the same region. Multiple tools are genotype recommendations such as AMMI, GGE, REML/BLUP, and principal components. These are effective in recommending soybean genotypes (Pradebon et al., 2023), white oats (Savicki et al., 2023; Loro et al., 2022), and wheat (Segatto, et al., 2023).

Evaluating genotype performance is one of the basic principles for recommending them to certain environments where the most adapted genotypes have higher productivity. This characteristic influences the genotype-environment interaction (Borges et al., 2013). Therefore, the study aimed to evaluate agronomic performance and select ideal soybean genotypes.

MATERIALS AND METHODS

The experiment occurred at the Missions Agronomic Research and Results Center (CPRAM), located at latitude 28º23'17.82” S and longitude 54º19'13.74” W at an altitude of 213 meters, located in Entre-Ijuís - Rio Grande do Sul, South Region of Brazil. The soil classification is typical dystrophic red Latosol - the humid subtropical Cfa environment according to Köppen. The experiment used random blocks with four different treatments. Each block was 40 square meters.

The treatments correspond to 36 soybean cultivars, they are: BMX COMPACTA (65I65RSF IPRO), BMX CROMO (57I59RSF IPRO), BMX DELTA IPRO (59I60RSF IPRO), BMX FIBRA (64I61RSF IPRO), BMX GARRA (63I64 IPRO), BMX LANÇA 58I60RSF IPRO, BMX LOTUS (61I63RSF IPRO, BMX VALENTE (6968RSF RR), BMX ZEUS (55I57RSF IPRO), BRS 5601 RR, BRS 5804 RR, C 2570 RR, C 2626 IPRO, DM 5958 RSF IPRO, DM 66I68 RSF IPRO RSF, HO AMAMBAY (54HO14MM IPRO), HO IGUAÇU (64HO133 IPRO), HO JACUÍ (59HO124 IPRO), HO JACUTINGA (57HO123 IPRO), HO PIRAPÓ (64HO114 IPRO), HO TERERE (64HO116 IPRO), M 5838 IPRO, NEO 610 IPRO, NS 5700 IPRO, NS 6010 IPRO, NS 6601 IPRO, NS 6909 IPRO, P 95R51 RR, P 95R95 IPRO, P 96R10 IPRO, TMG 2165 IPRO, TMG 2757 IPRO, TMG 7058 IPRO, TMG 7260 IPRO, TMG 902 and TMG 903.

Seeding happened in the second half of November 2019. The seeding density was 14 seeds per linear meter, with fertilization of 380 kg ha^{-1} of NPK (11-30-20) and 17 days after seeding, the coverage took place with 100 kg ha^{-1} of potassium chloride. Phytosanitary management was important to minimize biotic effects on the experiment outcome. The measurement of ten plants within the usable area of each experimental unit was necessary. The variables were: plant height (PH, cm), insertion of the first legume (IFL, cm), zone of production (ZP, cm), number of legumes on the stems (NLS, units), legumes in the zone of production (L_ZP, units), number of legumes in the branches (NLB, units), number of branches (NB, units), number of legumes per plant (NLP, units), number of grains per plant (NGP, units), and thousand grain weight (TGW, grams). Meteorological variables were: medium temperature (Tmed, ºC/d¹), maximum temperature (Tmax, ºC/d¹), minimum temperature (Tmin, ºC/d¹), relative air humidity (RH, %), precipitation (Prec., mm/d¹), and radiation (Rad, MJ/ m²/ d¹).

The data were submitted to analyze variance assumptions, such as homogeneity of residual variances by Bartlett's test and normality of errors by Shapiro Wilk. Then, descriptive analysis described the behavior of meteorological variables to understand the results obtained. The meteorological information was minimum temperature (Tmin), maximum temperature (Tmax), medium temperature (Tmed), relative air humidity (RH), precipitation (Prec.), and radiation (Rad.) (Nasa Power, 2021).

Genetic evaluation techniques based on mixed models of the BLUP type (Best Linear Unbiased Predictor) are essential for predicting additive and genotypic genetic values of individuals with the potential for selection. Subsequently, the Restricted Maximum Likelihood (REML) method was used, where the significance was obtained through the Deviance analysis at 5% probability by the Chi-square test. This model performs operations to estimate variance components and predict genetic values.

We estimated the phenotypic variance (σ^2P), broad sense heritability (H^2), mean genotype heritability (H^2mg), determination coefficient of genotype-environment interaction effects (GEI), genotypic correlation between genotype and performance environments, coefficient of genotypic variation (CVg*), residual coefficient of variation (CVr*) and the variation coefficient of the proportion between genotypic coefficient variation and productivity (CVratio*).

MGIDI model was used to perform the multi-trait estimate of the genotype-ideotype distance index (Olivoto e Nardino, 2021). Then, Pearson's linear correlation was necessary to show the linear trend of association between the characters with a significance of 5% by the t-test. For the preparation of the statistical analyses, the packages used: Exp.Des. pt, metan, and GGPLOt2, where the metan package was used to apply the MGIDI index and the correlation, while the GGPLOT2 package was used to develop the graphics through the Software R Core Team (2022).

RESULTS AND DISCUSSION

According to the meteorological data (Figure 1), from February to April, they had a behavior below the ideal. The maximum temperatures varied; November, December, and January had the highest peaks, reaching 40ºC. Temperatures above 40ºC cause the abortion of flowers and legumes (Zanon et al., 2018). In general, December, January, February, and March had the highest percentage of ideal soybean temperatures.

According to Figure 1, observe the total accumulation at 486 mm throughout the cycle, which is a low volume. According to Carvalho et al. (2013), soybean has a water demand of 450 to 850 mm throughout its cycle. Another important point is that in February and March, the averages were low, which possibly affected the development of the crop, coinciding with the grain-filling period when there was greater demand for water volumes.

Solar radiation, in addition to providing light energy for photosynthesis, also provides environmental signals for various physiological processes in soybeans. However, in the event of a water deficit, productivity may be higher in environments with a lower incidence of solar radiation. November and January were the ones with the highest average temperatures exceeding 400 MJ/m²/d¹, while December presented the greatest variations in radiation.

In the Deviance analysis (Table 1), which presents the variance parameters of the 36 soybean genotypes, there was significance ($p \leq 0.05$) for the characters' plant height (PH), insertion of the first legume (IFL), zone of production (ZP), number of legumes in the main stem (NLS), legumes in the zone of production (L_ZP), number of legumes in the branches (NLB), number of branches (NB), number of legumes per plant (NLP), number of grains per plant (NGP), thousand-grain weight (TGW) and grain yield (GY).

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plant (NGP), thousand-grain weight (TGW) and grain yield (GY).

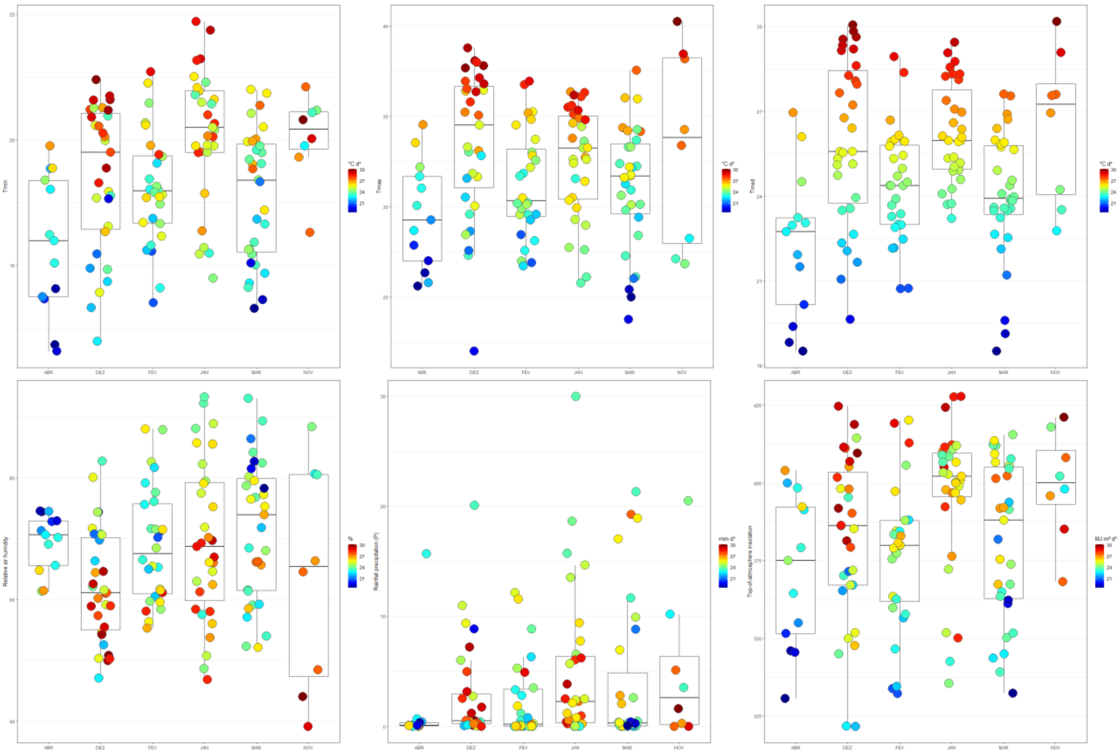

Figure 1. Meteorological data during the soybean cultivation cycle for minimum temperature (Tmin, ºC/d¹); maximum temperature (Tmax, ºC/d¹); medium temperature (Tmed, ºC/d¹); relative air humidity (RH, %); precipitation (Prec., mm/d¹); and radiation (Rad, MJ/m²/d¹).

Table 1. Deviance analysis in the identification of soybean variability.

PAR	PH	IFL	ZP	NLS	L_ZP	NLB	NB	NLP	NGP	TGW	GY
Deviance	*	*	*	*	*	*	*	*	*	*	*
Gen var	168.9	654	14160	98.44	0.01	32.01	0.76	150.6	602.3	296.3	24689
Gen (%)	88.68	65.08	86.9	87.01	67.91	55.19	56.22	75.52	75.52	56.17	69.2
Res_var	21.56	3.5	21.35	14.7	0.00	25.99	0.59	48.8	195.2	231.2	108042
Res (%)	11.32	34.92	13.1	14.7	32.09	44.81	43.78	24.48	24.48	43.83	30.8
σ²P	190.5	10.05	163	12.99	0.01	57.99	1.36	199.4	797.5	527.4	350731
H^2	0.88	0.65	0.86	0.87	0.67	0.55	0.56	0.75	0.75	0.56	0.69
H^2mg	0.96	0.88	0.96	0.96	0.89	0.83	0.83	0.92	0.92	0.83	0.89
Accuracy	0.98	0.93	0.98	0.98	0.94	0.91	0.91	0.96	0.96	0.91	0.94
CVg%	12.44	13.27	13.97	19.07	15.52	53.27	45.75	19.59	19.59	13.51	14.26
CVr%	4.44	9.71	5.42	7.36	10.67	48.00	40.38	11.15	11.15	11.94	9.51
Cv ratio	2.79	1.36	2.57	2.58	1.45	1.11	1.11	1.757	1.75	1.13	1.49

The parameters measured in the Deviance analysis are: genotypic variance (Gen_var); percentage of genotypic variance (Gen %); residual variance (Res_var); residual variance percentage (Res (%)); individual phenotypic variance (σ²P); heritability (H^2); mean genotype heritability (H^2mg); Accuracy; Genotypic variation coefficient (CVg); residual variation coefficient (CVr) ; coefficient of variation of the proportion between coefficient of genotypic and residual variation (CVratio); plant height (PH); insertion of the first legume (IFL); zone of production (ZP); number of legumes on the stem (NLS); legumes in the zone of production (L_ZP); number of legumes in the branches (NLB); number of branches (NB); number of legumes per plant (NLP); number of grains per plant (NGP); thousand grain weight (TGW); grain yields GY).

The variables plant height (PH), number of legumes on the main stem (NLS), and zone of production (ZP) showed the highest percentages of genotypic proportions, in which their values represent the greatest influence on the choice of genotype, with 88.68, 87.01, and 86.90%, respectively. The variables number of grains per plant (NGP), thousand-grain weight (TGW) and grain yield (GY) obtained the highest results for residual variation (Res_var), with values of 195.20, 231.20, and 108042, respectively. Likewise, for the individual phenotypic variation (σ^2P), these three parameters presented the respective values of 797.50, 527.40 and 350731.

For heritability (H^2), there were higher values for plant height (PH) at 88%, zone of production (ZP) at 86%, and number of legumes on the main stem (NLS) which obtained a value of 87%. The mean heritability (H2mg) of the genotypes represents the genetic contribution to the expression of the character, regardless of the evaluation environment. Thus, there are the variables plant height (PH), zone of production (ZP), and number of legumes on the stem (NLS), which obtained the highest values of the individual heritability genotype (H^2mg), with 96%.

There was a use of accuracy in genotype competition assays to determine experimental precision and to assess genotypic variation in the character. Therefore, in the analysis, all study variables had values above 90%, considered a high value, demonstrating the study's reliability. The genotypic variation coefficient (CVg) estimates the genetic variability of the trait available in the population, aiming for the highest possible values (Carvalho et al., 2016). The amplitude of the coefficient of genetic variation for the studied characters ranged from 12.44 to 53.27%, with the highest values for the number of legumes in the branch and number of branches, with values of 53.27 and 45.75, respectively.

Visualizing the coefficient of variation of the proportion between the coefficient of genotypic and residual variation (CVratio), values above one were observed for all characters evaluated. This data indicates that the number of genotypes used in this work was sufficient to select traits of agronomic interest (Leite et al., 2015, 2016). The variables plant height (PH), number of legumes on the stems (NLS) and zone of production (ZP) had the highest genotypic proportions, in which their values represented the greatest influence on the choice of genotype, with 88.68%, 87.01% and 86.90%, respectively (Figure 2).

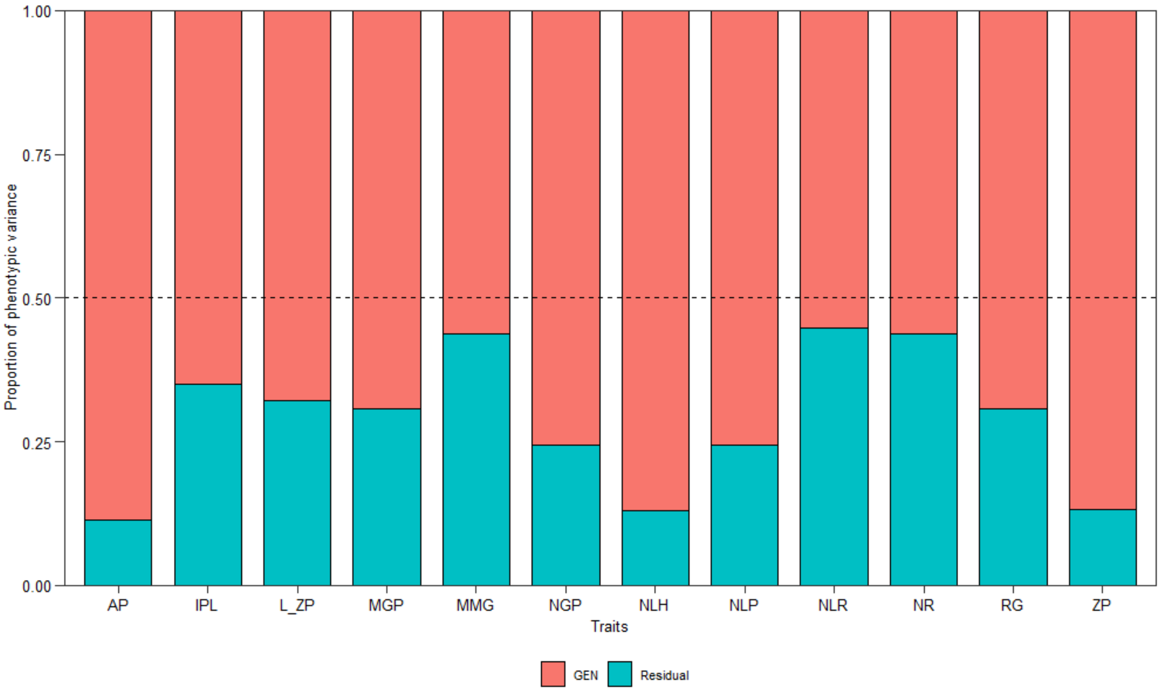

Figure 2. Phenotypic variance proportions for agronomic variables of soybean plant height (PH); insertion of the first legume (IFL); legumes in the zone of production (L_ZP); weight of grains per plant (WGP); thousand grain weight (TGW); number of grains per plant (NGP); number of legumes on stems (NLS); number of

legumes per plant (NLP); number of legumes in the branches (NLB); number of branches (NB); grain yield (GY); and zone of production (ZP).

The variables thousand-grain weight (TGW), number of legumes per plant (NLP), and number of branches (NB) presented the lowest values corresponding to the choice of genotype, being 56.17%, 55.19% and 56.22%, respectively.

The variables insertion of the first legume (IFL), legumes in the zone of production (L_ZP), weight of grains per plant (WGP), number of grains per plant (NGP), number of legumes per plant (NLP) and grain yield (GY) had median values compared to the proportions of genotype choice, with the respective values of 65.08, 67.91, 66, 75.2, 75.2 and 69.20%. The identification of genotypes with the characteristics desired by the breeder was through the evaluation of phenotypic data, which means phenotyping, to obtain a lineage that expresses all its genetic potential, reducing the environmental effect (Sousa et al., 2010).

Mixed models (BLUP) are fundamental for predicting genotype values and, thus, their recommendation for different productive regions (Ramalho e Araújo, 2011). For insertion of the first legume (IFL), the genotypes P 95R51, BRS 5804 RR and NS 5700 had the lowest heights, with values lower than 16 cm (Figure 3). The minimum height of the first legume must be above 10 cm to reduce losses at the time of soybean harvest (Rezende e Carvalho, 2007).

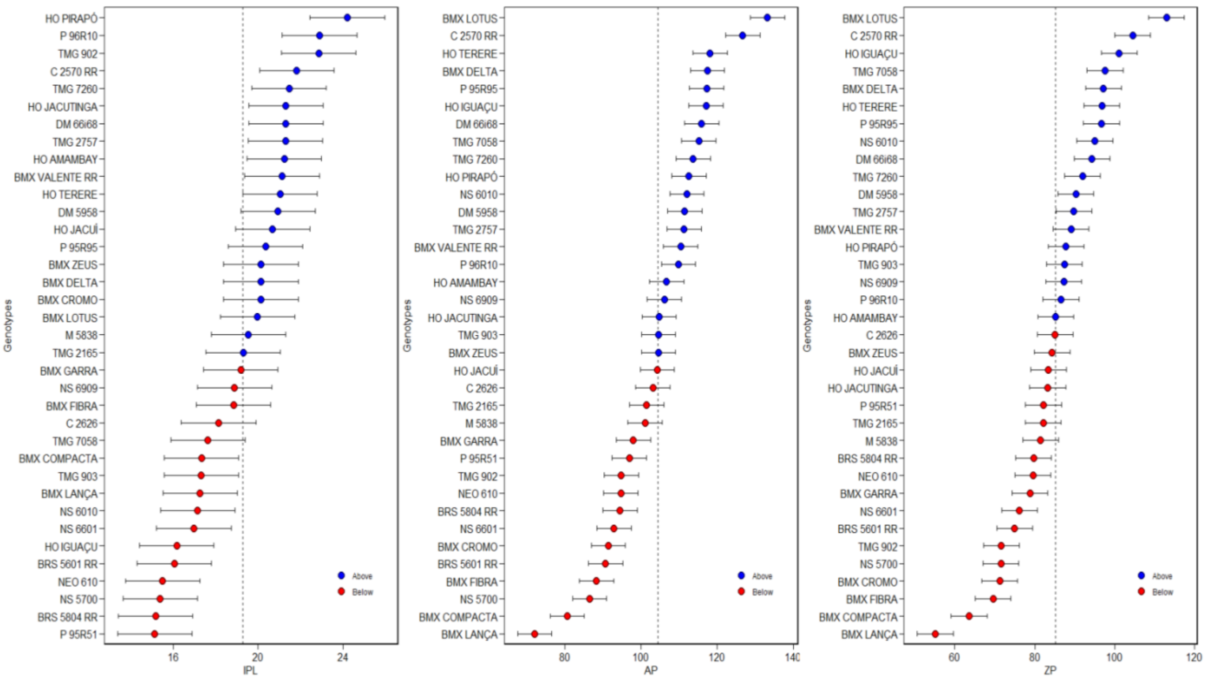

Figure 3. BLUP model for the variables insertion of the first legume (IFL, cm); plant height (PH, cm) and zone of production (ZP, cm) of soybean genotypes, represented by blue (higher than average) and red (lower than average) color.

For plant height, genotypes with intermediate heights are sought to reduce losses due to lodging and harvesting, for which plants taller than 80 cm can cause greater losses (Carvalho, et al., 2017). The genotypes BMX Compacta, NS5700, and BMX Fibra presented height close to the optimum of the culture. Regarding the zone of production, observe that the BMX Lotus, C 2570 RR, and HO Iguaçu genotypes presented the largest zones of production. However, this does not mean higher yields since genotypes with high stature direct greater amounts of photoassimilates to vegetative growth and, consequently, less legume development occurs.

For the number of legumes on the main stem (NLS), the genotypes showed lower average results: BMX DELTA IPRO, HO PIRAPÓ, HO IGUAÇU, BRS 5601RR, DM 66I68 RSF IPRO, HO JACUÍ, TMG 7058, TMG 2757, BMX LOTUS, HO TERERE,

NEO 610, P95R95, TMG 903, C2570RR, P 95R51, C 2626. For the variable number of legumes in the branches (NLB), the genotypes BRS 5804 RR, HO TERERE (64HO116 IPRO) and TMG 903 presented the highest values, being 23.92; 20.93 and 20.71 legumes respectively, while the genotypes HO AMANBAY IPRO, DM 59I58 RSF IPRO and HO JACUTINGA (57HO123 IPRO) had less than four legumes per branch. According to Szareski et al. (2015), approximately 66% of legumes are on the main stem, but management techniques and genotype characteristics influence this character.

The cultivars NEO 610, BRS 5601 RR and BRS 5804 RR had the highest number of pods in the production zone. The situation is different from what happens with the genotype BMX FIBRA and NS 6010, where there is an insertion of a reproductive node every 1.6 cm. According to reports by Nogueira et al. (2012), these characters present a positive and significant association with grain yield.

The number of branches lower than the average occurred for the genotypes TMG 903, NEO 610, HO IGUAÇU, BRS 5804RR, P 95R51, HO TERERE, BMX LOTUS, BMX CROMO, NS 5700, M5838, TMG 902, TMG 2165, BMX DELTA, TMG 7260, TMG 2757, P 95R95 (Figure 4). For number of legumes per plant and number of grains per plant, they showed a strong relationship, where the genotypes with the best results were HO IGUAÇU (87,02 NLP and 174.05 NGP), HO TERERE (81.10 NLP and 162.20 NGP) and BMX DELTA (80.89 NLP and 161.79 NGP). The genotypes with the lowest values for the variables number of legumes per plant and number of grains per plant are BMX LANÇA (41.49 units and 71.37 units), BMX FIBRA (41.49 units and 82.99 units), and COMPACT BMX (47.21 units and 94.43 units).

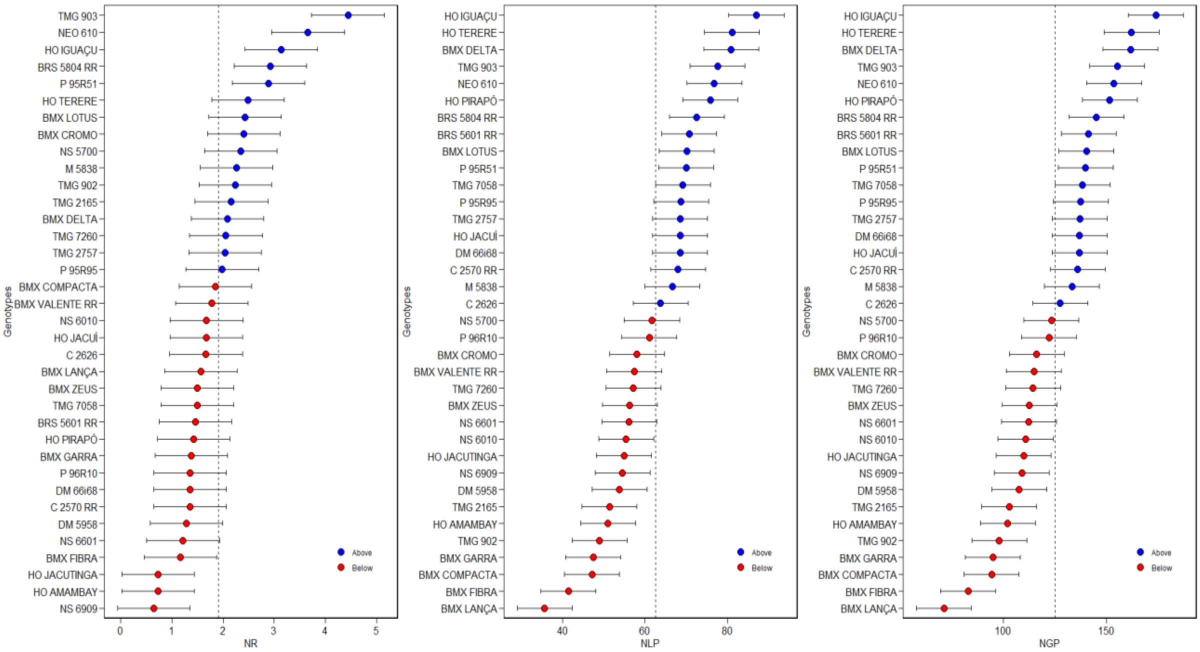

Figure 4. BLUP model for the number of branches (NB) variables, number of legumes per plant (NLP), and number of grains per plant (NGP) of soybean genotypes, represented by blue (higher than average) and red (lower than average) color.

The number of legumes per plant (NLP) is a variable that influences soybean yield, as it has a direct effect on the number of grains per plant. Nogueira et al. (2012) verified the direct effects of the number of legumes per plant on grain yield. Therefore, selecting soybean cultivars with the most legumes per plant will result in the indirect selection of genotypes with higher grain yield.

Using mixed models makes it possible to recommend genotypes broadly, considering only the genetic effect and increasing the probability of selecting the best genotypes (Pimentel et al., 2014). The conclusion is that genotypes weighing one thousand grains above 125g presented high performance (Figure 5). The genotypes NS6909, NS 6010, BMX LANÇA, M 5838, TMG 2757, NS 6601, BMX

ZEUS, HO AMANABAY, BMX VALENTE RR, TMG 902, BMX COMPACTA, BMX FIBRA, DM 5958, NS 5700, BRS 5804, BMX GARRA presented the largest mass of a thousand grains (MMG).

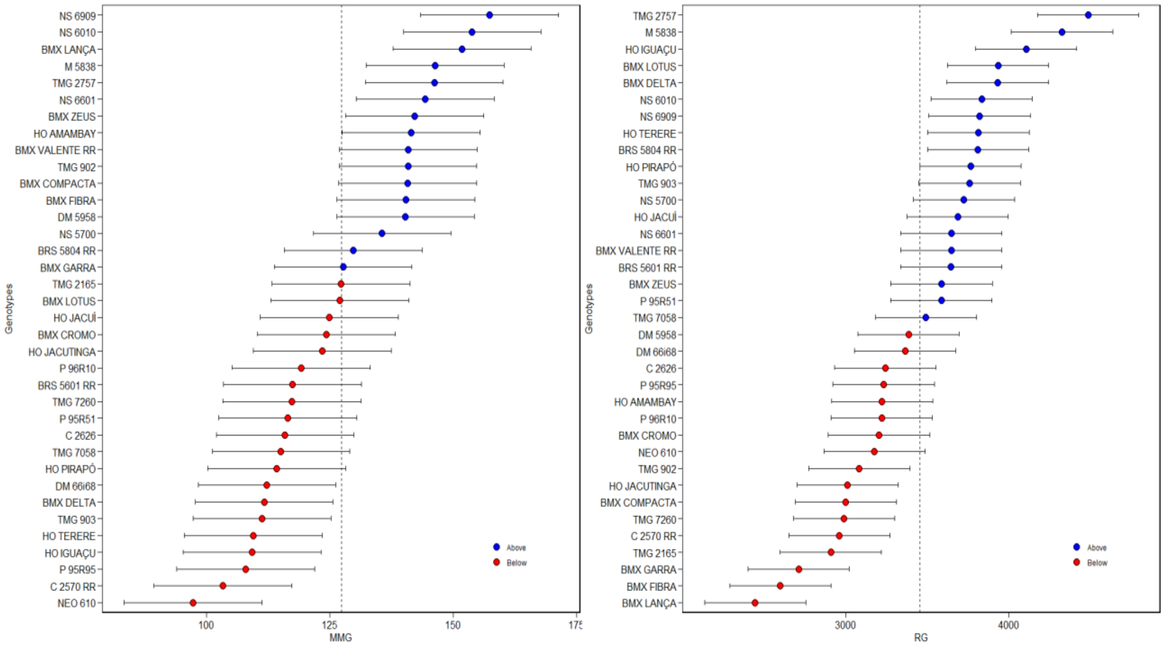

Figure 5. BLUP model for the variables thousand-grain weight (TGW) and grain yield (GY) of soybean genotypes, represented by blue (higher than average) and red (lower than average) color.

The genotypes TMG 2757 IPRO, M 5838 IPRO, and HO IGUAÇU (64HO133 IPRO) presented the highest averages of grain yields with 4484.11, 4104.79, and 4324.07 kg ha^{-1}, respectively. The opposite result occurred with the genotypes BMX LANÇA, BMX FIBRA, BMX GARRA, with productivity below 3000 kg ha^{-1}.

According to the multi-trait distance analysis (Table 2), the variables division was into two factors: when the number of legumes per plant (NLP), the number of grains per plant (NGP), and the thousand-grain weight (TGW) were represented by factor 1. The variables insertion of the first legume (IFL) and grain yield (GY) are represented by factor 2.

Table 2. Multi-trait genotype-ideotype distance analysis (MGDI) for the variables number of legumes per plant (NLP); number of grains per plant (NGP); thousand-grain weight (TGW); insertion of the first legume (IFL); and grain yield (GY).

VAR*	FACTOR	Xo	Xs	SD	SD Perc	H^2	SG	SG Perc	Sense	Objective
NLP	FA 1	58.4	61.2	2.74	4.68	0.858	2.35	4.02	Increase	100
NGP	FA 1	117	122	5.48	4.68	0.858	4.7	40.02	Decrease	100
TGW	FA 1	129	136	7.6	5.9	0.719	5.47	4.24	Increase	100
IFL	FA 2	18.8	17.2	-1.66	-8.79	0.663	-1.1	5.83	Decrease	100
GY	FA 2	3241	3537	296	9.12	0.581	172	5.3	Increase	100

*Variables (VAR); observed mean (Xo); desired mean (Xs); standard deviation (SD), standard deviation percentage (SDperc); heritability (H^2); genetic gain (SG); genetic gain percentage (SG Perc).

All variables, regardless of the factors, showed a difference between the obtained mean (Xo) and the desired mean (Xs). The average obtained from the number of legumes per plant (NLP) resulted in 58.4 grains, while the desired average obtained a value of 61.2. For the number of grains per plant, the average obtained was 117, while the desired average resulted in 122 grains. Another value observed was the average of 129 g of thousand grain weight and the desired average (Xs) was 136 grams.

The insertion of the first legume (IFL) behaves oppositely, as its desired direction is to decrease the average obtained (Xo) to 18.8 cm of insertion of the first legume (IFL). In comparison, the desired average (Xs) resulted in 17.2 cm. Grain yield (GY) also had an average (Xo) lower than the desired average (Xs), obtaining a difference of 296 kg.

For heritability (H^2), the variables that presented the highest results were the number of legumes per plant (NLP), the number of grains per plant (NGP), and the variable that resulted in the highest genetic gain (SG) was the number of grains per plant (NGP). Heritability (H^2) reveals the fraction of genetic variance in the phenotypic variance and can infer experimental reliability and precision for the phenotype (Ramalho et al., 2013).

In the multi-trait selection analysis (Figure 6), for the variables number of legumes per plant, number of grains per plant, thousand-grain weight, insertion of the first legume and grain yield, the materials were selected DM 5958 RSF IPRO, BMX ZEUS (55I57RSF IPRO), NS 6601 IPRO, BMX FIBRA (64I61RSF IPRO) and P 95R51. For the different factors, in Factor 1, which includes the variables number of legumes per plant (NLP), number of grains per plant (NGP) and the thousand-grain weight (TGW), the genotypes that stood out were the P 95R51 RR, BMX ZEUS (55I57RSF IPRO) and the DM 5958 RSF IPRO. Factor 2, represented by the variables insertion of the first legume (IFL) and grain yield (GY), the genotypes that had the best results were NS 6601 IPRO and BMX FIBRA (64I61RSF IPRO).

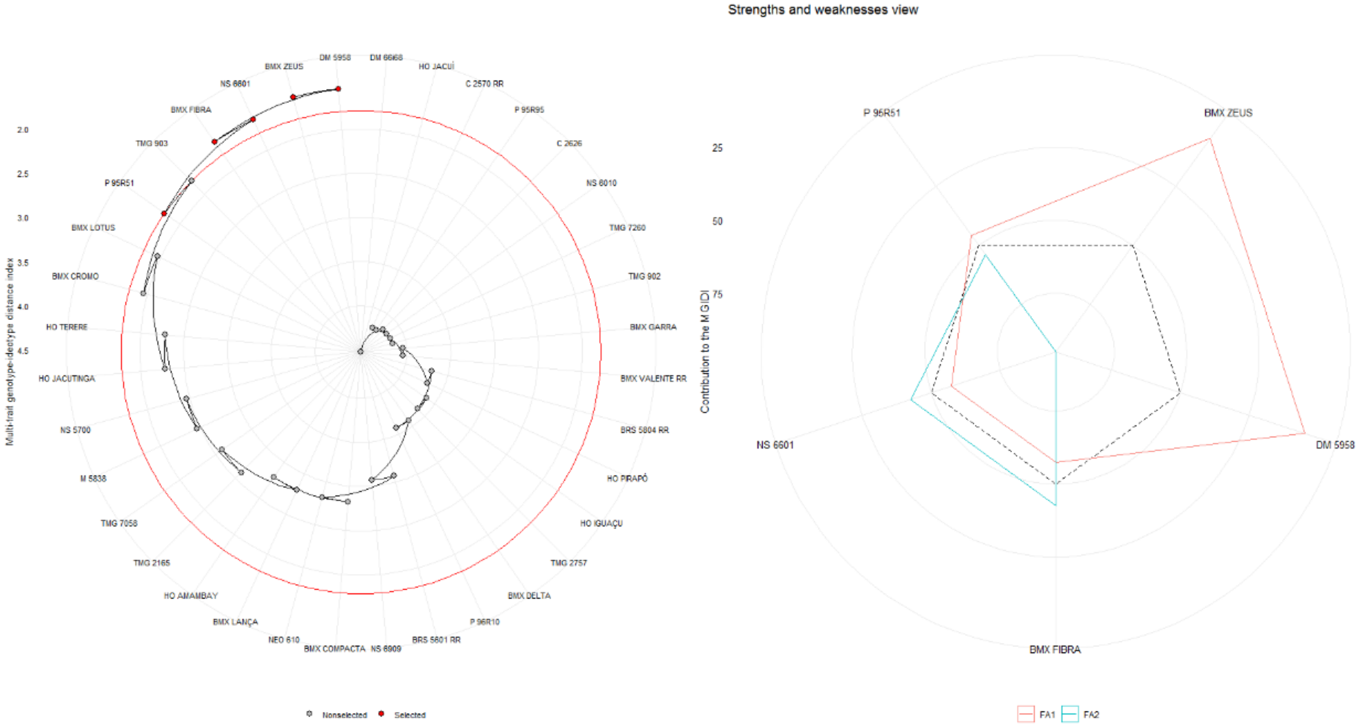

Figure 6. Multi-character selection of soybean genotypes by MGIDI methods for the variables number of legumes per plant (NLP); number of grains per plant (NGP); thousand grain weight (TGW); insertion of the first legume (IFL); and grain yield (GY).

Pearson's Linear Correlation is a technique used to identify the association between characters, presenting trends in the direction and magnitude of association between two characters (Meier et al., 2019). This presented 119 significant associations between the measured variables. However, only correlations of strong magnitudes are relevant.

There are strong and positive correlations between the variable number of legumes on the main stem (NLS), the number of legumes per plant (NLP) (0.85), the number of legumes on branches (NLB), and the number of branches (NB) (0.81) were observed (Figure 7). This type of association is desirable since these characters' considerations are important productivity components. Zuffo et al. (2018) and Nogueira et al. (2012) found a high correlation between the number of legumes per plant and productivity. There are correlations with strong associations between the number of legumes per plant (NLP) and legumes in the zone of production (L_ZP) (0.77). Figure 7 demonstrates correlations between plant height (PH) and zone of production (ZP), with a positive correlation of 0.97.

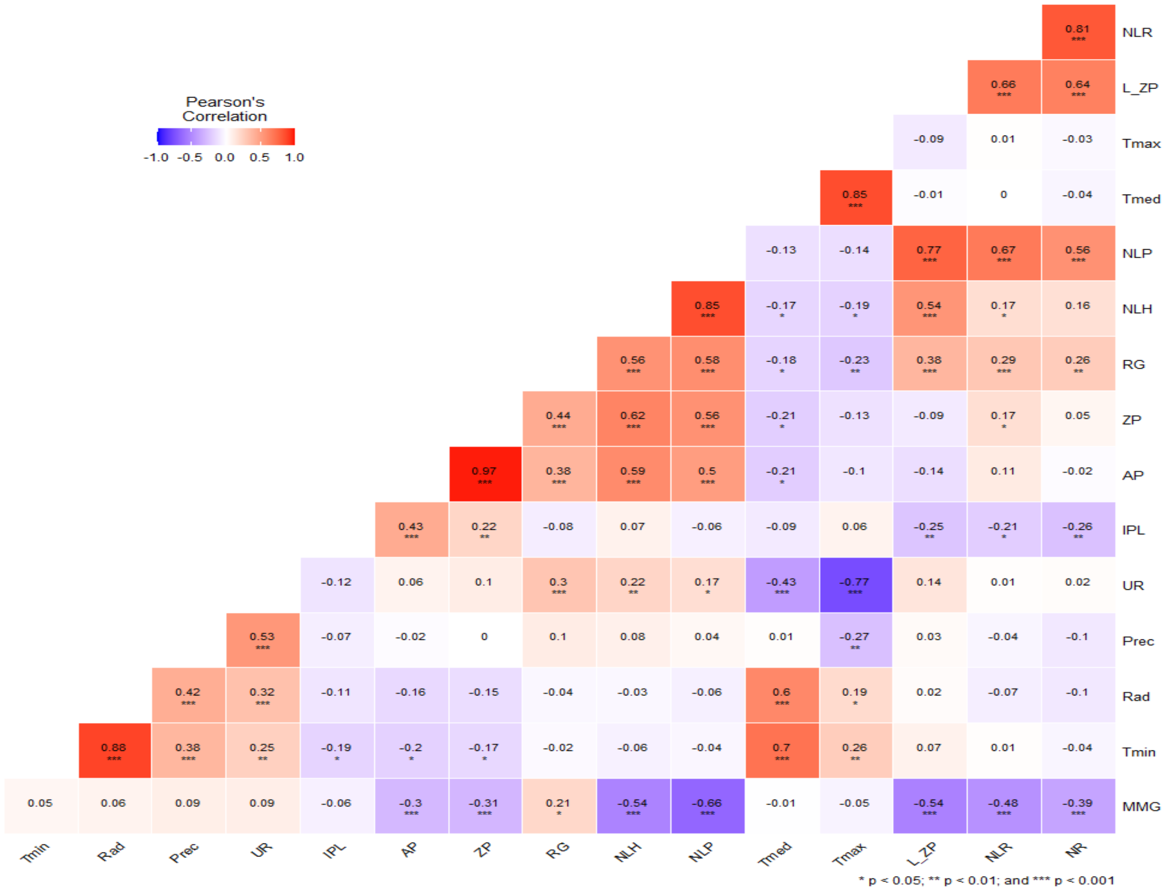

Figure 7. Pearson correlation for different soybean agronomic variables in the zone of production (L_ZP); number of legumes per plant (NLP); number of legumes on stems (NLS); grain yield (GY); zone of production (ZP); plant height (PH); insertion of the first legume (IFL); thousand grain weight (TGW); number of branches (NB); number of legumes in the branches (NLB); and the meteorological variables maximum temperature (Tmax); medium temperature(Tmed); minimum temperature (Tmin); relative humidity (RH); precipitation(Prec); radiation(Rad).

CONCLUSION

According to the BLUP analysis, the HO Iguaçu genotype was closer to the ideotype for culture, with a high number of legumes, number of grains, and high grain yield.

The genotypes DM 5958, BMX ZEUS, NS 6601, BMX FIBRA, and P 95R51 were selected by the MGIDI index by potentiating the variables number of legumes per plant, number of grains per plant, thousand-grain weight, and grain yield. The selection of genotypes with higher grain yield can be performed indirectly through the number of legumes per plant and legumes on the main stem.

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